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(54) Title: BASAL CELL MARKERS IN BREAST CANCER AND USES THEREOF

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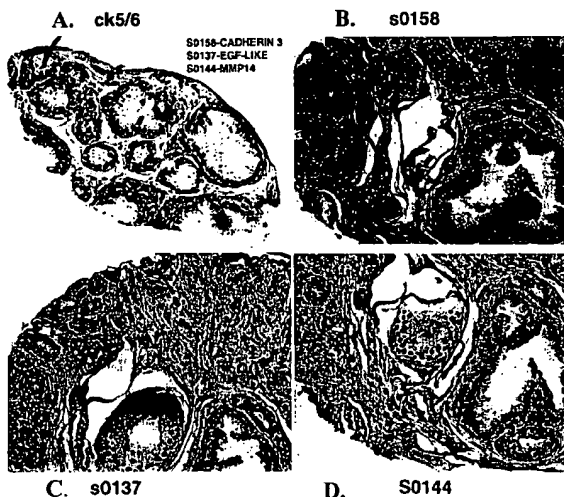
(57) **Abstract:** The invention provides a variety of reagents for use in the diagnosis and management of breast cancer. The invention utilizes cDNA microarray technology to identify genes whose expression profile across a large group of tumor samples correlates with that of cytokeratin 5 and cytokeratin 17, markers for basal cells of the normal mammary lactation gland. The invention demonstrates that tumors that express cytokeratin 5/6 and/or 17 have a poor prognosis relative to tumors overall. The invention provides basal marker genes and their expression products and uses of these genes for diagnosis of breast cancer and for identification of therapies for breast cancer. In particular, the invention provides basal marker genes including cadherin3, matrix metalloproteinase 14, and cadherin EGF LAG seven-pass G-type receptor 2. The invention provides antibodies to the polypeptides expressed by these genes and methods of use thereof.

SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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BASAL CELL MARKERS IN BREAST CANCER AND USES THEREOF

GOVERNMENT SUPPORT

The U.S. Government has a paid-up license in this invention and the right in
5   limited circumstances to require the patent owner to license others on reasonable
terms as provided for by the terms of Grant No. NIH CA 77097 awarded by the
National Cancer Institute.

CROSS-REFERENCE TO RELATED APPLICATIONS

10   . This application claims priority to provisional application U.S.S.N
60/220,967, filed July 26, 2000, which is incorporated herein by reference.

BACKGROUND OF THE INVENTION

A major challenge of cancer treatment is to target specific therapies to distinct
15   tumor types in order to maximize efficacy and minimize toxicity. A related challenge
lies in the attempt to provide accurate diagnostic, prognostic, and predictive
information. At present, tumors are described with the tumor-node-metastasis (TNM)
system. This system, which uses the size of the tumor, the presence or absence of
tumor in regional lymph nodes, and the presence or absence of distant metastases, to
20   assign a stage to the tumor is described in the American Joint Committee on Cancer:
AJCC Cancer Staging Manual. Philadelphia, Pa: Lippincott-Raven Publishers, 5th ed.,
1997, pp 171-180, and in Harris, JR: "Staging of breast carcinoma" in Harris, J.R.,
Hellman, S., Henderson, I.C., Kinne D.W. (eds.): *Breast Diseases*. Philadelphia,
Lippincott, 1991. The assigned stage is used as a basis for selection of appropriate
25   therapy and for prognostic purposes. In addition to the TNM parameters,
morphologic appearance is used to further classify tumors and thereby aid in selection
of appropriate therapy. However, this approach has serious limitations. Tumors with
similar histopathologic appearance can exhibit significant variability in terms of
clinical course and response to therapy. For example, some tumors are rapidly
30   progressive while others are not. Some tumors respond readily to hormonal therapy
or chemotherapy while others are resistant.

Assays for cell surface markers, e.g., using immunohistochemistry, have provided means for dividing certain tumor types into subclasses. For example, one factor considered in prognosis and in treatment decisions for breast cancer is the presence or absence of the estrogen receptor (ER) in tumor samples. ER-positive

5　breast cancers typically respond much more readily to hormonal therapies such as tamoxifen, which acts as an anti-estrogen in breast tissue, than ER-negative tumors. Though useful, these analyses only in part predict the clinical behavior of breast tumors. There is phenotypic diversity present in breast cancers that current diagnostic tools fail to detect. Therefore, there exists a need for improved methods for

10　classifying tumors.

Mutation or dysregulation of any of a large number of genes contributes to the development and progression of cancer as discussed in Hanahan, D. and Weinberg, R., The Hallmarks of Cancer, *Cell*, 100, 57-70, 2000. Genes that play a role in cancer can be divided into a number of broad classes including oncogenes, tumor suppressor

15　genes, and genes that regulate apoptosis. Oncogenes such as *ras* typically encode proteins whose activities promote cell growth and/or division, a function that is necessary for normal physiological processes such as development, tissue regeneration, and wound healing. However, inappropriate activity or expression of oncogenes can lead to the uncontrolled cell proliferation that is a feature of cancer.

20　Tumor suppressor genes such as *Rb* act as negative regulators of cell proliferation. Loss of their activity, e.g., due to mutations or decreased expression at the level of mRNA or protein, can lead to unrestrained cell division. A number of familial cancer syndromes and inherited susceptibility to cancer are believed to be caused by mutations in tumor suppressor genes. Apoptosis, or programmed cell death, plays

25　important roles both in normal development and in surveillance to eliminate cells whose survival may be deleterious to the organism, e.g., cells that have acquired DNA damage. Many chemotherapeutic agents are believed to work by activating the endogenous apoptosis pathway in tumor cells.

Although a substantial number of genes have been implicated as playing

30　important roles in cancer, the factors responsible for the phenotypic diversity of tumors remain largely unknown. In particular, understanding of the underlying differences in gene expression that may contribute to tumor phenotype is limited.

Understanding the differences in gene expression between normal and cancerous tissue and between different tumors of the same tissue type is of significant diagnostic, prognostic, and therapeutic utility. There is therefore a need for the identification of genes exhibiting differential expression between tumors. In

5   particular, there is a need for the identification of additional genes and proteins that can be used to classify tumors, especially genes and proteins that can provide diagnostic, prognostic, and/or predictive information in cancer. There is also a need for antibodies and other reagents for the detection and measurement of such genes and proteins.

10   Most of the commonly used chemotherapeutic agents act relatively nonselectively. Rather than specifically killing tumor cells, these agents target any dividing cell, resulting in a variety of adverse effects. In addition, current therapeutic strategies are of limited efficacy, and the mortality rate of breast cancer remains high. There is therefore a need for the identification of additional genes and proteins that

15   can be used as targets for the treatment of cancer. There is also a need for antibodies and other reagents that can modulate, regulate, or interact with these genes and proteins to provide new method of treatment for cancer.

SUMMARY OF THE INVENTION

20   The present invention relates to the identification of markers that are useful in classifying tumors, particularly breast tumors. The markers identify a class of tumors whose cells have characteristics of basal cells of normal breast lactation ducts. The markers were identified based on their expression profiles in human breast tumor samples, normal breast tissue, and cell lines as assessed using cDNA microarrays. In

25   particular, the basal cell markers of the present invention were identified based on the similarity of their mRNA expression patterns to the expression patterns of markers previously known to identify breast duct basal cells, e.g., cytokeratin 5 and cytokeratin 17, across a set of breast tumor samples. The basal markers include the three genes known as cadherin 3 or P-cadherin (SEQ ID NO:1; GenBank protein

30   accession number NP_001399; GenBank cDNA accession number NM_001408), matrix metalloproteinase 14 (SEQ ID NO:2; GenBank protein accession number NP_004986; GenBank cDNA accession number NM_004995); and cadherin EGF

LAG seven-pass G-type receptor 2 or EGF-Like Domain, Multiple 2 (SEQ ID NO:3; GenBank protein accession number NP_001784; GenBank cDNA accession number NM_001793). The invention further provides antibodies that specifically bind to the polypeptides encoded by the basal marker genes identified herein. The antibodies

5   recognize basal cells of normal mammary lactation glands.

The invention provides various diagnostic methods based on the reagents mentioned above. The diagnostic methods include methods for classifying a tumor. In particular, the invention allows classification of a breast tumor as belonging to a basal class of breast tumors. According to certain of the inventive methods the

10   presence or amount of a gene product, e.g., a polypeptide or a nucleic acid, encoded by a basal marker gene is detected in a sample derived from a subject (e.g., a sample of tissue or cells obtained from a tumor or a blood sample obtained from a subject). In general the subject is a human, however the subject may also be an animal of any other kind. The subject may be an individual who has or may have a tumor. The

15   sample may be subjected to various processing steps prior to or in the course of detection. In certain embodiments of the invention the gene product is a polypeptide that is detected using an antibody capable of binding to the polypeptide. In certain embodiments of the invention the antibody is used to perform immunohistochemical staining on a sample obtained from a subject. In certain embodiments of the invention

20   basal marker gene mRNA expression is measured using a microarray. In other embodiments of the invention basal marker gene mRNA expression is measured by . quantitative PCR using a set of primers designed to amplify a portion of the gene. Additional detection means that may be employed in the present invention are described in U.S. Patent No: 6,057,105. In any of the methods for tumor

25   classification and diagnosis, it may be advantageous to detect and/or measure expression of a set of basal markers rather than expression of a single marker.

By providing reagents that may reliably be used to classify tumors as belonging to a basal subclass, the invention enables a variety of methods for improving therapeutic options for patients with breast cancer. Much effort has and

30   continues to be expended on the discovery of new chemotherapeutic agents. These agents are tested for efficacy in clinical trials. In many such trials it is noticed that a small number of patients stabilize or improve while receiving the treatment, while

most patients do not appear to benefit. Most such agents are not further developed for a number of reasons. For example, the clinical trial results may not be adequate to gain approval by the Food and Drug Administration. In addition, a pharmaceutical company may determine that the potential market for the drug is too small to justify

5   further efforts. However, if it were possible to identify those patients likely to respond to the treatment, then it would be possible to design clinical trials that would show efficacy, and it would be possible to appropriately select patients who would benefit from the treatment. In addition, the availability of markers that can be used to classify breast tumors enables the retrospective examination of the thousands of breast

10   tumor samples archived in hospitals and pathology labs. These samples can be classified using the inventive reagents and classification scheme, and the results can be correlated with the clinical outcome, based on medical records. Thus it is possible to determine whether tumors that fall into a particular tumor class, e.g., a basal tumor class, are responsive to a particular treatment. This will enable the re-evaluation of

15   drugs that failed in clinical trials and may identify a subset of tumors that are likely to respond to a particular drug, and thus a subset of patients that are likely to benefit from treatment with that drug.

     The inventors have recognized that in order to achieve these goals it is necessary to develop new and improved methods for classifying breast tumors. The

20   inventive methods provide a molecular basis for classifying tumors, based on their underlying biology. While not wishing to be bound by any theory, the inventors postulate that tumors arising from a particular cell type within the breast are likely to display common features. Such features may include the prognosis (e.g., predicted survival time or likelihood that a patient's life expectancy exceeds a given length of

25   time) or likelihood that a tumor will respond to a particular therapy.

     In particular, tumors that display characteristics of basal cells of the normal breast lactation duct (also referred to herein as breast basal cells) form a distinct subclass (referred to herein as the basal subclass). Inventors have confirmed that patients with breast tumors whose cells display characteristics of breast basal cells,

30   e.g., expression of cytokeratin 5 and/or cytokeratin 17, have a poor clinical outcome relative to patients with breast tumors that do not express these markers. However, antibodies to these cytokeratins have been found (by the inventors and by other

investigators) to give spotty, focal staining patterns when used to perform immunohistochemistry on breast tumor samples. Thus the utility of cytokeratins 5 and 17 as markers and the utility of antibodies that bind to cytokeratin 5 or 17 for determining whether a tumor is a member of the basal subclass has been limited. The

5   inventors have therefore identified genes whose mRNA expression profiles across a large set of tumor samples correlate with, i.e. are similar to, the expression profiles of the known basal cell markers cytokeratins 5 and 17. These genes include the basal markers of the present invention mentioned above. As described in Examples 10 and 13, the inventors have generated antibodies to the proteins expressed by these genes

10   and shown that the antibodies stain basal cells of normal mammary lactation glands. Thus detection of one or more expression products of these genes may be used to identify tumors that fall within the basal tumor subclass.

The invention further provides therapeutic agents based on the identification of breast basal cell markers. The therapeutic agents include compounds that modulate

15   these genes or that modulate polypeptides encoded by these genes. In particular, the therapeutic agents include antibodies that bind to polypeptides encoded by the basal cell marker genes. The invention further includes agonists and antagonists to the basal marker genes, to the polynucleotides transcribed from those genes, and to their encoded polypeptides. The invention also provides methods for identifying such

20   agonists and antagonists. The invention further includes pharmaceutical compositions comprising such antibodies, agonists, and antagonists as well as methods of use of the pharmaceutical compositions in the treatment of cancer, particularly breast cancer.

According to one aspect, the invention provides a method of classifying a tumor comprising the steps of (i) providing a tumor sample, (ii) detecting expression

25   or activity of a gene encoding the polypeptide of SEQ ID NO:1 in the sample; and (iii) classifying the tumor as belonging to a tumor subclass based on the results of the detecting step. The invention also provides a method of classifying a tumor comprising the steps of (i) providing a tumor sample, (ii) detecting expression or activity of a gene encoding the polypeptide of SEQ ID NO:2 in the sample, and (iii)

30   classifying the tumor as belonging to a tumor subclass based on the results of the detecting step. In addition, the invention provides a method of classifying a tumor comprising the steps of (i) providing a tumor sample, (ii) detecting expression or

activity of a gene encoding the polypeptide of SEQ ID NO:3 in the sample, and (iii)

classifying the tumor as belonging to a tumor subclass based on the results of the

detecting step. The invention further includes a method of classifying a tumor

comprising the steps of (i) providing a tumor sample, (ii) detecting expression or

5   activity of at least two genes selected from the group consisting of: a gene encoding

the polypeptide of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3 in the sample,

and (iii) classifying the tumor as belonging to a tumor subclass based on the results of

the detecting step. In any of the foregoing methods the detecting step may comprise

detecting the polypeptide or polypeptides encoded by the genes. A variety of

10   detection techniques may be employed including, but not limited to,

immunohistochemical analysis, ELISA assay, antibody arrays, or detecting

modification of a substrate by the polypeptide.

In certain embodiments of the methods the tumor is a breast tumor and the

tumor subclass is a basal tumor subclass. The methods may further comprise

15   providing diagnostic, prognostic, or predictive information based on the classifying

step. Classifying may include stratifying the tumor (and thus stratifying a subject

having the tumor), e.g., for a clinical trial. The methods may further comprise

selecting a treatment based on the classifying step.

In another aspect, the invention provides a method of testing a subject

20   comprising the steps of (i) providing a sample isolated from a subject, (ii) detecting

expression or activity of a gene encoding the polypeptide of SEQ ID NO:1 in the

sample, and (iii) providing diagnostic, prognostic, or predictive information based on

the detecting step. The invention further provides a method of testing a subject

comprising the steps of (i) providing a sample isolated from a subject, (ii) detecting

25   expression or activity of a gene encoding the polypeptide of SEQ ID NO:2 in the

sample (iii) and providing diagnostic, prognostic, or predictive information based on

the detecting step. The invention further provides a method of testing a subject

comprising the steps of (i) providing a sample isolated from a subject, (ii) detecting

expression or activity of a gene encoding the polypeptide of SEQ ID NO:3 in the

30   sample (iii) and providing diagnostic, prognostic, or predictive information based on

the detecting step. The invention further includes a method of testing a subject

comprising the steps of (i) providing a sample isolated from the subject, (ii) detecting

expression or activity of at least two genes selected from the group consisting of: a gene encoding the polypeptide of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3 in the sample, and (iii) providing diagnostic, prognostic, or predictive information based on the detecting step. In any of these methods the detecting step may comprise

5   detecting the polypeptide or polypeptides. Detection may be performed using any appropriate technique including, but not limited to, immunohistochemistry, ELISA assay, protein array, or detecting modification of a substrate by the polypeptide.

The sample may comprise mRNA, in which case the detecting step may comprise hybridizing the mRNA or cDNA or RNA synthesized from the mRNA to a

10   microarray or detecting mRNA transcribed from the gene or detecting cDNA or RNA synthesized from mRNA transcribed from the gene. In any of the above methods, the sample may be a blood sample, a urine sample, a serum sample, an ascites sample, a saliva sample, a cell, and a portion of tissue.

In another aspect, the invention provides a kit for diagnosis of a tumor which

15   may include (i) primers for amplifying an mRNA transcribed from a gene that encodes the polypeptide of any of SEQ ID NO:1, SEQ ID NO:2; and SEQ ID NO:3 (ii) instructions for use of the kit; and/or (iii) control samples for testing the primers, wherein the control samples comprise nucleic acids that hybridize to the primers.

In another aspect, the invention provides an antibody that specifically binds to

20   an epitope found in a polypeptide whose amino acid sequence comprises the amino acid sequence of SEQ ID NO:1, and wherein the antibody recognizes basal cells in normal mammary lactation glands. According to certain embodiments of the invention the antibody distinguishes basal cells from luminal cells in normal mammary lactation gland. According to certain embodiments of the invention the

25   antibody recognizes an epitope found in a peptide having an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.

In another aspect, the invention provides an antibody that specifically binds to an epitope found in a polypeptide whose amino acid sequence comprises the amino

30   acid sequence of SEQ ID NO:2, and wherein the antibody recognizes basal cells in normal mammary lactation glands. According to certain embodiments of the invention the antibody distinguishes basal cells from luminal cells in normal

mammary lactation gland. According to certain embodiments of the invention the antibody recognizes an epitope found in a peptide having an amino acid sequence · selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8, and SEQ ID NO:9.

5   In another aspect, the invention provides an antibody that specifically binds to an epitope found in a polypeptide whose amino acid sequence the amino acid sequence of SEQ ID NO:3, and wherein the antibody recognizes basal cells in normal mammary lactation glands. According to certain embodiments of the invention the antibody distinguishes basal cells from luminal cells in normal mammary lactation

10   gland. According to certain embodiments of the invention the antibody recognizes an epitope found in a peptide having an amino acid sequence selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12.

       The invention further provides a kit for tumor diagnosis comprising one or more of the foregoing antibodies. The kit may further include instructions for use of

15   the kit and/or a control slide comprising breast tissue samples for testing reagents in the kit or such samples themselves.

       According to another aspect, the invention provides a method of testing a compound or a combination of compounds for activity against tumors comprising steps of (i) obtaining or providing tumor samples taken from subjects who have been

20   treated with the compound or combination of compounds, wherein the tumors fall within a tumor subclass, (ii) comparing the response rate of tumors that fall within the tumor subclass and have been treated with the compound with the overall response rate of tumors that have been treated with the compound or combination of compounds or with the response rate of tumors that do not fall within the subclass and

25   have been treated with the compound or combination of compounds and (iii) identifying the compound or combination of compounds as having selective activity against tumors in the tumor subclass if the response rate of tumors in the subclass is greater than the overall response rate or the response rate of tumors that do not fall within the subclass. In certain embodiments of the invention the tumors are breast

30   tumors. In certain embodiments of the invention the tumor subclass is a basal tumor subclass. The tumors may be classified according to any of the inventive classification methods described above. In certain embodiments of the invention the

classification is based on expression of the polypeptide of SEQ ID NO:1, 2, 3, or a combination of these.

The invention further provides a method of testing a compound or a combination of compounds for activity against tumors comprising steps of (i) treating

5   subjects in need of treatment for tumors with the compound or combination of compounds, (ii) comparing the response rate of tumors that fall within a tumor subclass with the overall response rate of tumors or with the response rate of tumors that do not fall within the subclass, and (iii) identifying the compound or combination of compounds as having selective activity against tumors in the tumor subclass if the

10   response rate of tumors in the subclass is greater than the overall response rate or the response rate of tumors that do not fall within the subclass. The method may further comprise various additional steps. For example, the method may comprise steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) determining whether the tumors fall within a tumor subclass, and (iii) stratifying the

15   subjects based on the results of the determining step prior to performing the treating step. The method may further comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding the polypeptide of SEQ ID NO:1 in the samples, and (iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step.

20   The method may further comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding the polypeptide of SEQ ID NO:2 in the samples, and (iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step. The method may further comprise the steps of (i) providing tumor samples from

25   subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding the polypeptide of SEQ ID NO:3 in the samples, and (iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step. The method may further comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene

30   encoding a polypeptide whose sequence comprises a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3 in the samples, and

(iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step.

In addition, the invention includes a method of testing a compound or a combination of compounds for activity against tumors comprising steps of (i) treating
5   subjects in need of treatment for tumors with the compound or combination of compounds or with an alternate compound, wherein the tumors fall within a tumor subclass, (ii) comparing the response rate of tumors treated with the compound or combination of compounds with the response rate of tumors treated with the alternate compound; and (iii) identifying the compound or combination of compounds as
10 having superior activity against tumors in the tumor subclass, as compared with the alternate compound, if the response rate of tumors treated with the compound or combination of compounds is greater than the response rate of tumors treated with the alternate compound. The method may further comprise various additional steps. For example, the method may comprise steps of (i) providing tumor samples from
15 subjects in need of treatment for tumors, (ii) determining whether the tumors fall within a tumor subclass, and (iii) stratifying the subjects based on the results of the determining step prior to performing the treating step. The method may further comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding the polypeptide of
20 SEQ ID NO:1 in the samples, and (iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step. The method may further comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding the polypeptide of SEQ ID NO:2 in the samples, and (iii) stratifying the subjects based on the results of
25 the detecting step prior to performing the treating step. The method may further comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding the polypeptide of SEQ ID NO:3 in the samples, and (iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step. The method may further
30 comprise the steps of (i) providing tumor samples from subjects in need of treatment for tumors, (ii) detecting expression or activity of a gene encoding a polypeptide whose sequence comprises a sequence selected from the group consisting of SEQ ID

NO:1, SEQ ID NO:2, and SEQ ID NO:3 in the samples, and (iii) stratifying the subjects based on the results of the detecting step prior to performing the treating step.

In certain embodiments of the invention the alternate compound is a compound approved by the U.S. Food and Drug administration for treatment of

5   tumors. The invention also provides a method of treating a subject comprising steps of (i) identifying a subject as having a tumor in a basal tumor subclass, and (ii) administering to the subject a compound identified according to any of the inventive methods for identifying a subject.

#In another aspect, the invention provides a method of treating a subject

10.   comprising steps of (i) providing a subject in need of treatment for cancer, (ii) administering to the subject an antibody that specifically binds to a polypeptide having an amino acid sequence comprising the sequence of SEQ ID NO:1, SEQ ID NO:2, or SEQ ID NO:3 or administering a combination of such antibodies. In certain embodiments of the invention the tumor is a breast tumor. In certain embodiments of

15   the invention the antibody is conjugated with a toxic molecule.

The invention further provides a method of treating a subject comprising steps of (i) providing a subject in need of treatment for cancer, (ii) administering to the subject a compound that activates or inhibits a gene that encodes an amino acid having a sequence comprising the sequence of SEQ ID NO:1, SEQ ID NO:2, or SEQ

20   ID NO:3, or that activates or inhibits an expression product of the gene.

In another aspect, the invention provides a composition comprising two or more compounds identified according to any of the methods described above for identifying compounds. The invention also provides a pharmaceutical composition comprising such a composition and a pharmaceutically acceptable carrier. The

25   invention also provides a composition comprising (i) a compound identified according to any of the methods described above for identifying compounds and (ii) a second compound, wherein the second compound is approved by the U.S. Food and Drug administration for the treatment of cancer or has shown potential efficacy against cancer in pre-clinical studies. The invention also provides a pharmaceutical

30   composition comprising such a composition and a pharmaceutically acceptable carrier.

The present application refers to various patents, publications, books, articles, and other references. The contents of all of these items are hereby incorporated by reference in their entirety. The present application also incorporates by reference six U.S. patent applications filed by inventors on July 26, 2001. These applications are

5   entitled "REAGENTS AND METHODS FOR USE IN MANAGING BREAST CANCER", "BSTP-RAS/RERG PROTEIN AND RELATED REAGENTS AND METHODS OF USE THEREOF", "BSTP-ECG1 PROTEIN AND RELATED REAGENTS AND METHODS OF USE THEREOF", "BSTP-CAD PROTEIN AND RELATED REAGENTS AND METHODS OF USE THEREOF", "BSTP-TRANS

10   PROTEIN AND RELATED REAGENTS AND METHODS OF USE THEREOF", "BSTP-5 PROTEINS AND RELATED REAGENTS AND METHODS OF USE THEREOF".

BRIEF DESCRIPTION OF THE DRAWING

15   Figure 1A presents the amino acid sequence of the polypeptide encoded by the basal marker gene known as cadherin 3 or P-cadherin (SEQ ID NO:1).

Figure 1B presents the amino acid sequence of the polypeptide encoded by the basal marker gene known as matrix metalloproteinase 14 (SEQ ID NO:2).

Figure 1C presents the amino acid sequence of the polypeptide encoded by the basal

20   marker gene known as cadherin EGF LAG seven-pass G-type receptor 2 or EGF-Like Domain, Multiple 2 (SEQ ID NO:3).

Figure 1D presents the amino acid sequences of peptides used to raise antibodies that recognize the cadherin 3, matrix metalloproteinase 14, cadherin EGF LAG seven-pass G-type receptor 2, and cytokeratin 17 proteins.

25   Figure 2 shows a comparison of dendrograms representing the results of hierarchical clustering of experimental samples using the intrinsic gene set and the epithelial-enriched gene set.

Figure 3 shows breast tissue immunohistochemistry results obtained using various antibodies.

30   Figure 3A shows tumor Stanford 2-P stained for immunoglobulin light chain.

Figure 3B shows tumor Stanford 16 stained for the T-lymphocyte cell surface antigen CD3.

Figure 3C shows normal mammary duct stained for the basal epithelial cell keratins 5/6.

Figure 3D shows normal mammary duct stained for the luminal cell keratins 8/18.

Figure 3E shows tumor New York 3 stained for keratin 5/6.

5   Figure 3F shows tumor Stanford 16 stained for keratins 8/18.

Figure 4A shows a Western blot demonstrating expression of the cadherin3 polypeptide in various cell lines.

Figure 4B shows a Western blot demonstrating expression of the matrix metalloproteinase 14 polypeptide in various cell lines.

10   Figure 4C shows a Western blot demonstrating expression of the cadherin EGF LAG seven-pass G-type receptor 2 polypeptide in various cell lines.

Figure 5A shows a Kaplan-Meier survival curve demonstrating poor outcome in cytokeratin 17 and/or cytokeratin 5/6 positive tumors (p = 0.012).

Figure 5B shows a Kaplan-Meier survival curve demonstrating poor outcome in

15   cytokeratin 17 and/or cytokeratin 5/6 positive tumors in lymph node negative patients (p = 0.006).

Figure 6 shows antibody staining of normal breast tissue cores in a breast tissue array.

Figure 6A shows staining with anti-cytokeratin 5/6 monoclonal antibody.

Figure 6B shows staining with anti-cadherin 3 polyclonal antibody.

20   Figure 6C shows staining with anti-EGF LAG seven-pass G-type receptor 2 polyclonal antibody.

Figure 6D shows staining with anti-metallproteinase 14 polyclonal antibody.

Figure 7 shows antibody staining of breast cancer tissue cores in a breast cancer tissue array.

25   Figure 7A shows antibody staining with anti-cytokeratin 5/6 monoclonal antibody.

Figure 7B shows antibody staining with anti-EGF LAG seven-pass G-type receptor 2 polyclonal antibody.

Figure 7C shows antibody staining with anti-cadherin 3 polyclonal antibody.

30   BRIEF DESCRIPTION OF THE TABLES

The tables contain the numerical data corresponding to microarray images. Some

tables list the individual genes in the various gene subsets or provide additional information.

5   Table 1 is a master data table for the 65 microarray experiments performed on individual tumor samples, in which rows represent I.M.A.G.E. clones that identify approximately 1753 genes whose expression varied by at least a factor of 4 and columns represent individual microarray experiments. The first 50 pages of the table consist of a reference list in which a descriptive name for each clone (where such a name exists) appears in the column entitled Name, followed by the Genbank

10   accession number for the clone. Each row in the reference list contains a number in the first column that numerically identifies the column. In the subsequent data portion of the table (pages 1 – 392), each row is similarly identified by a number in the first column so that the name and Genbank accession number for the clone for which data appears in that row may be determined by consulting the reference list. In the data

15   portion of the table, the column headings in the first row identify the tumor samples. Each data cell in the table represents the measured Cy5/Cy3 fluorescence ratio at the corresponding target element on the appropriate array. Empty cells indicate insufficient or missing data. All ratio values are log transformed (base 2) to treat inductions or repressions of identical magnitude as numerically equal but with

20   opposite sign.

       Table 2 is a master data table for the 19 microarray experiments performed on cell line samples, in which rows represent I.M.A.G.E. clones that identify approximately 1753 genes whose expression varied by at least a factor of 4 and columns represent

25   individual microarray experiments. This table contains only a data portion, in which the column headings in the first row identify the cell lines. Each row in the table is identified by a number which appears in the first column. The same reference list that forms part of Table 1 may be consulted to determine the name and Genbank accession number for the clone for which data appears in that row. Each data cell in the table

30   represents the measured Cy5/Cy3 fluorescence ratio at the corresponding target element on the appropriate array. Empty cells indicate insufficient or missing data. All ratio values are log transformed (base 2) to treat inductions or repressions of

identical magnitude as numerically equal but with opposite sign.

Table 3 presents a listing and description of the 11 cell lines used to create the common reference sample.

5

Table 4 presents a complete listing of the 84 experimental samples that were assayed versus the common reference sample. The table includes a list of alternate names (in the column entitled Sample ID/old name) for the same tumors. The alternate names are used to identify the tumor samples in certain contexts, and the table allows

10 conversion between the two sets of names.

Table 5 lists the tumors used in the experiments described herein, along with clinical and pathological information about each tumor/patient.

15 Table 6 is a master data table for the 84 microarray experiments performed on individual tumor, tissue, and cell line samples, in which rows represent I.M.A.G.E. clones that identify the 496 genes in the intrinsic gene set, and columns represent individual microarray experiments. The first 15 pages of the table consist of a reference list in which a descriptive name for each clone (where such a name exists)

20 appears in the column entitled Name, followed by the Genbank accession number for the clone. Each row in the reference list contains a number in the first column that numerically identifies the column. In the subsequent data portion of the table (pages 1 – 91), each row is similarly identified by a number in the first column so that the name and Genbank accession number for the clone for which data appears in that row

25 may be determined by consulting the reference list. In the data portion of the table, the column headings in the first row identify the tumor samples. Each data cell in the table represents the measured Cy5/Cy3 fluorescence ratio at the corresponding target element on the appropriate array. Empty cells indicate insufficient or missing data. All ratio values are log transformed (base 2) to treat inductions or repressions of

30 identical magnitude as numerically equal but with opposite sign.

Table 7 is a listing of the 374 clones that identify genes selected for the epithelial

enriched gene set including Genbank accession numbers.

Table 8 is a listing of the clones that identify genes that comprise the luminal subset including Genbank accession numbers.

5

Tables 9-1 and 9-2 are listings of the two groups of clones that identify genes that comprise the basal subset including Genbank accession numbers.

Table 10 is a listing of the clones that identify genes that comprise the *ErbB2* subset

10   including Genbank accession numbers.

Table 11 is a listing of the clones that identify genes that comprise the endothelial gene subset including Genbank accession numbers.

15   Table 12 is a listing of the clones that identify genes that comprise the stromal/fibroblast gene subset including Genbank accession numbers.

Table 13 is a listing of the clones that identify genes that comprise the B-cell gene subset including Genbank accession numbers.

20

Table 14 is a listing of the clones that identify genes that comprise the adipose-enriched/normal breast gene subset including Genbank accession numbers.

Table 15 is a listing of the clones that identify genes that comprise the macrophage

25   gene subset including Genbank accession numbers.

Table 16 is a listing of the clones that identify genes that comprise the T-cell gene subset including Genbank accession numbers.

30   In Table 1, the Genbank accession number for each clone appears in the column entitled "Name", following a brief descriptive name for the gene identified by the clone, where available. In some cases the descriptive name is a number corresponding

to an I.M.A.G.E. clone ID number. As is well known and accepted in the art, the Genbank accession number represents a means of definitively identifying a particular clone, since Genbank accession numbers will be maintained permanently or, if changed, the change will be accomplished in such a manner as to allow unambiguous

5   correlation between any new numbering system and the numbering system currently in use.

Note that Tables 1, 2, and 6 are provided for purposes of presenting the clone identifications and the data that was used to perform hierarchical clustering analysis, and that the format of the tables may not correspond exactly with the format required

10   by software developed for the analysis of the data. Appropriate format will, in general, depend upon the particular computer program. See, for example, the Web site http://genome-www.stanford.edu/~sherlock/tutorial.html for discussion of the appropriate format for one particular analysis program.

15   In Tables 7 – 16, each entry identifies a clone. The first portion of each entry is a brief descriptive name for the gene identified by the clone. The Genbank accession number for the clone appears on the last line of the entry for that clone.

DETAILED DESCRIPTION OF CERTAIN EMBODIMENTS
20   ## DEFINITIONS

To facilitate understanding of the invention, the following definitions are provided. It is to be understood that, in general, terms not otherwise defined are to be given their meaning or meanings as generally accepted in the art.

25

Agonist: As used herein, the term "agonist" refers to a molecule that increases or prolongs the duration of the effect of a polypeptide or a nucleic acid. Agonists may include proteins, nucleic acids, carbohydrates, lipids, small molecules, ions, or any other molecules that modulate the effect of the polypeptide or nucleic acid. An

30   agonist may be a direct agonist, in which case it is a molecule that exerts its effect by binding to the polypeptide or nucleic acid, or an indirect agonist, in which case it exerts its effect via a mechanism other than binding to the polypeptide or nucleic acid

(e.g., by altering expression or stability of the polypeptide or nucleic acid, by altering the expression or activity of a target of the polypeptide or nucleic acid, by interacting with an intermediate in a pathway involving the polypeptide or nucleic acid, etc.)

5   Antagonist: As used herein, the term "antagonist" refers to a molecule that decreases or reduces the duration of the effect of a polypeptide or a nucleic acid. Antagonists may include proteins, nucleic acids, carbohydrates, or any other molecules that modulate the effect of the polypeptide or nucleic acid. An antagonist may be a direct antagonist, in which case it is a molecule that exerts its effect by binding to the

10   polypeptide or nucleic acid, or an indirect antagonist, in which case it exerts its effect via a mechanism other than binding to the polypeptide or nucleic acid (e.g., by altering expression or stability of the polypeptide or nucleic acid, by altering the expression or activity of a target of the polypeptide or nucleic acid, by interacting with an intermediate in a pathway involving the polypeptide or nucleic acid, etc.)

15

Basal cell: The term "basal cell" is a general term applied to any stratified or pseudostratified epithelium. It refers to cells which are juxtaposed to the basement membrane and under one or more additional epithelial layers. Mammary tissue can have both a two cell layer epithelium (basal and luminal cells) or in the duct system, a

20   single layered epithelium. In the two cell layer, the cells adjacent to the basement membrane are termed "basal cells" and express basal cell markers (e.g., cytokeratin 17 and cytokeratin 5/6). In pseudostratified epitheum "non-basal" cells can also contact the basement membrane but since normal breast epithelium is not, in general, pseudostratified, breast basal cells are cells located adjacent to basement membrane

25   and under one or more additional layers of epithelial cells. As used herein, the term "basal cell" is distinct from "myoepithelial cell" in that myoepithelial cell refers to cells that have the contractual apparatus for milk excretion by the ducts (i.e., they express contractile proteins).

30

Breast basal cell marker: A gene whose expression is characteristic of basal cells of normal breast lactation ducts, or an expression product of such a gene (e.g., an mRNA

or polypeptide). The marker may be used to distinguish basal cells from other cells in the breast, e.g., luminal cells. In the case of a marker that is a polypeptide, antibodies to the polypeptide stain cells in the basal layer of normal breast lactation ducts when used to perform immunohistochemistry on breast tissue samples. Since the present

5 invention is concerned primarily with breast cancer, the term "basal cell marker" is used interchangeably with "breast basal cell marker" herein unless otherwise indicated. Examples of basal cell markers include the cytokeratin 5 and cytokeratin 17 genes, mRNAs, and proteins, in addition to the newly identified basal cell markers described herein.

10

Breast basal tumor marker: A gene whose expression is characteristic of basal cells in the normal breast lactation duct and which is also expressed in a subset of breast tumors, or an expression product of such a gene. These genes include cytokeratin 5 and cytokeratin 17, which are known from the prior art to distinguish breast basal

15 cells from other breast tissue cells, and the genes identified herein. Antibodies to the proteins encoded by these genes identify basal breast cells when used to perform immunohistochemical staining of normal breast tissue, i.e., they stain cells in the basal epithelial layer. The term "basal tumor marker" is used interchangeably with "breast basal tumor marker" herein unless otherwise indicated.

20

Breast basal tumor subclass: The breast basal tumor subclass, as used herein, refers to breast tumors that display characteristics of basal cells of normal breast lactation ducts. Such characteristics include expression of genes whose expression has been shown to discriminate between normal basal cells of breast lactation ducts and other

25 cells in the breast, including luminal cells of breast lactation ducts. These genes include cytokeratin 5 and cytokeratin 17, which are known from the prior art to distinguish breast basal cells from other breast tissue cells, and the genes identified herein. Antibodies to the proteins encoded by these genes identify basal breast cells when used to perform immunohistochemical staining of normal breast tissue, i.e., they

30 stain cells in the basal epithelial layer. The term "breast basal tumor subclass" is used interchangeably with "basal tumor subclass" herein unless otherwise indicated.

Diagnostic information: As used herein, diagnostic information or information for use in diagnosis is any information that is useful in determining whether a patient has a disease or condition and/or in classifying the disease or condition into a phenotypic category or any category having significance with regards to the prognosis of or likely.

5   response to treatment (either treatment in general or any particular treatment) of the disease or condition. Similarly, diagnosis refers to providing any type of diagnostic information, including, but not limited to, whether a subject is likely to have a condition (such as a tumor), information related to the nature or classification of a tumor, information related to prognosis and/or information useful in selecting an

10   appropriate treatment. Selection of treatment may include the choice of a particular chemotherapeutic agent or other treatment modality such as surgery, radiation, etc., a choice about whether to withhold or deliver therapy, etc.

Differential expression: A gene exhibits differential expression at the RNA level if its

15   RNA transcript varies in abundance between different samples in a sample set. A gene exhibits differential expression at the protein level, if a polypeptide encoded by the gene varies in abundance between different samples in a sample set. In the context of a microarray experiment, differential expression generally refers to differential expression at the RNA level.

20

Gene: For the purposes of the present invention, the term "gene" has its meaning as understood in the art. However, it will be appreciated by those of ordinary skill in the art that the term "gene" has a variety of meanings in the art, some of which include gene regulatory sequences (e.g., promoters, enhancers, etc.) and/or intron sequences,

25   and others of which are limited to coding sequences. It will further be appreciated that definitions of "gene" include references to nucleic acids that do not encode proteins but rather encode functional RNA molecules such as tRNAs. For the purpose of clarity we note that, as used in the present application, the term "gene" generally refers to a portion of a nucleic acid that encodes a protein; the term may optionally

30   encompass regulatory sequences. This definition is not intended to exclude application of the term "gene" to non-protein coding expression units but rather to

clarify that, in most cases, the term as used in this document refers to a protein coding nucleic acid.

Gene product or expression product: A gene product or expression product is, in

5   general, an RNA transcribed from the gene or a polypeptide encoded by an RNA transcribed from the gene.

Marker: A marker, as used herein, refers to a gene whose expression is characteristic of a particular cell type. The term may also refer to a product of gene expression, e.g.,

10   an RNA transcribed from the gene or a translation product of such an RNA, the production of which is characteristic of a particular cell type. The cell type may be defined based on any phenotypic criterion. For example, a normal breast basal cell is defined based on its position within an epithelial layer. In some cases expression of a marker gene may be the sole criterion used to define the cell type. The statistical

15   significance of the presence or absence of a marker gene expression product may vary depending upon the particular marker. In some cases the detection of a marker is highly specific in that it reflects a high probability that the cell is of a particular type. This specificity may come at the cost of sensitivity, i.e., a negative result may occur even if the cell is a cell that would be expected to express the marker. Conversely,

20   markers with a high degree of sensitivity may be less specific than those with lower sensitivity. Thus it will be appreciated that a useful marker need not distinguish cells of a particular type with 100% accuracy. Furthemore, it will be appreciated that the use of multiple markers may improve the specificity and/or sensitivity with which a cell can be identified as being of a particular cell type. The concept of a marker may

25   be applied not only to individual cells, but also to tumors or to other disease states. In the case of tumors, a marker for a particular tumor class is a gene whose expression is characteristic of a particular tumor type, i.e., a gene whose expression is characteristic of some or all of the cells in the tumor. The term may also refer to a product of gene expression, e.g., an RNA transcribed from the gene or a translation product of such an

30   RNA, the production of which is characteristic of a particular tumor type, i.e., of some or all of the cells in the tumor.

Prognostic information and predictive information: As used herein the terms prognostic information and predictive information are used interchangeably to refer to any information that may be used to foretell any aspect of the course of a disease or condition either in the absence or presence of treatment. Such information may

5   include, but is not limited to, the average life expectancy of a patient, the likelihood that a patient will survive for a given amount of time (e.g., 6 months, 1 year, 5 years, etc.), the likelihood that a patient will be cured of a disease, the likelihood that a patient's disease will respond to a particular therapy (wherein response may be defined in any of a variety of ways). Prognostic and predictive information are

10   included within the broad category of diagnostic information.

Response: As used herein a response to treatment may refer to any beneficial alteration in a subject's condition that occurs as a result of treatment. Such alteration may include stabilization of the condition (e.g., prevention of deterioration that would

15   have taken place in the absence of the treatment), amelioration of symptoms of the condition, improvement in the prospects for cure of the condition, etc. One may refer to a subject's response or to a tumor's response. In general these concepts are used interchangeably herein. Tumor or subject response may be measured according to a wide variety of criteria, including clinical criteria and objective criteria. Techniques

20   for assessing response include, but are not limited to, clinical examination, chest X-ray, CT scan, MRI, ultrasound, endoscopy, laparoscopy, presence or level of tumor markers in a sample obtained from a subject, cytology, histology. Many of these techniques attempt to determine the size of a tumor or otherwise determine the total tumor burden. Methods and guidelines for assessing response to treatment are

25   discussed in Therasse P., et al., "New guidelines to evaluate the response to treatment in solid tumors", European Organization for Research and Treatment of Cancer, National Cancer Institute of the United States, National Cancer Institute of Canada. J Natl Cancer Inst, Feb 2;92(3):205-16, 2000. The exact response criterion can be selected in any appropriate manner, provided that when comparing groups of tumors

30   and/or patients, the groups to be compared are assessed based on the same or comparable criteria for determining response rate. One of ordinary skill in the art will be able to select appropriate criteria.

Sample: As used herein, a sample obtained from a subject may include, but is not limited to, any or all of the following: a cell or cells, a portion of tissue, blood, serum, ascites, urine, saliva, and other body fluids, secretions, or excretions. The term

5 "sample" also includes any material derived by processing such a sample. Derived samples may include nucleic acids or proteins extracted from the sample or obtained by subjecting the sample to techniques such as amplification or reverse transcription of mRNA, etc.

10 Specific binding: As used herein, the term refers to an interaction between a target polypeptide (or, more generally, a target molecule) and a binding molecule such as an antibody, agonist, or antagonist. The interaction is typically dependent upon the presence of a particular structural feature of the target polypeptide such as an antigenic determinant or epitope recognized by the binding molecule. For example, if

15 an antibody is specific for epitope A, the presence of a polypeptide containing epitope A or the presence of free unlabeled A in a reaction containing both free labeled A and the antibody thereto, will reduce the amount of labeled A that binds to the antibody. It is to be understood that specificity need not be absolute. For example, it is well known in the art that numerous antibodies cross-react with other epitopes in addition

20 to those present in the target molecule. Such cross-reactivity may be acceptable depending upon the application for which the antibody is to be used. One of ordinary skill in the art will be able to select antibodies having a sufficient degree of specificity to perform appropriately in any given application (e.g., for detection of a target molecule, for therapeutic purposes, etc). It is also to be understood that specificity

25 may be evaluated in the context of additional factors such as the affinity of the binding molecule for the target polypeptide versus the affinity of the binding molecule for other targets, e.g., competitors. If a binding molecule exhibits a high affinity for a target molecule that it is desired to detect and low affinity for nontarget molecules, the antibody will likely be an acceptable reagent for immunodiagnostic purposes. Once

30 the specificity of a binding molecule is established in one or more contexts, it may be employed in other, preferably similar, contexts without necessarily re-evaluating its specificity.

Treating a tumor: As used herein, treating a tumor is taken to mean treating a subject who has the tumor.

5   Tumor sample: The term "tumor sample" as used herein is taken broadly to include cell or tissue samples removed from a tumor, cells (or their progeny) derived from a tumor that may be located elsewhere in the body (e.g., cells in the bloodstream or at a site of metastasis), or any material derived by processing such a sample. Derived tumor samples may include nucleic acids or proteins extracted from the sample or
10   obtained by subjecting the sample to techniques such as amplification or reverse transcription of mRNA, etc.

Tumor subclass: A tumor subclass, also referred to herein as a tumor subset or tumor class, is the group of tumors that display one or more phenotypic or genotypic
15   characteristics that distinguish members of the group from other tumors.

I. Overview and Description of the Basal Marker Genes, Polynucleotides, and Polypeptides

        The present invention provides new reagents and methods for the management
20   (e.g., detection, classification, provision of diagnostic and prognostic information, treatment, etc.) of breast cancer. Significant progress has been made in understanding risk factors, including genetic factors, that may contribute to breast cancer (See, for example, Vogelstein, B. and Kinzler, eds., "Breast Cancer", by Couch, F. and Weber, B. in *The Genetic Basis of Human Cancer*, McGraw Hill, 1998), but the relevance of
25   these factors to clinical outcome remains unclear. The most powerful prognosticators are clinical features such as lymph node status, tumor size, and tumor grade. In addition, the expression level and antibody staining pattern of several proteins are predictive of outcome and of the likelihood of response to therapy. However, the clinical outcome of individual patients remains uncertain. In addition, the ability to
30   predict which patients are likely to benefit from a particular type of therapy (e.g., a certain drug or class of drug) remains elusive.

The invention encompasses the realization that high throughput analysis techniques, e.g., those involving the use of cDNA microarrays, can be used to provide new insights into the biology of breast cancer. By analyzing the transcriptional profiles of a large number of breast tumor samples and by undertaking comparisons,

5   e.g., between tumors associated with varying prognoses, between primary tumors and metastases, between tumors before and after treatment, and between tumors with differing responses to therapy, the present invention provides new tools and methods for classifying tumors and defines new classes of tumors based on these methods. The invention identifies genes and gene subsets that are useful in classifying breast

10   tumors. In addition, the methods described herein identify genes that are likely to play a role in breast cancer development, progression, and/or response to therapy. Classification based on expression of particular genes may be used to predict clinical course or to predict sensitivity to chemotherapeutic agents. Ultimately such classification may be used to guide selection of appropriate therapy. As described

15   herein, detection of mRNA and protein corresponding to differentially expressed genes provides new methods of use in cancer prognosis, diagnosis, and treatment selection. In addition, differentially expressed genes and their encoded proteins provide targets for the identification of new therapies for breast cancer.

As described in further detail below, the invention employs methods for

20   clustering genes into groups by determining their expression patterns across a set of samples obtained from breast tumors and from normal breast tissue. The invention also clusters the breast tumor and normal breast tissue samples into groups based on similarities in their expression of a set of genes. This two-dimensional clustering approach permits the association of particular classes of tumors with particular subsets

25   of genes that, for example, show relatively high levels of expression in the tumors. Correlation with clinical information indicates that the tumor classes have clinical significance in terms of prognosis or response to chemotherapy.

Genes that are relatively overexpressed in tumors may be particularly appropriate targets for the development of new therapeutic agents. Any gene (or

30   combination of genes) that is overexpressed in some tumors forms a basis by which tumors can be divided into different groups. As demonstrated herein, when particular sets of genes are used such groups have clinical significance in that, for example, they

26

display differences in prognosis. However, regardless of whether the resulting division has significance in terms of known clinical parameters, therapeutic agents directed towards such genes or towards their encoded proteins would be expected to be specific for the tumors that overexpress the genes. Thus the invention offers an

5   opportunity for the development and selection of therapeutic agents based on specific properties of a tumor. In other words, any gene that is overexpressed in a subset of tumors can be used to define that subclass and is a potential target for the development of a therapeutic agent that is specific for that tumor subclass.

In particular, tumors that display characteristics of basal cells of the normal

10   breast lactation gland (also referred to herein as breast basal cells) form a distinct subclass (referred to herein as the basal subclass). It is known in the art that two distinct types of epithelial cells are found in the adult human mammary gland: basal cells and luminal epithelial cells. Expression of cytokeratin 5 and/or cytokeratin 17 is a characteristic of basal cells of the normal mammary lactation gland, while

15   cytokeratins 8 and 18 are expressed in luminal cells. Cytokeratins are a family of intermediate filament proteins, members of which are found in most or all epithelial cell types (Moll, R., et al., "The catalog of human cytokeratins: patterns of expression in normal epithelia, tumors, and cultured cells", Cell, 31(1), 11-24, 1982. Intermediate-sized filaments are morphologically similar but biochemically and

20   immunologically distinguishable cytoplasmic proteins of which five major filament types have been identified (cytokeratin, vimentin, desmin, neurofilament protein, glia filament protein), and antibodies to these proteins have been used for distinguishing different cell types and tumors derived therefrom. Epithelial and carcinoma cells are characterized by the presence of cytokeratin filaments that can be identified by

25   antibodies. These antibodies can be used to distinguish between different cell and tumor types (Dobus, E., et al., "Immunohistochemical distinction of human carcinomas by cytokeratin typing with monoclonal antibodies", Am J. Pathol., 114(1): 121-30, 1984). In particular, antibodies against cytokeratins 5/6, 17, 8, and 18 may be used to distinguish between breast basal and luminal cell types in normal breast and in

30   tumors (See, e.g., Purkis, P., et al., "Antibody markers of basal cells in complex epithelia", J. Clin. Pathol., 48:26-32, 1990; Taylor,-Papadimitriou and Lane, E., "Keratin expression in the mammary gland" in Neville, M and Daniel C, eds. The

Mammary Gland: Development, Regulation, and Function. New York: Plenum, pp. 181-215, 1987; Dairkee, S., *et al.*, "Immunolocalization of a human basal epithelium-specific keratin in benign and malignant breast disease. *Breast Cancer Res. Treat.*, 10:11-20, 1987.)

5   Several previous studies suggested that expression of basal cell keratins is associated with a poor clinical outcome (Dairkee, S.H., *et al.*, "Monoclonal antibody that predicts early recurrence of breast cancer", *Lancet*, 1:514, 1987; Malzahn, K., *et al.*, "Biological and prognostic significance of stratified epithelial cytokeratins in infiltrating ductal breast carcinomas", *Virchows Archiv*, 433:119-29, 1998). Inventors

10   have confirmed, in a large-scale study, that patients with breast tumors whose cells display characteristics of breast basal cells, e.g., expression of cytokeratin 5 and/or cytokeratin 17, have a poor clinical outcome relative to patients with breast tumors that do not express these markers. However, antibodies to these cytokeratins have been found (by the inventors and by other investigators) to give spotty, focal staining

15   patterns when used to perform immunohistochemistry on breast tumor samples. Thus the utility of cytokeratins 5 and 17 as markers and the utility of antibodies that bind to cytokeratin 5 or 17 for determining whether a tumor is a member of the basal subclass has been limited.

        The inventors have therefore identified genes whose mRNA expression profiles

20   across a large set of tumor samples correlate with, i.e., are similar to, the expression profiles of the known basal cell markers cytokeratins 5 and 17. These genes include the basal marker genes of the present invention, i.e., genes that encode cadherin3 or P-cadherin (SEQ ID NO:1; GenBank protein accession number NP_001399; GenBank cDNA accession number NM_001408), matrix metalloproteinase 14 (SEQ ID NO:2;

25   GenBank protein accession number NP_004986; GenBank cDNA accession number NM_004995); and cadherin EGF LAG seven-pass G-type receptor 2 or EGF-Like Domain, Multiple 2 (SEQ ID NO:3; GenBank protein accession number NP_001784; GenBank cDNA accession number NM_001793). A portion of the cadherin3 gene was present as I.M.A.G.E. clone 777301 on the cDNA microarray described below.

30   This clone is entry #421 in Table 1. A portion of the matrix metalloproteinase 14 gene was present as I.M.A.G.E. clone 270505 on the cDNA microarray described below. This clone is entry #424 in Table 1. A portion of the cadherin EGF LAG

seven-pass G-type receptor 2 gene was present as I.M.A.G.E. clone 175103 on the cDNA microarray described below. This clone is entry #1443 in Table 1. Information about these genes may be found at NCBI's LocusLink (http://www.ncbi.nlm.nih.gov/LocusLink), among other sources. As described in

5   Examples 10 and 13, the inventors have generated antibodies to the proteins expressed by these genes and shown that the antibodies stain basal cells of normal mammary lactation glands. Thus detection of one or more expression products of these genes may be used to identify tumors that fall within the basal tumor subclass.

As is well known in the art, breast carcinomas lose the typical histology and

10   architecture of normal breast glands. Generally, carcinoma cells overgrow the normal cells and lose their ability to differentiate into glandular like structures. The degree of loss of differentiation in general is related to the aggressiveness of the tumor. For example, "in situ" carcinoma by definition retains the basement membrane intact, whereas as it progresses to "invasive", the tumor shows breakout of basement

15   membranes. Thus one would not expect to see, within breast carcinomas, staining of a discrete layer of basal cells as seen in normal breast tissue. For a discussion of the physiology and histology of normal breast and breast carcinoma, see Ronnov-Jessen, L., Petersen, O. W. & Bissell, M. J. Cellular changes involved in conversion of normal to malignant breast: importance of the stromal reaction. Physiol Rev 76, 69-

20   125 (1996).

The basal marker genes provided herein are expressed in the best model of basal cells (HMECs, Human Mammary Epithelial Cells) and based on antibody staining, in normal breast basal cells. Therefore describing them as basal markers is

25   appropriate. However, in addition to their specific staining properties, a major characteristic that makes these genes and their expression products useful is their variation in expression across cohorts of breast carcinoma patients, which portends their utility in stratification of breast carcinoma patients. While not wanting to be limited by the implications of having chosen a particular

30   descriptor (i.e. "basal") inventors refer to the set of genes, proteins, and antibody reactivity patterns as "basal" as it serves as a reminder of their utility in recognizing breast tumor cells that have characteristics

reminiscent of normal breast basal cells. Breast tumors containing such cells are likewise referred to as "basal" without intending any limitations thereby.

Two of the basal marker genes, cadherin3 and cadherin EGF LAG seven-pass G-type receptor 2 encode members of the cadherin superfamily. The cadherin EGF

5　LAG seven-pass G-type receptor 2 or EGF-Like Domain, Multiple 2 protein is a member of the flamingo subfamily, part of the cadherin superfamily. The cadherins are a large family of proteins with critical roles in the regulation of cell-cell adhesion. Generally expressed in development- or tissue-specific manners, these factors have been shown to have important roles in development, cellular proliferation, and

10　differentiation. The cadherin superfamily include classic cadherins, desmogleins, desmocollins, protocadherins, CNRs, Fats, and seven-pass transmembrane cadherins (for review see Nollet *et al.* 2000). Typically transmembrane proteins, the cadherins are characterized by the unique cadherin, or EC, domain. These cadherin domains, which are involved in Ca^{++} binding (Takeichi 1990), are repeated in the extracellular

15　region of all of the family members. The amino acid sequences of other regions shows significant divergence among members, suggesting functional diversity amongst the various cadherin proteins. However, amid the members of each subfamily, the cytoplasmic domains are conserved. In the classic cadherins, which are components of adherens junctions and desmoplakin plaques, this region interacts with catenin p120[ctn],

20　and plakoglobin or β-catenin. The latter binds to α-catenin, and this molecular complex further associates with α-actinin, F-actin and other cytoskeletal proteins. Consistent with their roles in regulating cell-cell adhesion events, altered expression of cadherin genes has been associated with human cancer. Alteration of cadherin function may lead to subsequent metastasis by disaggregation of tumor cells, and one

25　proposed role of many cadherins studied to date is as tumor- and invasion-suppressors. Further discussion of some of the many members of the cadherin superfamily and their possible role in cancer is found in references 53-61.

The flamingo subfamily consists of nonclassic-type cadherins; a subpopulation that does not interact with catenins. The flamingo cadherins are located at the plasma

30　membrane and have nine cadherin domains, seven epidermal growth factor-like repeats and two laminin A G-type repeats in their ectodomain. They also have seven transmembrane domains, a characteristic unique to this subfamily. While not wishing

to be bound by any theory, it is postulated that these proteins are receptors involved in contact-mediated communication, with cadherin domains acting as homophilic binding regions and the EGF-like domains involved in cell adhesion and receptor-ligand interactions. The cadherin EGF LAG seven-pass G-type receptor 2 gene (also

5   known as CELSR2) has not been as extensively studied as the classic cadherins, but is implicated in cell signaling. The *Drosophila* homolog of this gene has been studied in more detail, and is clearly important in regulating different cellular events (Usui T, Shima Y, Shimada Y, Hirano S, Burgess RW, Schwarz TL, Takeichi M, Uemura T, "Flamingo, a seven-pass transmembrane cadherin, regulates planar cell polarity under

10   the control of Frizzled", *Cell* 1999 Sep 98:585-95.

While not wishing to be bound by any theory, it is postulated that this protein is a receptor involved in contact-mediated communication, with the cadherin domains acting as homophilic binding regions and the EGF-like domains involved in cell adhesion and receptor-ligand interactions.

15   Proteins of the matrix metalloproteinase (MMP) family are involved in the breakdown of extracellular matrix in normal physiological processes, such as embryonic development, reproduction, and tissue remodeling, as well as in disease processes, such as arthritis and metastasis. Most MMP's are secreted as inactive proproteins which are activated when cleaved by extracellular proteinases. However,

20   matrix metalloproteinase 14 protein is a member of the membrane-type MMP (MT-MMP) subfamily; each member of this subfamily contains a potential transmembrane domain suggesting that these proteins are expressed at the cell surface rather than secreted. This protein activates MMP2 protein, and this

25   activity may be involved in tumor invasion.

Cadherin3 is predicted to be membrane-bound, with an extracellular portion. As indicated by the presence of seven putative transmembrane domains, cadherin EGF LAG seven-pass G-type receptor 2 is also likely to be a membrane bound protein. The presence of a predicted transmembrane domain indicates that matrix

30   metalloproteinase 14 is also membrane bound. The likelihood that the proteins encoded by the basal marker genes are membrane bound makes them attractive candidate for the application of serological assays for diagnostic purposes. In addition,

the likelihood that cadherin3, cadherin EGF LAG seven-pass G-type receptor 2, and matrix metalloproteinase 14 are membrane bound makes them attractive candidates for antibody therapeutics.

The invention provides antibodies that specifically bind to the polypeptide

5   expression products of the basal marker genes, i.e., the polypeptides of SEQ ID NO:1, 2, and 3. The antibodies stain basal cells of the normal mammary lactation gland. In certain embodiments of the invention the antibodies distinguish basal cells from luminal cells in normal mammary lactation glands.

The antibodies are potentially useful as therapeutic reagents for cancer,

10   particularly breast cancer, either by themselves or when conjugated to or delivered with another molecule such as a toxic compound. The invention further provides pharmaceutical compositions comprising agonists or antagonists of the polynucleotides and their encoded polypeptides, and methods of use thereof for the treatment of cancer. The invention includes a variety of methods for providing

15   information of use in the prognosis, classification, diagnosis, etc. of cancer, particularly breast cancer.

In order that the manner in which the basal cell marker genes of the present invention were identified may be better understood, a description of cDNA microarray technology is provided below. Following this description the specific experimental

20   approach employed herein is described. Certain aspects of the invention are then described in further detail.

II. cDNA Microarray Technology

cDNA microarrays consist of multiple (usually thousands) of different cDNAs

25   spotted (usually using a robotic spotting device) onto known locations on a solid support, such as a glass microscope slide. The cDNAs are typically obtained by PCR amplification of plasmid library inserts using primers complementary to the vector backbone portion of the plasmid or to the gene itself for genes where sequence is known. PCR products suitable for production of microarrays are typically between

30   0.5 and 2.5 kB in length. Full length cDNAs, expressed sequence tags (ESTs), or randomly chosen cDNAs from any library of interest can be chosen. ESTs are partially sequenced cDNAs as described, for example, in L. Hillier, et al., Generation

and analysis of 280,000 human expressed sequence tags, *Genome Research*, 6, 807-828, 1996. The afore-mentioned article is herein incorporated by reference, as are the entire teachings of all other patents and journal articles mentioned herein, for all purposes and not just those related to the particular context in which they are

5   mentioned. Although some ESTs correspond to known genes, frequently very little or no information regarding any particular EST is available except for a small amount of 3' and/or 5' sequence and, possibly, the tissue of origin of the mRNA from which the EST was derived. As will be appreciated by one of ordinary skill in the art, in general the cDNAs contain sufficient sequence information to uniquely identify a gene within

10   the human genome. Furthermore, in general the cDNAs are of sufficient length to hybridize, preferably specifically and yet more preferably uniquely, to cDNA obtained from mRNA derived from a single gene under the hybridization conditions of the experiment.

In a typical microarray experiment, a microarray is hybridized with

15   differentially labeled RNA or DNA populations derived from two different samples. Most commonly RNA (either total RNA or poly A^+ RNA) is isolated from cells or tissues of interest and is reverse transcribed to yield cDNA. Labeling is usually performed during reverse transcription by incorporating a labeled nucleotide in the reaction mixture. Although various labels can be used, most commonly the

20   nucleotide is conjugated with the fluorescent dyes Cy3 or Cy5. For example, Cy5-dUTP and Cy3-dUTP can be used. cDNA derived from one sample (representing, for example, a particular cell type, tissue type or growth condition) is labeled with one fluor while cDNA derived from a second sample (representing, for example, a different cell type, tissue type, or growth condition) is labeled with the second fluor.

25   Similar amounts of labeled material from the two samples are cohybridized to the microarray. In the case of a microarray experiment in which the samples are labeled with Cy5 (which fluoresces red) and Cy3 (which fluoresces green), the primary data (obtained by scanning the microarray using a detector capable of quantitatively detecting fluorescence intensity) are ratios of fluorescence intensity (red/green, R/G).

30   These ratios represent the relative concentrations of cDNA molecules that hybridized to the cDNAs represented on the microarray and thus reflect the relative expression levels of the mRNA corresponding to each cDNA/gene represented on the microarray.

Each microarray experiment can provide tens of thousands of data points, each representing the relative expression of a particular gene in the two samples. Appropriate organization and analysis of the data is of key importance. Various computer programs that incorporate standard statistical tools have been developed to

5 facilitate data analysis. One basis for organizing gene expression data is to group genes with similar expression patterns together into clusters. A method for performing hierarchical cluster analysis and display of data derived from microarray experiments is described in Eisen, M., Spellman, P., Brown, P., and Botstein, D., Cluster analysis and display of genome-wide expression patterns, *Proc. Natl. Acad.*

10 *Sci. USA*, 95: 14863-14868, 1998. As described therein, clustering can be combined with a graphical representation of the primary data in which each data point is represented with a color that quantitatively and qualitatively represents that data point. By converting the data from a large table of numbers into a visual format, this process facilitates an intuitive analysis of the data. Additional information and details

15 regarding the mathematical tools and/or the clustering approach itself may be found, for example, in Sokal, R.R. & Sneath, P.H.A. Principles of numerical taxonomy, xvi, 359, W. H. Freeman, San Francisco,1963; Hartigan, J.A. Clustering algorithms, xiii, 351, Wiley, New York, 1975; Paull, K.D. et al. Display and analysis of patterns of differential activity of drugs against human tumor cell lines: development of mean

20 graph and COMPARE algorithm. *J Natl Cancer Inst* 81, 1088-92,1989; Weinstein, J.N. et al. Neural computing in cancer drug development: predicting mechanism of action. *Science* 258, 447-51, 1992; van Osdol, W.W., Myers, T.G., Paull, K.D., Kohn, K.W. & Weinstein, J.N. Use of the Kohonen self-organizing map to study the mechanisms of action of chemotherapeutic agents. *J Natl Cancer Inst* 86, 1853-9,

25 1994; and Weinstein, J.N. *et al.* An information-intensive approach to the molecular pharmacology of cancer. *Science*, 275, 343-9, 1997.

Further details of the experimental methods used in the present invention are found in the Examples. Additional information describing methods for fabricating and using microarrays is found in U.S. Patent No. 5,807,522, which is herein

30 incorporated by reference. Instructions for constructing microarray hardware (e.g., arrayers and scanners) using commercially available parts can be found at http://cmgm.stanford.edu/pbrown/ and in Cheung, V., Morley, M., Aguilar, F.,

Massimi, A., Kucherlapati, R., and Childs, G., Making and reading microarrays,
Nature Genetics Supplement, 21:15-19, 1999, which are herein incorporated by
reference. Additional discussions of microarray technology and protocols for
preparing samples and performing microrarray experiments are found in, for example,

5   DNA arrays for analysis of gene expression, *Methods Enzymol,* 303:179-205, 1999;
Fluorescence-based expression monitoring using microarrays, *Methods Enzymol,* 306:
3-18, 1999; and M. Schena (ed.), DNA Microarrays: A Practical Approach, Oxford
University Press, Oxford, UK, 1999. Descriptions of how to use an arrayer and the
associated software are found at

10   http://cmgm.stanford.edu/pbrown/mguide/arrayerHTML/ArrayerDocs.html, which is
herein incorporated by reference.

III. Experimental Approach of the Invention

15   The present invention encompasses the realization that genes that are
differentially expressed are of use in classifying tumors. Differentially expressed
genes are likely to be responsible for the different phenotypic characteristics of
tumors. The present invention identifies such genes. In general, a differentially
expressed gene is a gene whose transcript abundance varies between different

20   samples, e.g., between different tumor samples, between normal versus tumor
samples, etc. In the case of the experiment described herein, the transcript level of a
differentially expressed gene varies by at least 4-fold from its average abundance in a
given sample set in at least 3 of the samples. However, genes that display smaller
variations in expression are also within the scope of the invention. In general, the

25   amount by which the expression varies and the number of samples in which the
expression varies by that amount will depend upon the number of samples and the
particular characteristics of the samples. One skilled in the art will be able to
determine, based on knowledge of the samples, what constitutes a significant degree
of differential expression.

30   While analysis of multiple genes is of use in developing a robust classification
of tumors, each of the differentially expressed genes and their encoded proteins is a
target for the development of diagnostic and therapeutic agents. Investigation of

variation in individual genes in breast tumors reveals that molecular variation can be
related to important features of clinical variation. For example, expression of the
estrogen receptor alpha gene (*ESR1*), the *Erb-B2/HER2/neu* oncogene, and the
mutational status at the *TP53, BRCA1* and *BRCA2* loci have shown that molecular

5   variation can be related to important features of clinical variation. (Discussed, for
example, in Osborne, C.K., *et al.*, The value of estrogen and progesterone receptors in
the treatment of breast cancer, *Cancer* 46, 2884-2888, 1980; Ingvarsson, S.,
Molecular genetics of breast cancer progression, *Seminars in Cancer Biology*, 9, 277-
288, 1999;

10   Breast Cancer Linkage Consortium, Pathology of familial breast cancer: differences
between breast cancers in carriers of *BRCA1* and *BRCA2* mutations and sporadic
cases, *Lancet*, 349, 1505-1510, 1997; Anderson, T. I., et al., Prognostic significance of
TP53 alterations in breast carcinoma. *Br J Cancer*, 68, 540-548, 1993 and references
cited in these articles). In particular, approximately 60% to 70% of breast tumors

15   express the estrogen receptor, and this expression has been shown to be a favorable
prognostic factor (reviewed in Allred, D.C., et al. Prognostic and Predictive Factors in
Breast Cancer by Immunohistochemical Analysis, *Modern Pathology*, 11(2), 155-168,
1998).

       As described in more detail in Examples 1, 2, and 4, cDNA microarrays each
20   representing the same set of approximately 8100 different human genes were
produced. The human cDNA clones used to produce the microarrays contained
approximately 4000 named genes, 2000 genes with homology to named genes in other
species, and approximately 2000 ESTs of unknown function. An mRNA sample was
obtained from each of a set of 84 tissue samples or cell lines. The expression levels of

25   the approximately 8100 genes were measured in each mRNA sample by hybridization
to an individual microarray, yielding an expression profile for each gene across the
experimental samples. Although more details will be found in the Examples, an
overview of the experimental procedure is presented here so that the invention may be
better understood.

30   Variation in patterns of gene expression were characterized in 62 breast tumor
samples from 40 different patients, 3 normal breast tissue samples, and 19 samples
from 17 cultured human cell lines (one of which was sampled 3 times under different

conditions). Twenty of the tumors had been sampled twice, before and after a 16 week course of doxorubicin chemotherapy, and two tumors were paired with a lymph node metastasis from the same patient. The other 18 tumor samples were single samples from individual tumors. A detailed listing of the tumor samples and various

5   characteristics including clinical estrogen receptor and Erb-B2 status as assessed using antibody staining, estrogen receptor and Erb-B2 status as assessed by microarray result, tumor grade, differentiation, survival status and time, age at diagnosis, doxorubicin response, and p53 status is presented in Table 5. A listing of the cell lines including description and ATCC (American Tissue Culture Collection) number

10   or reference is presented in Table 3. The cell lines provided a framework for interpreting the variation in gene expression patterns seen in the tumor samples and included gene expression models for many of the cell types encountered in tumors.

As described in more detail in Example 2, mRNA was isolated from each sample. cDNA labeled with the fluorescent dye Cy5 was prepared from each

15   experimental sample separately. Fluorescently labeled cDNA, labeled using a second distinguishable dye (Cy3), was prepared from a pool of mRNAs isolated from 11 different cultured cell lines. The pooled mRNA sample served as a reference to provide a common internal standard against which each gene's expression in each experimental sample was measured.

20   Comparative expression measurements were made by separately mixing Cy5-labeled experimental cDNA derived from each of the 84 samples with a portion of the Cy3-labeled reference cDNA, and hybridizing each mixture to an individual cDNA microarray. The ratio of Cy5 fluorescence to Cy3 fluorescence measured at each cDNA element on the microarray was then quantitatively measured. The use of a

25   common reference standard in each hybridization allowed the fluorescence ratios to be treated as comparative measurements of the expression level of each gene across all the experimental samples.

A hierarchical clustering method (Eisen, et al., 1998) was used to group genes based on similarity in the pattern with which their expression varied over all

30   experimental samples. The same clustering method was used to group the experimental samples (tissue and cell lines separately) based on the similarity in their patterns of expression. Interpretation of the data obtained from the clustering

algorithm was facilitated by displaying the data in the form of tumor and gene dendrograms. In the tumor dendrograms, the pattern and length of the branches reflects the relatedness of the tumor samples with respect to their expression of genes represented on the microarray. Microarray images and tumor and gene dendrograms

5   are available in Perou, et al, *Nature,* 2000, and at inventors' Web site (http://genome-www.stanford.edu/molecularportraits/). In general, the similarity of the gene expression profiles of individual tumor samples or groups of tumor samples to one another is inversely related to the length of the branches that connect them. Thus, for example, adjacent tumor samples connected to one another by short vertical branches

10   descending from a common horizontal branch (e.g., tumor samples Norway 48-BE and Norway 48-AF close to the right of the tumor dendrogram) are more closely related to one another in terms of their gene expression profiles than adjacent tumor samples connected to one another by longer vertical branches descending from a common horizontal branch (e.g., tumor samples Norway 100-BE and Norway 100-AF

15   at the left side of the tumor dendrogram). To the extent that the gene expression programs dictate the biological properties and behavior of the tumors and reflect their physiological state and environment, it is expected that the clustering of the tumors reflects phenotypic relationships among them, e.g., tumor samples connected by short horizontal branches (i.e., located in close proximity to one another) are expected to

20   exhibit similar phenotypic features. In the gene dendrograms, the pattern and length of the branches reflects the relatedness of the genes with respect to their expression profiles across the tumor samples. Similarly to the tumor samples, genes connected by short vertical branches are more similar to one another in terms of expression profile than genes connected by longer vertical branches.

25   The expression patterns of the genes were also displayed using a matrix format, with each row representing all of the hybridization results for a single cDNA element on the array and each column representing the measured expression levels for all genes in a single sample. In this format, tumor samples with similar patterns of expression across the gene set are close to each other along the horizontal dimension.

30   Similarly, genes with similar expression patterns across the set of samples are close to each other along the vertical dimension. To allow the patterns of expression to be visualized, the normalized expression value of each gene was represented by a colored

box, using red to represent expression levels greater than the median and green to represent expression levels less than the median. In all images the brightest red color represents transcript levels at least 16-fold greater than the median, and the brightest green color represents transcript levels at least 16-fold below the median. This

5 display format facilitates comparisons between genes and the recognition of significant patterns.

As described herein, systematic investigation of gene expression patterns in human breast tumors and their correlation to specific features of phenotypic variation offers a basis for an improved molecular taxonomy of breast cancers. Such a

10 taxonomy has significant clinical utility. For example, correlation of gene expression patterns with outcome in the absence of treatment is of use in deciding whether a patient should receive adjuvant chemotherapy after surgery. As another example, genes whose expression level varies between tumors that are sensitive to chemotherapy and tumors that are resistant to chemotherapy are of use in predicting

15 likelihood of response and in selection of appropriate treatment. Genes whose expression level varies between tumor samples taken before and after therapy are of use in understanding the response of tumors to treatment.

IV. Further Aspects of the Invention

20 A. Basal tumor subclasses and corresponding gene subsets

Gene and tumor dendrograms were derived from data obtained by performing a microarray analysis on the set of breast tumor and breast tissue samples described above, using a set of genes (the "intrinsic" gene set) described further below and in Example 8. Appendices A and C present the resulting tumor dendrograms and color

25 matrix displays of the gene expression profiles obtained. Although technically the dendrograms identify groups of tumor samples, since each sample is obtained from a specific tumor the dendrograms also identify groups of tumors. Thus, in general, a group of tumor samples corresponds to a group of tumors. Therefore, throughout most of the discussion herein reference will be made to tumor groups, classes, etc.,

30 rather than tumor sample groups, classes, etc. The clustering method permits the identification of subsets of genes with related expression profiles across a set of tumors and the identification of groups or classes of tumors with similar expression

profiles across a set of genes. Although the existence of gene subsets is revealed by the display of the data in dendrogram format, understanding the significance of the gene subsets obtained in experiments such as those described above requires interpretation in light of knowledge about the genes and tumor samples. Groups of

5   tumors identified based on their expression patterns of sets of genes (e.g., groups of tumors that overexpress genes in particular gene subsets) can be designated as tumor classes when deemed significantly distinct to warrant a distinct classification.

Table 5 includes information regarding the clinical outcome of the tumors from which the samples were obtained. In particular, the table includes survival time

10   of the patients and, for some of the tumors, whether or not the tumor responded to chemotherapy (doxorubicin). Such information was used to demonstrate that the basal tumor class is characterized by a poor clinical outcome relative to the other tumors. Differences in survival between groups of patients was demonstrated using the Kaplan-Meier technique for survival analysis, which is implemented in computer

15   software such as the SAS package (SAS Institute, Inc, Cary, NC) and described in the accompanying manual. Of course various other statistical techniques can be used to detect differences in survival or any other clinical parameters between groups of tumors. Various appropriate statistical techniques useful for analyzing survival are discussed, for example, in Lawless, J.F., *Statistical Models and Methods for Lifetime*

20   *Data.* New York: John Wiley & Sons, 1982. Lee, Elisa T. *Statistical Methods for Survival Data Analysis.* 2nd ed. New York: John Wiley & Sons, 1992. Marubini, Ettore, and Valsecchi, Maria Grazia, *Analysing Survival Data from Clinical Trials and Observational Studies.* New York: John Wiley & Sons, 1995. Miller, Rupert G. Jr. *Survival Analysis.* New York: John Wiley & Sons, 1981. Rosner, Bernard,

25   *Fundamentals of Biostatistics.* 4th ed. Belmont, California: Duxbury Press, 1995.) Other clinical parameters of importance include response to therapy, time to recurrence, etc.

As will be appreciated by one of ordinary skill in the art, the correlation of particular tumor groups with survival or other parameters of clinical importance can be

30   strengthened by the inclusion of data obtained from additional tumor samples.

The invention identifies genes and gene subsets that are associated with the basal tumor subclass. The genes and gene subsets are identified in part by the

overexpression of certain members of each subset in a particular tumor group and are also defined in part based on the proximity of genes within each subset to one another in a gene dendrogram. As used herein unless otherwise stated, a gene is overexpressed in a tissue sample at the RNA level if a mRNA corresponding to (i.e.,

5   transcribed from) the gene is present in excess relative to the median abundance of that mRNA across the set of analyzed specimens. A gene is overexpressed in a tissue sample at the protein level if a polypeptide corresponding to (i.e., translated from a mRNA that was transcribed from) the gene is present in excess relative to the abundance of that polypeptide across the set of analyzed specimens. The

10   measurement of relative abundance using cDNA microarrays relies upon the comparison of all samples relative to a common reference sample that provides cognate mRNA for as many genes as possible with the goal of providing a common denominator for the measured ratios across all samples. Each tested sample can be compared to all other tested samples in ratio units relative to the reference. This

15   allows reproducible determination of gene expression in each tested sample relative to the median gene expression across any given sample set (Ross, DT, et al., Systematic variation in gene expression patterns in human cancer cell lines, *Nat Genet.* 2000 Mar;24(3):227-35, 2000). In general, an appropriate reference sample comprises a renewable source of diverse cell samples such as a mixture of cells obtained from the

20   panel of 11 cell lines listed in Table 3. A particularly preferred reference sample is one in which all relevant genes are represented in significant abundance above measured background. This provides for a reproducible measurement of reference signal for all relevant genes. As is well known in the art, there is generally a correlation between overexpression or underexpression at the RNA level and

25   overexpression or underexpression at the protein level. In other words, if a mRNA is overexpressed then it is highly likely that the corresponding polypeptide is also overexpressed, and if a mRNA is underexpressed then it is highly likely that the corresponding polypeptide is underexpressed. Therefore, detection of either mRNA or a corresponding polypeptide is generally sufficient to determine whether a

30   particular gene is over or underexpressed. However, as is well known in the art, in certain situations it may be more convenient and/or practical to detect mRNA while in other situations it may be more convenient and/or practical to detect polypeptides.

As mentioned above, genes that are overexpressed in one or more samples
may be identified by examining the microarray data displayed in matrix format,
wherein red squares indicate overexpression. The basal gene subset includes a
number of genes known to be expressed in basal epithelial cells (e.g., cytokeratins 5

5   and 17) and is characterized in that certain of the genes in the subset are
overexpressed at the RNA level in samples obtained from a subset of tumors that had
a poor prognosis relative to the entire group of tumors (the basal group). Referring to
Perou, et al, Nature, 2000, the basal gene subset comprises two subsets identified with
a blue bar and a green bar along the side of the color matrices. Genes in the basal

10   gene subset are, in general, overexpressed in tumors in the basal tumor group
(identified with orange dendrogram branches). Of course it will be appreciated that
additional genes, not necessarily falling into either of the two basal gene subsets, also
have an expression pattern similar to that of cytokeratin 5 and/or cytokeratin 17.

It will be appreciated that not all of the genes are overexpressed to a similar

15   extent within a particular group of tumors and that expression of any given gene will
likely vary between different tumors in a group. For example, genes identified as
"Cytochrome P450, subfamily IIA" and "Lymphoid nuclear protein related to AF4"
are significantly overexpressed in tumors at the far right of the luminal tumor group
(Stanford 24, Norway 27, 28, 26, and 56) while they are expressed at lesser levels in

20   other members of the luminal tumor group. Conversely, genes identified as "417081"
and "Homo Sapiens PWD gene mRNA, 3' end" are, in general, relatively
underexpressed in these tumors. However, the overall expression patterns of genes in
each subset over all tissue samples, are sufficiently similar to cause them to cluster in
close proximity on the gene dendrogram. Thus whether a gene is a member of one of

25   the inventive gene subsets is not determined solely on the basis of the overexpression
of that gene within a tumor subset but also on the relationship of the overall
expression pattern of the gene to the expression pattern of other genes within the
subset. It will further be appreciated that a gene may be overexpressed in more than
one tumor group. For example, certain of the genes in the basal subset are expressed

30   in a group identified with green dendrogram branches, which includes both tumor and
normal tissue samples, in addition to being overexpressed in the basal tumor group.

B. Diagnostics and methods of use thereof

The invention provides reagents for detecting expression products of the basal marker genes described herein, i.e., cadherin3, matrix metalloproteinase 14, and cadherin EGF LAG seven-pass G-type receptor 2. Detection of these expression

5 products identifies tumors in the basal tumor subclass. While not wishing to be bound by any theory, inventors suggest that breast carcinoma with basal cell like features has · distinguishing biology that could be targeted in therapeutic development. Once therapeutics targeted at such tumors are identified (as described elsewhere herein), detection of these expression products allows identification of subjects likely to

10 benefit from these therapeutics. In addition, since the invention has established a correlation between the expression of the three basal marker genes and the expression of cytokeratin17 and also established that cytokeratin 5/6 and/or cytokeratin 17 expression in breast tumors correlates with a poor outcome, detection of expression of the basal marker genes is useful in guiding therapeutic decisions in general. If it is

15 known that a patient has a tumor that falls into the basal tumor subclass and thus has a poor prognosis, a more aggressive approach to therapy may be warranted than in tumors not falling within the basal subclass. For example, in patients where there is no evidence of disease in lymph nodes (node-negative patients), a decision must be made regarding whether to administer chemotherapy (adjuvant therapy) following

20 surgical removal of the tumor. While some patients are likely to benefit from such treatment, it has significant side effects. Presently it is difficult or impossible to predict which patients would benefit. Knowing that a patient falls into a poor prognosis category may help in this decision. Of note, inventors showed that in node-negative patients cytokeratin 5/6 and/or 17 expression was a prognostic factor

25 independent of tumor size and tumor grade. See Example 13 for further discussion of these issues and inventor's findings. Detecting expression of the basal marker genes of the present invention may provide information related to tumor progression. It is well known that as tumors progress, their phenotypic characteristics may change. The invention contemplates the possibility that breast tumors may evolve from luminal-

30 like to basal-like (or vice versa), and that detection of expression products of the basal marker genes can be used to detect such progression.

It is well known in the art that some tumors respond to certain therapies while others do not. In general there is very little information that may be used to determine, prior to treatment, the likelihood that a specific tumor will respond to a given therapeutic agent. Many compounds have been tested for anti-tumor activity and appear to be

5   effective in only a small percentage of tumors. Due to the current inability to predict which tumors will respond to a given agent, these compounds have not been developed into marketed therapeutics. This problem reflects the fact that current methods of classifying tumors are limited. However, the present invention offers the possibility of identifying tumor subgroups characterized by a significant likelihood of

10   response to a given agent. Tumor sample archives containing tissue samples obtained from patients that have undergone therapy with various agents are available along with information regarding the results of such therapy. In general such archives consist of tumor samples embedded in paraffin blocks. These tumor samples can be analyzed for their expression of polypeptides encoded by the basal marker genes of

15   the present invention. For example, immunohistochemistry can be performed using antibodies that bind to the polypeptides. Tumors belonging to the basal tumor subclass may then be identified on the basis of this information. It is then possible to correlate the expression of the basal marker genes with the response of the tumor to therapy, thereby identifying particular compounds that show a superior efficacy in

20   tumors in this class as compared with their efficacy in tumors overall or in tumors not falling within the basal tumor subclass. Once such compounds are identified it will be possible to select patients whose tumors fall into the basal tumor subclass for additional clinical trials using these compounds. Such clinical trials, performed on a selected group of patients, are more likely to demonstrate efficacy. The reagents

25   provided herein, therefore, are valuable both for retrospective and prospective trials.

In the case of prospective trials, detection of expression products of one or more of the marker genes may be used to stratify patients prior to their entry into the trial or while they are enrolled in the trial. In clinical research, stratification is the process or result of describing or separating a patient population into more

30   homogeneous subpopulations according to specified criteria. Stratifying patients initially rather than after the trial is frequently preferred, e.g., by regulatory agencies such as the U.S. Food and Drug Administration that may be involved in the approval

44

process for a medication. In some cases stratification may be required by the study design. Various stratification criteria may be employed in conjunction with detection of expression of one or more basal marker genes. Commonly used criteria include age, family history, lymph node status, tumor size, tumor grade, etc. Other criteria

5 including, but not limited to, tumor aggressiveness, prior therapy received by the patient, ER and/or PR positivity, Her2neu status, p53 status, various other biomarkers, etc., may also be used. Stratification is frequently useful in performing statistical analysis of the results of a trial. Ultimately, once compounds that exhibit superior efficacy against breast basal tumors are identified, reagents for detecting expression of

10 the basal marker genes may be used to guide the selection of appropriate chemotherapeutic agent(s).

In summary, by providing reagents and methods for classifying tumors based on their expression of the basal marker genes, the present invention offers a means to individualize therapy. The invention further provides a means to identify a patient

15 population that may benefit from potentially promising therapies that have been abandoned due to inability to identify the patients who would benefit from their use.

Information regarding the expression of the basal marker genes is useful even in the absence of specific information regarding their biological function or role in tumor development, progression, maintenance, or response to therapy. Although the

20 reagents disclosed herein find particular application with respect to breast cancer, the invention also contemplates their use to provide diagnostic and/or prognostic information for other cancer types. As is well known in the art, mutations in a single gene (e.g., the p53 gene) may play a role in the development of multiple cancer types.

Thus it is contemplated that some or all of the basal marker genes described herein

25 will be important both in breast cancer and in one or more other tumor types, particularly since basal cells are a feature of epithelia throughout the body.

In one aspect, the invention provides a method of classifying tumors by detecting the presence of one or more of the inventive gene products encoded by the cadherin3, matrix metalloproteinase 14, and cadherin EGF LAG seven-pass G-type

30 receptor 2 genes. As is well known in the art, a polypeptide may be detected using a variety of techniques that employ an antibody that binds to the polypeptide. As described further below, these techniques include enzyme-linked immunosorbent

assay (ELISA), immunoblot, and immunohistochemistry. The invention encompasses the use of protein arrays, including antibody arrays, for detection of the polypeptide. The use of antibody arrays is described, for example, in Haab, B., *et al.*, "Protein microarrays for highly parallel detection and quantitation of specific proteins and

5   antibodies in complex solutions", *Genome Biol.* 2001;2(2), 2001. Other types of protein arrays are known in the art.

In addition, in certain embodiments of the invention the polypeptides are detected using other modalities known in the art for the detection of polypeptides, such as aptamers (Aptamers, *Molecular Diagnosis*, Vol. 4, No. 4, 1999), reagents

10   derived from combinatorial libraries for specific detection of proteins in complex mixtures, random peptide affinity reagents, etc. In general, any appropriate method for detecting a polypeptide may be used in conjunction with the present invention, although antibodies may represent a particularly appropriate modality.

The invention provides antibodies to the polypeptides encoded by the encoded

15   by the cadherin3, matrix metalloproteinase 14, and cadherin EGF LAG seven-pass G-type receptor 2 genes. Example 10 describes the generation of polyclonal antibodies to these polypeptides. In general, antibodies (either monoclonal or polyclonal) may be generated by methods well known in the art and described, for example, in Harlow, E., Lane, E., and Harlow, E., (eds.) *Using Antibodies: A Laboratory Manual*, Cold

20   Spring Harbor Laboratory Press, Cold Spring Harbor, 1998. Details and references for the production of antibodies based on an inventive polypeptide may also be found in U.S. Patent No. 6,008,337. Antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric (e.g., "humanized"), and single chain antibodies, and Fab fragments, antibodies generated using phage display technology, etc. The

25   invention encompasses "fully human" antibodies produced using the XenoMouse™ technology (AbGenix Corp., Fremont, CA) according to the techniques described in U.S. Patent No. 6,075,181.

The invention encompasses a number of uses for these antibodies. Detection of the basal marker polypeptides may be used to provide diagnostic information. As

30   used herein the term "diagnostic information" includes, but is not limited to, any type of information that is useful in determining whether a patient has, or is at increased risk for developing, a disease or disorder; for providing a prognosis for a patient

having a disease or disorder; for classifying a disease or disorder; for monitoring a patient for recurrence of a disease or disorder; for selecting a preferred therapy; for predicting the likelihood of response to a therapy, etc. In certain embodiments of the invention, the antibodies are used for providing diagnostic information for cancer, ·

5   particularly for breast cancer, but they may also be of use for providing diagnostic information for other diseases, e.g., other types of cancer.

In general, diagnostic assays in which the antibodies may be employed include methods that use the antibody to detect the polypeptide in a tissue sample, cell sample, body fluid sample (e.g., serum), cell extract, etc. Such methods typically

10   involve the use of a labeled secondary antibody that recognizes the primary antibody (i.e., the antibody that binds to the polypeptide being detected). Depending upon the nature of the sample, appropriate methods include, but are not limited to, immunohistochemistry, radioimmunoassay, ELISA, immunoblotting, and FACS analysis. In the case where the polypeptide is to be detected in a tissue sample, e.g., a

15   biopsy sample, immunohistochemistry is a particularly appropriate detection method. Techniques for obtaining tissue and cell samples and performing immunohistochemistry and FACS are well known in the art. Such techniques are routinely used, for example, to detect the ER in breast tumor tissue or cell samples. In general, such tests will include a negative control, which can involve applying the test

20   to normal tissue so that the signal obtained thereby can be compared with the signal obtained from the sample being tested. In tests in which a secondary antibody is used to detect the antibody that binds to the polypeptide of interest, an appropriate negative control can involve performing the test on a portion of the sample with the omission of the antibody that binds to the polypeptide to be detected, i.e., with the omission of

25   the primary antibody. Antibodies suitable for use as diagnostics generally exhibit high specificity for the target polypeptide and low background. In general, monoclonal antibodies are preferred for diagnostic purposes.

In general, the results of such a test can be presented in any of a variety of formats. The results can be presented in a qualitative fashion. For example, the test

30   report may indicate only whether or not a particular polypeptide was detected, perhaps also with an indication of the limits of detection. The results may be presented in a semi-quantitative fashion. For example, various ranges may be defined, and the

ranges may be assigned a score (e.g., 1+ to 4+) that provides a certain degree of quantitative information. Such a score may reflect various factors, e.g., the number of cells in which the polypeptide is detected, the intensity of the signal (which may indicate the level of expression of the polypeptide), etc. The results may be presented

5   in a quantitative fashion, e.g., as a percentage of cells in which the polypeptide is detected, as a protein concentration, etc. As will be appreciated by one of ordinary skill in the art, the type of output provided by a test will vary depending upon the technical limitations of the test and the biological significance associated with detection of the polypeptide. For example, in the case of certain polypeptides a purely

10   qualitative output (e.g., whether or not the polypeptide is detected at a certain detection level) provides significant information. In other cases a more quantitative output (e.g., a ratio of the level of expression of the polypeptide in the sample being tested versus the normal level) is necessary.

      Sequence analysis of two of the basal marker proteins, matrix

15   metalloproteinase 14 and cadherin EGF LAG seven-pass G-type receptor 2 indicates that they possess one or more transmembrane domains and an extracellular portion. Sequence analysis of the third basal marker protein, cadherin3, indicates that it also has an extracellular portion. The invention encompasses the recognition that since these proteins have an extracellular domain, the likelihood exists that a portion of

20   these proteins may therefore be present in serum (e.g., the portion may be cleaved by endogenous proteases and released into the bloodstream), enabling their detection through a blood test rather than requiring a biopsy specimen. Regardless of whether the proteins are present in serum, the likelihood that cadherin3, cadherin EGF LAG seven-pass G-type receptor 2, and matrix metalloproteinase 14 are membrane bound

25   makes them attractive candidates for antibody diagnostics. The proteins may be detected on cells that enter the bloodstream or in samples obtained from a tumor site (e.g., cell or tissue samples).

      Measurement of prostate specific antigen (PSA) in serum using an immunoassay technique is widely used as a method for early detection of prostate

30   cancer and for monitoring recurrence or progression after therapy, etc. Methods and considerations in the use of this clinical marker are described, for example, in Chen DW, *et al*. Prostate-specific antigen as a marker for prostate cancer: A monoclonal

and polyclonal immunoassay compared. *Clin Chem* , 33:1916-1920, 1987; Oesterling
JE, *et al.* Free, complexed and total serum prostate specific antigen: The
establishment of appropriate reference ranges for their concentrations and ratios. *J*
Urol 154:1090-1095, 1995; Hybritech Tandem®-MP Free PSA. Package insert. March

5   1998 and Hybritech Tandem® Total PSA. Package insert., Hybritech, Inc., San Diego,
CA. One of ordinary skill in the art will readily be able to develop appropriate assays
for polypeptides encoded by the basal marker genes described herein and to apply
them to the detection of such polypeptides in serum. Such assays may be used as
screening tests for cancer, to detect recurrence or progression of cancer, to monitor the

10   response of cancer to therapy, to classify and/or provide prognostic information
regarding a tumor, etc.

        In certain embodiments of the inventive methods a single antibody is used
whereas in other embodiments of the invention multiple antibodies, directed either
against the same or against different polypeptides can be used to increase the

15   sensitivity or specificity of the test or to provide more detailed information than that
provided by a single antibody. Thus the invention encompasses the use of a battery of
antibodies that bind to polypeptides encoded by the basal marker genes identified
herein. Of course these antibodies can also be used in conjunction with antibodies
against other polypeptides, including antibodies that bind to cytokeratin 5/6 or 17.

20   Various other techniques for detecting the basal marker polypeptides identified
herein are within the scope of the invention. For example, a basal marker polypeptide
may be detected using an assay for a biochemical activity of the polypeptide, e.g., an
enzymatic activity. This type of assay may be especially convenient for tests on
samples such as blood or other body fluids. Such an approach may be particularly

25   attractive in the case of matrix metalloproteinase 14. As described above, matrix
metalloproteinases are involved in cleavage of various proteins in the extracellular
matrix. The cleavage specificity of this protein may readily be determined, and an
appropriate substrate prepared. (See, e.g., Turk, B., *et al.*, "Determination of protease
cleavage site motifs using mixture-based oriented peptide libraries", *Nature*

30   *Biotechnology*, 19(7): 661-667, 2001, which discusses cleavage site motifs for various
metalloproteases including MMP14, referred to as MT1-MMP therein.) Cleavage of
this substrate may then be detected. In certain embodiments of the invention the

substrate includes a fluorescent moiety for convenient detection. The invention contemplates use of fluorescent resonance energy transfer (FRET) assays to detect matrix metalloproteinase 14 (see http://www.aurorabio.com).

Although in many cases detection of polypeptides using antibodies represents

5   the most convenient means of determining whether a gene is expressed (or overexpressed) in a particular sample, the invention also encompasses the use of polynucleotides for this purpose. Microarray analysis is but one means by which polynucleotides can be used to detect or measure gene expression. Expression of a gene can also be measured by a variety of techniques that make use of a

10   polynucleotide corresponding to part or all of the gene rather than an antibody that binds to a polypeptide encoded by the gene. Appropriate techniques include, but are not limited to, *in situ* hybridization, Northern blot, and various nucleic acid amplification techniques such as PCR, quantitative PCR, and the ligase chain reaction.

15   One detection method involves performing quantitative PCR on a diagnostic sample using a set of oligonucleotide primers designed to amplify the genes in one or more of the inventive gene sets of gene subsets. (Considerations for primer design are well known in the art and are described, for example, in Newton, et al. (eds.) *PCR: Essential data Series*, John Wiley & Sons; *PCR Primer: A Laboratory Manual*, Cold

20   Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1995; White, et al.. (eds.) *PCR Protocols: Current methods and Applications,* Methods in Molecular Biology, The Humana Press, Totowa, NJ, 1993. In addition, a variety of computer programs known in the art may be used to select appropriate primers.)

According to one embodiment of this method the diagnostic sample is

25   distributed into multiple vessels, e.g., multiple wells of a 396 well microtiter plate. A pair of primers designed to amplify a portion of a gene in one of the inventive gene sets or subsets is added to each well, and PCR amplification is performed. The resulting product can then be detected using any of a number of methods known in the art depending upon the particular method of performing quantitative PCR that is

30   employed. Primers sufficient for amplification of genes that allow quantitation of different cell types within the sample may also be included in the set of primers.

The invention also encompasses the detection of mutations within any of the basal marker genes or within a regulatory region of a basal marker gene. Such mutations may include, but are not limited to, deletions, additions, substitutions, and amplification of regions of genomic DNA that include all or part of a gene. Methods

5   for detecting such mutations are well known in the art. Such mutations may result in overexpression or inappropriate expression of the gene. Detection of mutations can be used, for example, to predict the likelihood that an individual will develop a condition associated with the mutation.

Another aspect of the invention comprises a kit to test for the presence of any

10   of the inventive polynucleotides or polypeptides, e.g., in a tissue sample or in a body fluid. The kit can comprise, for example, an antibody for detection of a polypeptide or a probe for detection of a polynucleotide. In addition, the kit can comprise a reference or control sample, instructions for processing samples, performing the test and interpreting the results, buffers and other reagents necessary for performing the

15   test. In certain embodiments of the invention the kit comprises a panel of antibodies. In certain embodiments of the invention the kit comprises pairs of primers for detecting expression of one or more of the basal marker genes. In certain embodiments of the invention the kit comprises a cDNA or oligonucleotide array for detecting expression of one or more of the basal marker genes.

20

D. Therapeutics

The invention encompasses the use of the basal marker genes and their expression products as targets for the development of therapeutics. The invention specifically encompasses antagonists to the basal marker genes and their expression

25   products. Such antagonists (which include, but are not limited to, antibodies, small molecules, antisense nucleic acids) may be produced or identified using any of a variety of methods known in the art. For example, a purified polypeptide or fragment thereof may be used to raise antibodies or to screen libraries of compounds to identify those that specifically bind to the polypeptide. The likelihood that cadherin3,

30   cadherin EGF LAG seven-pass G-type receptor 2, and matrix metalloproteinase 14 are membrane bound makes them attractive candidates for antibody therapeutics.

Preferably antibodies suitable for use as therapeutics exhibit high specificity for the target polypeptide and low background binding to other polypeptides. In general, monoclonal antibodies are preferred for therapeutic purposes. In the case of breast cancer, antibodies against the HER2/neu/ErbB2 polypeptide (a polypeptide homologous to the epidermal growth factor receptor) represent a paradigm in terms of the development of therapeutic antibodies. The *HER2/neu/ErbB2* gene is overexpressed in approximately 25 to 30 percent of metastatic breast tumors, and an antibody against the HER2/neu/ErbB2 polypeptide, Herceptin® (Trastuzumab) is approved for the treatment of certain patients with metastatic breast cancer, confirming the utility of therapeutic antibodies directed against polypeptides that are specifically overexpressed in particular tumors subsets. Proteins that are expressed on the cell surface, such as the basal marker proteins described herein, represent preferred targets for the development of therapeutic agents, particularly therapeutic antibodies. The presence of these proteins on the cell surface can be confirmed using immunohistochemisty.

Antibodies directed against a polypeptide expressed by a cell may have a number of mechanisms of action. In certain instances, e.g., in the case of a polypeptide that exerts a growth stimulatory effect on a cell, antibodies may directly antagonize the effect of the polypeptide and thereby arrest tumor progression, trigger apoptosis, etc. While not wishing to be bound by any theory, it may be particularly likely that certain genes that are overexpressed in tumors having a poor prognosis (e.g., genes in the basal gene subsets) encode polypeptides that have a growth stimulatory effect on tumor cells or facilitate the growth of such cells in some other way, e.g., by enhancing angiogenesis, by allowing cells to overcome normal growth regulatory mechanisms, or by blocking mechanisms that would normally lead to elimination of mutated or otherwise abnormal cells.

In certain embodiments of the invention the antibody may serve to target a toxic moiety to the cell. Thus the invention encompasses the use of antibodies that have been conjugated with a cytotoxic agent, e.g., a toxin such as ricin or diphtheria toxin, a radioactive moiety, etc. Such antibodies can be used to direct the cytotoxic agent specifically to cells that express the inventive polypeptide, particularly in the case of a polypeptide that is expressed on the cell surface.

Although certain antagonists may function through direct interaction with a polypeptide, e.g., by inhibiting its activity, others may function by affecting expression of the polypeptide. Reduction in expression of an endogenously produced polypeptide may be achieved by the administration of antisense nucleic acids (e.g.,

5   oligonucleotides, RNA, DNA, most typically oligonucleotides that have been modified to improve stability or targeting) or peptide nucleic acids comprising sequences complementary to those of the mRNA that encodes the polypeptide. Antisense technology and its applications are described in Phillips, M.I. (ed.) *Antisense Technology*, Methods Enzymol., Volumes 313 and 314, Academic Press,

10   San Diego, 2000, and references mentioned therein. Ribozymes (catalytic RNA molecules that are capable of cleaving other RNA molecules) represent another approach to reducing gene expression. Such ribozymes can be designed to cleave specific mRNAs corresponding to a gene of interest. Their use is described in U.S. Patent No. 5,972,621, and references therein. The invention encompasses the delivery

15   of antisense and/or ribozyme molecules via a gene therapy approach in which vectors or cells expressing the antisense molecules are administered to an individual.

It may also be desirable to increase the expression of a gene in an inventive gene subset or to increase the activity of the corresponding polypeptide. For example, in the case of genes that are overexpressed in tumors having a good prognosis, e.g.,

20   certain genes in the luminal subset, it may be desirable to increase the expression of such genes or the activity of the corresponding polypeptides in tumors that fail to express these genes.

Small molecule modulators (e.g., inhibitors or activators) of gene expression are also within the scope of the invention and may be detected by screening libraries

25   of compounds using, for example, cell lines that express the polypeptide or a version of the polypeptide that has been modified to include a readily detectable moiety. Methods for identifying compounds capable of modulating gene expression are described, for example, in U.S. Patent No. 5,976,793. The screening methods described therein are particularly appropriate for identifying compounds that do not

30   naturally occur within cells and that modulate the expression of genes of interest whose expression is associated with a defined physiological or pathological effect within a multicellular organism.

More generally, the invention encompasses compounds that modulate the activity of a basal marker gene of the present invention. Methods of screening for such interacting compounds are well known in the art and depend, to a certain degree, on the particular properties and activities of the polypeptide encoded by the gene.

5   Representative examples of such screening methods may be found, for example, in U.S. Patent No. 5,985,829, U.S. Patent No. 5,726,025, U.S. Patent No. 5,972,621, and U.S. Patent No. 6,015,692. The skilled practitioner will readily be able to modify and adapt these methods as appropriate for a given polypeptide. Thus the invention encompasses methods of screening for molecules that modulate the activity of a

10   polypeptide encoded by a basal marker gene.

The invention also encompasses the use of polynucleotide sequences corresponding to basal marker genes, or portions thereof, as DNA vaccines. Such vaccines comprise polynucleotide sequences, typically inserted into vectors, that direct the expression of an antigenic polypeptide within the body of the individual

15   being immunized. Details regarding the development of vaccines, including DNA vaccines for various forms of cancer may be found, for example, in Brinckerhoff L.H., Thompson L.W., Slingluff C.L., Jr., Melanoma Vaccines, *Curr Opin Oncol*, 12(2):163-73, 2000 and in Stevenson, F.K., DNA vaccines against cancer: from genes to therapy, *Ann. Oncol.*, 10(12): 1413-8, 1999 and references therein. The

20   polypeptides, or fragments thereof, that are encoded by genes in the inventive gene subsets may also find use as cancer vaccines. Such vaccines may be used for the prevention and/or treatment of cancer.

The invention includes pharmaceutical compositions comprising the inventive antibodies, or small molecule inhibitors, agonists, or antagonists described above. In

25   general, a pharmaceutical composition will include an active agent in addition to one or more inactive agents such as a sterile, biocompatible carrier including, but not limited to, sterile water, saline, buffered saline, or dextrose solution. The pharmaceutical compositions may be administered either alone or in combination with other therapeutic agents including other chemotherapeutic agents, hormones, vaccines,

30   and/or radiation therapy. By "in combination with", it is not intended to imply that the agents must be administered at the same time or formulated for delivery together, although these methods of delivery are within the scope of the invention. In general,

each agent will be administered at a dose and on a time schedule determined for that agent. Additionally, the invention encompasses the delivery of the inventive pharmaceutical compositions in combination with agents that may improve their bioavailability, reduce or modify their metabolism, inhibit their excretion, or modify

5 their distribution within the body. The invention encompasses treating cancer, particularly breast cancer, by administering the pharmaceutical compositions of the invention. Although the pharmaceutical compositions of the present invention can be used for treatment of any subject (e.g., any animal) in need thereof, they are most preferably used in the treatment of humans.

10 The pharmaceutical compositions of this invention can be administered to humans and other animals by a variety of routes including oral, intravenous, intramuscular, intraarterial, subcutaneous, intraventricular, transdermal, rectal intravaginal, intraperitoneal, topical (as by powders, ointments, or drops), bucal, or as an oral or nasal spray or aerosol. In general the most appropriate route of

15 administration will depend upon a variety of factors including the nature of the compound (e.g., its stability in the environment of the gastrointestinal tract), the condition of the patient (e.g., whether the patient is able to tolerate oral administration), etc. At present the intravenous route is most commonly used to deliver therapeutic antibodies and nucleic acids. However, the invention encompasses

20 the delivery of the inventive pharmaceutical composition by any appropriate route taking into consideration likely advances in the sciences of drug delivery.

General considerations in the formulation and manufacture of pharmaceutical agents may be found, for example, in *Remington's Pharmaceutical Sciences*, 19th ed., Mack Publishing Co., Easton, PA, 1995. It will be appreciated that certain of the

25 compounds of the present invention can exist in free form for treatment, or, where appropriate, in salt form, as discussed in more detail below. Compounds to be utilized in the pharmaceutical compositions include compounds existing in free form or pharmaceutically acceptable derivatives thereof, as defined herein, such as pharmaceutically acceptable salts, esters, salts of such esters, or any other adduct or

30 derivative, which upon administration to a patient in need, is capable of providing, directly or indirectly, a compound as otherwise described herein, or a metabolite or residue thereof, e.g., a prodrug. Thus, as used herein, the term "pharmaceutically

acceptable salt" refers to those salts which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of humans and lower animals without undue toxicity, irritation, allergic response and the like, and are commensurate with a reasonable benefit/risk ratio. Pharmaceutically acceptable salts

5   are well known in the art. For example, S. M. Berge, et al. describe pharmaceutically acceptable salts in detail in *J. Pharmaceutical Sciences*, 66: 1-19 (1977), incorporated herein by reference. The salts can be prepared in situ during the final isolation and purification of the compounds of the invention, or separately by reacting the free base function with a suitable organic acid. Examples of pharmaceutically acceptable,

10   nontoxic acid addition salts are salts of an amino group formed with inorganic acids such as hydrochloric acid, hydrobromic acid, phosphoric acid, sulfuric acid and perchloric acid or with organic acids such as acetic acid, oxalic acid, maleic acid, tartaric acid, citric acid, succinic acid, or malonic acid or by using other methods used in the art such as ion exchange. Other pharmaceutically acceptable salts include

15   adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, formate, fumarate, glucoheptonate, glycerophosphate, gluconate, hemisulfate, heptanoate, hexanoate, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate,

20   malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, p-toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium,

25   and the like. Further pharmaceutically acceptable salts include, when appropriate, nontoxic ammonium, quaternary ammonium, and amine cations formed using counterions such as halide, hydroxide, carboxylate, sulfate, phosphate, nitrate, lower alkyl sulfonate and aryl sulfonate.

Additionally, as used herein, the term "pharmaceutically acceptable ester"

30   refers to esters that hydrolyze in vivo and include those that break down readily in the human body to leave the parent compound or a salt thereof. Suitable ester groups include, for example, those derived from pharmaceutically acceptable aliphatic

carboxylic acids, particularly alkanoic, alkenoic, cycloalkanoic and alkanedioic acids, in which each alkyl or alkenyl moiety advantageously has not more than 6 carbon atoms. Examples of particular suitable esters includes formates, acetates, propionates, butyrates, acrylates and ethylsuccinates.

5   Furthermore, the term "pharmaceutically acceptable prodrugs" as used herein refers to those prodrugs of the compounds of the present invention that are, within the scope of sound medical judgment, suitable for use in contact with the tissues of humans and lower animals without undue toxicity, irritation, allergic response, and the like, commensurate with a reasonable benefit/risk ratio, and effective for their

10   intended use, as well as the zwitterionic forms, where possible, of the compounds of the invention. The term "prodrug" refers to compounds that are rapidly transformed *in vivo* to yield a particular active compound, for example by hydrolysis in blood. A thorough discussion is provided in T. Higuchi and V. Stella, "Pro-drugs as Novel Delivery Systems", Vol. 14 of the A.C.S. Symposium Series, and in Edward B.

15   Roche, ed., *Bioreversible Carriers in Drug Design*, American Pharmaceutical Association and Pergamon Press, 1987, both of which are incorporated herein by reference.

          As mentioned above, the pharmaceutical compositions of the present invention additionally comprise a pharmaceutically acceptable carrier, which, as used herein,

20   means a non-toxic, inert solid, semi-solid or liquid filler, diluent, encapsulating material, or formulation auxiliary of any type. Some examples of materials which can serve as pharmaceutically acceptable carriers are sugars such as lactose, glucose and sucrose; starches such as corn starch and potato starch; cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate;

25   powdered tragacanth; malt; gelatin; talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil; safflower oil; sesame oil; olive oil; corn oil and soybean oil; glycols; such a propylene glycol; esters such as ethyl oleate and ethyl laurate; agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; water; isotonic saline; Ringer's solution; ethyl

30   alcohol, and phosphate buffer solutions, dextrose solutions, as well as other non-toxic compatible lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening, flavoring and

perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator.

Liquid dosage forms for oral administration include pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and elixirs. In

5   addition to the active compounds, the liquid dosage forms may contain inert diluents commonly used in the art such as, for example, water or other solvents, solubilizing agents and emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils (in particular, cottonseed, groundnut, corn, germ, olive,

10   castor, and sesame oils), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof. Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, and perfuming agents.

Injectable preparations, for example, sterile injectable aqueous or oleaginous

15   suspensions may be formulated according to the known art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution, suspension or emulsion in a nontoxic parenterally acceptable diluent or solvent, for example, as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution,

20   U.S.P. and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid are used in the preparation of injectables.

The injectable formulations can be sterilized, for example, by filtration

25   through a bacterial-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium prior to use.

In order to prolong the effect of a drug, it is often desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be

30   accomplished by the use of a liquid suspension of crystalline or amorphous material with poor water solubility. The rate of absorption of the drug then depends upon its rate of dissolution which, in turn, may depend upon crystal size and crystalline form.

Alternatively, delayed absorption of a parenterally administered drug form is
accomplished by dissolving or suspending the drug in an oil vehicle. Injectable depot
forms are made by forming microencapsulated matrices of the drug in biodegradable
polymers such as polylactide-polyglycolide. Depending upon the ratio of drug to
5   polymer and the nature of the particular polymer employed, the rate of drug release
can be controlled. Examples of other biodegradable polymers include
poly(orthoesters) and poly(anhydrides). Depot injectable formulations are also
prepared by entrapping the drug in liposomes or microemulsions which are
compatible with body tissues.

10   Compositions for rectal or vaginal administration are preferably suppositories
which can be prepared by mixing the compounds of this invention with suitable non-
irritating excipients or carriers such as cocoa butter, polyethylene glycol or a
suppository wax which are solid at ambient temperature but liquid at body
temperature and therefore melt in the rectum or vaginal cavity and release the active
15   compound.

Solid dosage forms for oral administration include capsules, tablets, pills,
powders, and granules. In such solid dosage forms, the active compound is mixed
with at least one inert, pharmaceutically acceptable excipient or carrier such as sodium
citrate or dicalcium phosphate and/or a) fillers or extenders such as starches, lactose,
20   sucrose, glucose, mannitol, and silicic acid, b) binders such as, for example,
carboxymethylcellulose, alginates, gelatin, polyvinylpyrrolidinone, sucrose, and
acacia, c) humectants such as glycerol, d) disintegrating agents such as agar--agar,
calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium
carbonate, e) solution retarding agents such as paraffin, f) absorption accelerators such
25   as quaternary ammonium compounds, g) wetting agents such as, for example, cetyl
alcohol and glycerol monostearate, h) absorbents such as kaolin and bentonite clay,
and i) lubricants such as talc, calcium stearate, magnesium stearate, solid polyethylene
glycols, sodium lauryl sulfate, and mixtures thereof. In the case of capsules, tablets
and pills, the dosage form may also comprise buffering agents.
30   Solid compositions of a similar type may also be employed as fillers in soft
and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well
as high molecular weight polyethylene glycols and the like. The solid dosage forms of

tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings and other coatings well known in the pharmaceutical formulating art. They may optionally contain opacifying agents and can also be of a composition that they release the active ingredient(s) only, or preferentially, in a

5   certain part of the intestinal tract, optionally, in a delayed manner. Examples of embedding compositions that can be used include polymeric substances and waxes. Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well as high molecular weight polethylene glycols and the like.

10   The active compounds can also be in micro-encapsulated form with one or more excipients as noted above. The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings, release controlling coatings, and other coatings well known in the pharmaceutical formulating art. In such solid dosage forms the active compound may be admixed

15   with at least one inert diluent such as sucrose, lactose or starch. Such dosage forms may also comprise, as is normal practice, additional substances other than inert diluents, e.g., tableting lubricants and other tableting aids such a magnesium stearate and microcrystalline cellulose. In the case of capsules, tablets and pills, the dosage forms may also comprise buffering agents. They may optionally contain opacifying

20   agents and can also be of a composition that they release the active ingredient(s) only, or preferentially, in a certain part of the intestinal tract, optionally, in a delayed manner. Examples of embedding compositions that can be used include polymeric substances and waxes.

         Dosage forms for topical or transdermal administration of a compound of this

25   invention include ointments, pastes, creams, lotions, gels, powders, solutions, sprays, inhalants or patches. The active component is admixed under sterile conditions with a pharmaceutically acceptable carrier and any needed preservatives or buffers as may be required. Ophthalmic formulation and ear drops are also contemplated as being within the scope of this invention. The ointments, pastes, creams and gels may contain, in

30   addition to an active compound of this invention, excipients such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or

mixtures thereof. Powders and sprays can contain, in addition to the compounds of this invention, excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain propellants known in the art such as chlorofluorohydrocarbons.

5   Transdermal patches have the added advantage of providing controlled delivery of a compound to the body. Such dosage forms can be made by dissolving or dispensing the compound in the proper medium. Absorption enhancers can also be used to increase the flux of the compound across the skin. The rate can be controlled by either providing a rate controlling membrane or by dispersing the compound in a

10   polymer matrix or gel.

In yet another aspect, the present invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention, and in certain embodiments, includes an additional approved therapeutic agent for use as a

15   combination therapy. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceutical products, which notice reflects approval by the agency of manufacture, use or sale for human administration. Instructions for use of the compound(s) may also be included.

20   According to the methods of treatment of the present invention, cancer, particularly breast cancer, is treated or prevented in a patient such as a human or other mammal by administering to the patient a therapeutically effective amount of a compound of the invention, in such amounts and for such time as is necessary to achieve the desired result. By a "therapeutically effective amount" of a compound of

25   the invention is meant a sufficient amount of the compound to treat (e.g. to ameliorate the symptoms of, delay progression of, prevent recurrence of, cure, etc.) cancer, particularly breast cancer, at a reasonable benefit/risk ratio, which involves a balancing of the efficacy and toxicity of the compound. In general, therapeutic efficacy and toxicity may be determined by standard pharmacological procedures in

30   cell cultures or with experimental animals, e.g., by calculating the ED_{50} (the dose that is therapeutically effective in 50% of the treated subjects) and the LD_{50} (the dose that is lethal to 50% of treated subjects). The ED_{50}/LD_{50} represents the therapeutic index

of the compound. Although in general drugs having a large therapeutic index are preferred, as is well known in the art, a smaller therapeutic index may be acceptable in the case of a serious disease, particularly in the absence of alternative therapeutic options. Ultimate selection of an appropriate range of doses for administration to

5   humans is determined in the course of clinical trials.

It will be understood that the total daily usage of the compounds and compositions of the present invention for any given patient will be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective dose level for any particular patient will depend upon a

10   variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific compound employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific compound employed; the duration of the treatment; drugs used in combination or coincidental

15   with the specific compound employed; and like factors well known in the medical arts.

The total daily dose of the compounds of this invention administered to a human or other mammal in single or in divided doses can be in amounts, for example, from 0.01 to 50 mg/kg body weight or more usually from 0.1 to 25 mg/kg body

20   weight. Single dose compositions may contain such amounts or submultiples thereof to make up the daily dose. In general, treatment regimens according to the present invention comprise administration to a patient in need of such treatment from about 0.1 μg to about 2000 mg of the compound(s) of the invention per day in single or multiple doses.

25

EXAMPLES

Note: A numbered list of references appears following the Examples, all of which are
incorporated herein by reference.

5   Example 1

Preparation of Microarrays Containing 8498 Human cDNAs

The human cDNA clones used in this study were obtained from Research Genetics
(Huntsville AB, USA) as bacterial colonies in 96-well microtiter plates. The clones
10   were chosen from a set of 15,000 cDNA clones that corresponded to the Research
Genetics Human Gene Filters sets GF200-202 (http://www.resgen.com/). These
clones form part of a set of clones assembled by the I.M.A.G.E. consortium (Lennon,
G.G., Auffray, C., Polymeropoulos, M., Soares, M.B. The I.M.A.G.E. Consortium:
An Integrated Molecular Analysis of Genomes and their Expression. Genomics
15   33:151-152,1996) and are identified by I.M.A.G.E. clone ID numbers. All clones
printed on these arrays were sequence validated as part of a product offered at
Research Genetics, Inc. We estimate that greater than 97% of the clones on the array
are correctly identified.

A detailed protocol for the production of the cDNA microarrays used in this
20   study is available at http://cmgm.stanford.edu/pbrown/protocols.html and is
reproduced below with insubstantial changes. As described below, the protocol
includes steps of (1) cleaning the glass slides onto which the DNAs (e.g., products of
PCR reactions) are to be spotted; (2) spotting the DNAs onto the glass slides with an
arrayer; (3) Post processing to prepare arrays containing spotted DNAs for
25   hybridization. All procedures are done at room temperature and with double distilled
water unless otherwise stated. Unless otherwise stated, in this Example and the
following Examples, reagents are prepared according to protocols available in
Maniatis, T., Sambrook, J. and Fritsch, E., *Molecular Cloning: A Laboratory Manual*
(3 Volume Set), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1989.
30

Cleaning Slides

Use 30 slide racks in 350mL glass dishes

1. Dissolve 50g of NaOH pellets into 150ml ddH2O

2. Add 200ml of 95% EtOH, stir until completely mixed

3. If solution remains cloudy, add ddH2O until clear

4. Pour solution into glass slide box.

5. Drop in 30 slides in a metal rack. (Gold Seal slides, Cat. 3010)

6. Let soak on an orbital shaker for at least two hours

7. Rinse slides by transferring rack to slide dish filled with ddH2O

8. Repeat ddH2O rinses x3. It's important to remove all traces of the

NaOH-ethanol.

9. Prepare Poly-l-lysine solution: Use Sigma Poly-l-lysine solution. Cat. No.

8920

10. Add 70mL poly-l-lysine to 280ml of water

11. Transfer slides to poly-l-lysine solution and let soak for 1 hour.

12. Remove excess liquid from slides by spinning the rack of slides on microtiter

plate

carriers at 500rpm.

13. Dry slides at 40 degrees C for 5 minutes in a vacuum oven.

14. Store slides in a closed box for at least two weeks prior to use.

15. Before printing arrays, check a sample slide to make sure it's hydrophobic

(water should bead off it) but the lysine coating is not turning opaque.

Arraying

1. Transfer PCR reactions to 96-well V-bottom tissue culture plates (Costar).

Add 1/10 vol. 3M sodium acetate (pH 5.2) and equal volume isopropanol. Store at -20

C for a few hours.

2. Centrifuge in Sorvall at 3500 RPM for 45 min. Rinse with 70% EtOH,

centrifuge again and dry.

2. Resuspend DNA in 12ul 3X SSC for a few hours and transfer to flexible

U-bottom printing plates.

4. Spot DNA onto poly-l-lysine slides with an arrayer.

Post processing

    1. Rehydrate arrays by suspending slides over a dish of warm ddH2O. (~1 minute)

    2. Snap-dry each array (DNA side up) on a 100C hot plate for 3 seconds.

5   3. UV cross-link DNA to the glass by using a Stratalinker set for 60 milliJoules

    4. Dissolve 5g of succinic anhydride (Aldrich) in 315mL of n-methyl-pyrrolidinone.

    5. To this, add 35mL of 0.2M NaBorate pH 8.0 (made by dissolving boric acid in water and adjusting the pH with NaOH), and stir until dissolved.

10   6. Soak arrays in this solution for 15 minutes with shaking.

    7. Transfer arrays to 95C water bath for 2 minutes

    8. Quickly transfer arrays to 95% EtOH for 1 minute.

    9. Remove excess liquid from slides by spinning the rack of slides on microtiter plate

15   carriers at 500rpm.

    10. Arrays can be used immediately.

Reagent Suppliers

20   Microscope slides Goldseal brand. (Cat. 3010)

Poly-l-lysine solution Sigma product number P8920

Succinic Anhydride Aldrich product number 23,969-0

N-Methyl-Pyrrolidinone Aldrich product number 32,863-4

25   Microarrays were prepared according to the above protocol using the 8498 cDNA clones described above. All microarrays used in the experiments described herein were from a single print run batch of microarrays.

Example 2

30

Cell Lines, Breast Tissue, and Breast Tumor Samples for Microarray Analysis and Preparation of mRNA Samples

Common Reference Sample

Each of the 84 experimental samples tested here was analyzed by a
comparative hybridization, using a common reference RNA pool as a standard; this
5   reference sample was composed of equal mixtures of mRNA isolated from 11
established cell lines derived from human tissue (MCF7, Hs578T, OVCAR3, HepG2,
NTERA2, MOLT4, RPMI-8226, NB4+ATRA, UACC-62, SW872, and Colo205: also
see Table 3 for more details). The 11 cell lines were all grown to 70-90% confluence
in RPMI medium, containing 10% Fetal Calf Serum and Penicillin/Streptomycin. The
10   cells were harvested either by scraping or centrifugation, quickly resuspended in RNA
lysis buffer and mRNA prepared using the FastTrack™ 2.0 mRNA Isolation Kit
(Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. In each case,
multiple individual mRNA preparations were collected for each cell line, which were
then pooled together and analyzed via Northern analysis before final mixing to ensure
15   the quality of the input mRNAs (e.g., to confirm that the mRNA exhibited a size
distribution indicating that it was substantially nondegraded). The 11 mRNA samples
were then mixed together in equal amounts, aliquoted in 10mM Tris (7.4), and stored
at -80 C until use (2 micrograms of common reference sample was used per
microarray hybridization and was always labeled using Cy3).
20

Normal Breast Tissue

Three samples of normal breast tissue were analyzed. Two of the samples
were obtained from Clontech (Palo Alto, CA) and were pools of six (Normal1) or two
(Normal2) whole normal breasts. The third sample (Normal3) was obtained from a
25   single individual.

Breast Tumor Samples

The 40 individual breast tumor samples were collected at either Stanford
University in Stanford CA, USA, or in the Haukeland University Hospital in Bergen,
30   Norway. Twenty of the forty breast tumors were sampled twice as part of a larger
Norwegian study on locally advanced breast cancers (T3/T4 and/or N2 tumors) and
have been described previously (Aas, T., et al., *Nat. Med.*, 2, 811-814, 1996, the

contents of which are incorporated herein by reference) ; these patients underwent an

open surgical biopsy before treatment with doxorubicin monotherapy (range 12-23

weeks), followed by the definitive surgical resection of the remaining tumor after

therapy, and were evaluated for clinical responses according to UICC criteria

5   (Hayward, J., et al., *Br. J. Cancer*, 35, 292-298, 1977). In addition to the 20 pairs,

there were 8 additional "before" specimens from Norway and 10 tumor specimens

from Stanford (all Stanford tumors tested had a diameter of 3 cm or larger). Finally, 2

of the 10 Stanford tumor specimens assayed were also paired with a lymph node

metastasis from the same patient.

10

mRNA Isolation from Breast Tumor and Tissue Samples

Following their excision, breast tumor samples were rapidly frozen in liquid

N2 and then stored at -80 C until use. mRNA was isolated from breast tumors and

normal breast tissue using the Trizol Reagent (Gibco-BRL) and Invitrogen FastTrack

15   2.0 Kit (all Stanford samples, and see http://genome-

www.stanford.edu/sbcmp/web.shtml for the detailed protocol) or using the Trizol

Reagent followed by Dynal bead separation for the mRNA purification step (all

Norway tissue samples). Briefly, frozen tumor samples were cut into small pieces and

immediately placed into 12 ml of Trizol Reagent. Each tumor sample in Trizol was

20   homogenized using a PowerGen 125 Tissue Homogenizer (Fisher Scientific), and

total RNA was isolated according to the Trizol reagent manufacturer's protocol.

Tumor mRNA was isolated according to the manufacturer's protocols using the

FastTrack 2.0 Kit (Invitrogen) or Dynal beads.

25   Example 3

Characterization of Breast Tissue and Tumor Samples

For all but two of the tumor specimens (i.e. New York 1 and New York 2), the

mutational status of the *TP53* gene was determined using published methods (Aas, T.,

30   *et al.*).

A single pathologist (applicant Matt van de Rijn) reviewed hematoxylin and

eosin (H&E) sections of each tumor, including all before and after pairs, and made a

histological evaluation of each while blinded to the source. Tumors were graded using a modified version of the Bloom-Richardson method (Robbins, P., et al., *Hum Pathol*, 26, 873-879, 1995). These data are displayed in Table 4. Representative H&E sections of each tumor are posted on Applicants' website at http://genome-

5   www.stanford.edu/molecularportraits/.

Immunohistochemistry was performed as described previously (Perou, C., *et al.*, 1999; Bindl, J. and Warnke, R., *Am J Clin Pathol*, 85, 490-493, 1986, and Natkunam, Y., *et al.*, Am. J. Path., 156(1), 2000). The antibodies used included the commercially available monoclonal antibodies CAM5.2 (specific for keratins 8/18,

10   available from Becton Dickinson), anti-keratin 5/6 (available originally from Boehringer Mannheim, Indianapolis, IN, cat. no. 1273396 and now from Chemicon International, Temekula, CA), anti-keratin 17 (clone E3, available from Dako, Carpinteria, CA, cat. no. M7046), anti-CD3 (available from Dako), and anti-immunoglobulin light chain (A191, A193, available from Dako). These

15   immunohistochemical methods were applied for all the immunohistochemical studies described in the present application unless otherwise stated. Results are presented in Figure 3 and are described in further examples as appropriate.

20   Example 4

cDNA Synthesis and Labeling and Microarray Hybridization

mRNA was isolated from breast tissue, breast tumor samples, and cell lines as described in Example 2. Fluorescently labeled cDNA was synthesized from the

25   mRNA using a reverse transcriptase reaction that included dUTP labeled with either Cy3 or Cy5. For each hybridization experiment differentially labeled cDNA samples (an experimental sample and a reference sample) were pooled and hybridized to a cDNA microarray, which was then scanned as described in Example 4. The protocol below provides details of the steps performed for cDNA synthesis and labeling and

30   for microarray hybridization.

1. To set up for the reverse transcriptase (RT) reaction, combine the following (e.g., in an Eppendorf tube):

    (a) Anchored Oligo dT primer - 2 microliters at 2.5 micrograms/microliter or control - 2 microliters.

    (b) mRNA - (whatever volume is needed to reach 1.5-2 micrograms)

    (c) DEPC/H2O - add sufficient volume so that final volume is 16 microliters

2. Heat at 70° C for 10 minutes

3. Chill on ice for 1-2 minutes

4. Add the following RT reaction components to each individual tube:

    (a) 5X RT Buffer - 6 microliters

    (b) 50X dNTPs - 0.7 microliters - (500mm A,C,G, 200mm T)

    (c) Cy Dyes dUTP - 3 microliters - (either Cy3 or Cy5)

    (d) DTT Stock - 3 microliters - (comes with RT setup)

    (e) Superscript II RT—1.7 microliters - (cat# 18064-014 Gibco-BRL)

5. Mix well

6. Incubate at 42° C for 1 hour

7. Add another 1 microliter of Superscript II RT and mix

8. Incubate at 42° C for 1 more hour

9. Degrade mRNA with 1.5 microliters of 1M NaOH / 2mM EDTA

10. Incubate at 65° C for 8 minutes (do NOT go TOO long here)

11. Add 15 microliters of 0.1M HCL

12. Add 450 microliters of TE (pH 7.4) to each sample and place each sample into a microcon-30 filter.

13. Add 15 microliters of Human COT1 DNA (Gibco-BRL = 1 microgram/microliter) to each sample in the microcon filter.

14. Spin in Eppendorf centrifuge until volume equals about 50 microliters (8-10')

15. Remove flowthroughs, and pool Cy3 and Cy5 flowthroughs together for future recovery of Cy dyes (store at –20 ° C).

16. Invert microcons, recover labeled samples, and pool Cy3 and Cy5 samples together that will be used for an individual experiment, in a single microcon filter that was used in step 15.

17. Add 500 microliters of T.E again, and spin until final volume equals 8 microliters or less (BE VERY CAREFUL TO NOT SPIN THE SAMPLE DRY!!!)

18. To the 8 microliter combined Cy3 + Cy5 sample, add the following:

5   (a) Yeast tRNA - 1 microliter - (10 micrograms/microliter)

(b) PolyA DNA - 2 microliters - (10 micrograms/microliter)

(c) 20XSSC - 2 microliters - (FINAL SSC concentration approximately 3X)

(d) 10% SDS - 0.3 microliters

FINAL VOLUME = 13.3 MICROLITERS

10   19. Mix well.

20. Heat sample at 100° C for 2 minutes, spin very briefly.

21. Place samples at 42° C for 20-30 minutes.

22. During Step 21, prepare the necessary number of hybridization chambers (Custom made by Die-Tech, San Jose, CA (see "Drawings for custom parts at

15   http://cmgm.stanford.edu/pbrown/mguide/HybChamber.pdf") or purchased at Corning Costar, Acton, MA (CTM™ Hybridization Chamber, #2551), get 22mm X 22mm coverslips ready, and get arrays ready.

23. Add the 13 microliters of probe (i.e., labeled cDNA mixture) onto the center of the array while NOT actually touching the array face with the pipette tip.

20   24. Quickly and gently place the 22mm X 22mm glass#1 coverslip onto the array face.

25. Add about 15-20 microliters of 3XSSC in two drops onto the end of the array slide away from the actual array for hydration purposes.

26. Assemble the hybridization chamber with the array slide in it, and place into a 65

25   C water bath overnight.

27. Pull out the hybridization chamber and dry off the excess H_2O.

28. Disassemble the hybridization chamber, and quickly place the slides into a slide washing chamber that contains 2XSSC/0.05%SDS. Jiggle the slide holder up and down until the slide coverslip falls off. Repeat this individually for each array, one at

30   a time, until all are done

29. Wash slides in 1XSSC for 3-5 minutes.

30. Wash slides in 50 C 0.2XSSC for 3-5 minutes, twice.

31. Spin slides down in centrifuge at 200 RPM for 2 minutes.

32. SCAN immediately.

Example 5

5   Collection, Processing, and Analysis of Data from Microarray Hybridizations

The cDNA microarrays were scanned with either a General Scanning
(Watertown, MA) ScanArray 3000 at 20 microns resolution, or with a prototype Axon
Instruments (Foster City, CA) GenePix Scanner at 10 micron resolution. The output
10   files, which were TIFF images, were then analyzed using the program ScanAlyze (M.
Eisen; available at http://www.microarrays.org/software). Fluorescent ratios and
quantitative data on spot quality (see ScanAlyze manual) were stored in a prototype of
the AMAD database (M. Eisen; available at http://www.microarrays.org/software).
Areas of the array with obvious blemishes were manually flagged and excluded from
15   subsequent analyses. The primary data tables can be downloaded at http://genome-
www.stanford.edu/molecularportraits/, in text/tab delimited format after obtaining a
password.

Data were extracted from the database in a single table, with each row
representing an array element, each column a hybridization, and each cell the
20   observed fluorescent ratio for the array element in the appropriate hybridization.
Previously flagged spots were excluded, as were spots that did not pass quality
control. This table had 9216 rows and 84 columns. Array elements were removed if
they were not well measured in at least 80% of the hybridizations. The data table was
split into tumors and cell lines, and the two subtables were separately median polished
25   (the rows and columns were iteratively adjusted to have median 0) before being
rejoined into a single table. Genes whose expression varied by at least 4-fold from the
median in this sample set in at least three of the samples tested were selected for the
analyses described in the Detailed Description and in Examples 6 and 7 (1753 genes
satisfied these conditions).

30   Average-linkage hierarchical clustering, as implemented in the program
Cluster (M. Eisen; http://www.microarrays.org/software), was applied separately to

both the genes and arrays. The results were analyzed, and images generated, using

TreeView (M. Eisen; http://www.microarrays.org/software).

5   Example 6

Molecular Portraits of Tumors Based on Variation in Expression of 1753 Genes

Methods

A hierarchical clustering method (Eisen, 1998) was used to group 1753

differentially expressed genes (i.e., those genes whose expression varied by at least 4-

10   fold from the median in the sample set in at least three of the samples tested) based on

similarity in the pattern with which their expression varied over all samples. The

same clustering method was used to group the experimental samples (tissues and cell

lines separately) based on the similarity in their patterns of expression. The data are

conveniently presented in a matrix format, with each row representing a single gene,

15   and each column representing an experimental sample. The ratio of the abundance of

transcripts of each gene, in each sample, to the median abundance of the gene's

transcript among all the cell lines (left panel) or to its median abundance across all the

clinical samples (right panel) is represented by the color of the corresponding cell in

the matrix. Green squares represent transcript levels below the median; black squares

20   represent transcript levels equal to the median; red squares represent transcript levels

greater than the median; gray squares indicate technically inadequate or missing data.

The color saturation reflects the magnitude of the ratio relative to the median for each

set of samples (see scale at bottom left). In all images the brightest red color

represents transcript levels at least 16-fold greater than the median, and the brightest

25   green color represents transcript levels at least 16-fold below the median.

Results

(i) Molecular Portraits of Tumors

Three striking general features of the tumors' gene expression patterns are

30   evident in Appendices A and D. First, the breast tumors show remarkable variation in

their patterns of gene expression. Second, this variation is multidimensional, that is,

many different sets of genes show largely independent patterns of variation. Third,

the patterns of gene expression have a pervasive order reflecting relationships among the genes, relationships among the tumors, and connections between specific genes and specific tumors.

The hierarchical clustering algorithm organized the experimental samples
5   based only on overall similarity in their gene expression patterns; relationships among the experimental samples are summarized in a dendrogram , in which the pattern and length of the branches reflect the relatedness of the samples (Eisen, M., *et al.*, 1998). Fifteen of the 20 pairs of samples taken from the same tumor before and after *doxorubicin chemotherapy (red dendrogram branches), and both pairs of samples*
10 taken from a primary tumor and an associated lymph node metastasis (blue branches) were clustered together on adjacent terminal branches in the dendrogram. The three clustered normal breast samples are highlighted in green. The branches representing the four breast luminal epithelial cell lines are displayed in pink; breast basal epithelial cell lines are displayed in orange, the endothelial cell lines in blue, the
15 mesynchemal-like cell lines in dark green, and the lymphocyte-derived cell lines in dark red.

Application of the clustering method to the samples and genes identified the two members of each primary tumor/metastasis pair as being closely related to one another based on similarity in gene expression. Thus this method can provide
20 information useful in determining whether a tumor sample obtained from a second tumor is a metastasis originating from a first tumor or is an independent primary tumor. In addition, despite the potential confounding effects of an interval of 16 weeks, independent surgical procedures and cytotoxic chemotherapy, the independent samples taken from the same tumor before and after chemotherapy were in most cases
25 recognizably more similar to each other in their overall pattern of gene expression than either was to any of the other samples.

Closer examination of the five before and after pairs that were not matched by the clustering algorithm provided further insight. In three instances, the after chemotherapy specimens (i.e. Norway 47, 61, and 101) were clustered into a branch
30 of the dendrogram that contained the three normal breast samples along with five additional tumor samples; we know from the clinical data that these three tumors were all classified as doxorubicin responders (Table 5 and Aas, T., *et al.*). Thus, in most

cases, independent tumor biopsies from the same individual could be recognized as such solely on the basis of gene expression patterns. This implies that the patterns of gene expression are homogeneous and stable in each breast tumor, and yet, sufficiently diverse between tumors, so that they can be viewed as molecular portraits

5 of each tumor.

(ii) Specific Properties of the Tumors

The molecular portraits revealed in the patterns of gene expression not only uncovered similarities and differences among the tumors but, in many cases, pointed

10 to a biological interpretation. As discussed below, variation in growth rate, in the activity of specific signaling pathways, and in the cellular composition of the tumors were all reflected in corresponding variations in the expression of specific subsets of genes.

15 Growth and Proliferation. The largest distinct subset of genes among the 1753 genes was the proliferation subset, which is a group of approximately 120 genes whose level of expression correlates with cellular proliferation rates (See Perou, C., et al., 1999; Ross, D., et al., Nature Genetics, 24(3): 227-35, 2000.). Expression of this subset of genes varied widely among the tumor samples, and was generally well correlated with

20 a standard pathological index of tumor cell proliferation, namely the mitotic index. The mitotic grade of each tumor, as determined by evaluating mitotic index, is displayed in a color-coded format below the tumor name, with green indicating mitotic grade 1, black indicating mitotic grade 2, red indicating mitotic grade 3, and gray indicating that mitotic grade was not evaluated. The growth and proliferation

25 cluster also included the genes encoding two widely used immunohistochemical markers of cell proliferation (Ki-67 and PCNA, names in blue/purple letters).

Diverse proliferation-related functions are represented in the genes comprising this subset, including macromolecular synthesis, cell-cycle regulation, mitosis and cytokinesis. Many genes in which alterations in sequence or expression that are

30 associated with tumorigenesis were also found in this gene subset, in particular, numerous genes implicated in chromosomal instability and/or anueploidy (names in

pink letters)[22]. These genes included the spindle checkpoint gene *hBUB1*[23], the human *MAD2* homologue[24], the *STK15/IPL1* kinase[25], and the *PLK1/HSTPK13* kinase[26].

The importance of this clustered set of genes in cancer biology is further highlighted by its inclusion of genes encoding the molecular targets of widely used

5 anticancer agents (names in orange letters), including both subunits of ribonucleotide reductase, topoisomerase II alpha, and dihydrofolate reductase. The many uncharacterized genes in this subset, therefore, are candidates for important roles in the regulation and execution of the cell's program for growth and proliferation, and potential targets for oncogenic mutations or antiproliferative drugs. Thus the

10 clustering method, by generating a set of genes known to be involved in proliferation and/or known to be targets for antiproliferative drugs and further identifying a set of unknown genes whose expression patterns cause them to fall within the subset, identifies potential targets for the development of new chemotherapeutic agents.

15 Variation in signaling pathways. Several groups of co-expressed genes provided views of the activities of specific signaling and/or regulatory systems.

(a) Interferon signaling: A large subset of genes known to be regulated by the interferon pathway (including *STAT1*) showed substantial variation in expression among the tumors.

20 (b) Estrogen receptor: Variation in expression of the estrogen receptor alpha gene (*ESR1*) correlated well with the direct clinical measurement of the estrogen receptor protein levels in the tumors (Table 5, concordance in 36/38 tumors tested), and paralleled variation in the expression of a larger group of genes that included three other transcription factors (GATA-binding protein 3, X-box binding protein 1 and

25 hepatocyte nuclear factor 3 alpha (see also references 27 and 28). In a specific subset of the estrogen receptor positive tumors, the *BCL2* gene and two previously known estrogen regulated genes (*LIV1* and trefoil factor 1[29]) were also highly expressed (See Appendices C and D). The regulatory program reflected in the expression of this *ESR1*-containing subset of genes may play an important role in the clinical course of a

30 breast tumor, as the loss of expression of the estrogen receptor is known to be associated with a poor prognosis[17], while high levels of expression of both *BCL2* and *ESR1* are associated with a more favorable prognosis[30,31].

(c) <u>Erb-B2</u>: *HER2/neu*, also known as the *Erb-B2* oncogene, is a gene whose aberrant expression is thought to contribute to tumorigenesis in the breast[16]. The *Erb-B2* receptor-tyrosine kinase is known to be overexpressed in 20-30% of all breast tumors, usually associated with DNA amplification of the chromosomal locus (17q12-q22)

5   that contains the *ERB-B2* gene[32,33]. Interestingly, most of the other genes contained within the *Erb-B2* cluster

were also located in this same small region of Chromosome 17. These expression data suggested, and the results of microarray comparative genomic hybridization confirmed, that these other closely linked genes were also amplified on the genomic

10   DNA level and, consequently, overexpressed on the mRNA level in tumors with an amplified *Erb-B2* gene[33-35].

(d) <u>Fos/Jun Signaling</u>: A subset of genes that included *c-Fos, JunB*, and other genes involved in the "immediate-early" response to serum, co-varied in expression among the tumor specimens; these genes were most highly expressed in the three normal

15   breast samples. Applicants have found that this set of genes is characteristically induced by prolonged handling of the samples following surgical resection. The observed variation in the expression of this set of genes may therefore reflect variation in post surgical handling rather than true *in vivo* differences.

20   Example 7

Identification of Cell Type Specific Components Within Tumors Based on Variation

in Expression of 1753 Genes

<u>Methods and Rationale</u>

25   Clustering was performed as described in the previous Example. The resulting dendrogram and matrix were used to identify gene expression patterns indicative of the presence of certain cell types within the samples. Human breast tumors are histologically complex tissues, containing a variety of cell types in addition to the carcinoma cells[18]. In analyzing the gene expression patterns in tumors and tissues,

30   two lines of reasoning were used to infer the lineage of the cells that accounted for apparently cell-type specific expression of particular clustered groups of genes. First, such gene subsets usually included genes whose expression patterns have been well

characterized by previous workers, and have consistently pointed to a specific cell type. Second, these inferences were often corroborated by observing comparable expression of the same group of genes in one or more of the cultured cell lines (reference 21). Some of the prominent patterns of gene expression that appear, on this

5   basis, to indicate the variable abundance of particular cell types in these tissue samples are summarized below.

Immunohistochemistry was performed as described in Example 3.

Results

10   At least eight subsets of genes appeared to reflect variation in specific cell types present within the tumors. The notion that developmental lineage has a pervasive influence on gene expression patterns is highlighted by the clustering pattern of the cultured cell lines. For example, the three lymphocyte cell lines comprise one branch, the two endothelial cell lines constitute another and the

15   mesenchymal cell lines form a third. Cell lines derived from two distinct types of breast epithelial cells (basal and luminal) also formed distinct dendrogram branches. Some of the prominent patterns of gene expression that appear to indicate the variable abundance of particular cell types within a tumor sample are summarized in the remainder of this Example.

20

(a) Endothelial cells: A subset of genes characteristically expressed by endothelial cells, including CD34, CD31 and von Willebrand Factor[36,37] were also strongly expressed in the two endothelial cell lines HUVEC and HMVEC. Variation among the tumor samples in the abundance of transcripts from this subset of genes may

25   therefore reflect variation in the vascularity or angiogenic activity within the tumors.

(b) Stromal cells: A previously characterized subset of genes that included multiple isoforms of collagen and other genes encoding extracellular matrix components, many of which are characteristically expressed by mesenchymal cells, showed significant variation in expression among the tumor samples[8,21].

30   (c) Adipose-Enriched/Normal Breast: A subset of genes that included fatty acid binding protein 4 and PPARγ may represent the presence of adipose cells in the tumor samples[38,39]. This subset of genes was most highly expressed in the three normal breast

samples. As we have no cell line guide for this cluster, the exact nature of the cell type underlying expression of these genes cannot be unequivocally determined.

(d) B-lymphocytes: Variation in expression of a subset of genes that were highly expressed in RPMI-8226 (a multiple myeloma-derived cell line), including many

5   immunoglobulin genes, appears to represent variable B-cell infiltration of the tumors. This interpretation was corroborated by immunohistochemistry)[8,21].

(e) T-lymphocytes: One subset of co-expressed genes included CD3, and two subunits of the T-cell receptor. Most of the genes in this subset were expressed at their highest levels in the T-cell leukemia derived cell line, MOLT-4. Variation in expression of

10   this subset of genes was therefore interpreted as representing variation in T-lymphocyte populations in the tumors. Immunohistochemical staining of tumor samples, using anti-CD3 antibodies, confirmed that tumors with the highest levels of expression of this subset of genes contained numerous CD3-positive lymphocytes (Figure 3b).

15   (f) Macrophages: A subset of genes that appeared to be markers of macrophage/monocyte populations included CD68, acid phosphatase 5, chitinase, and lysozyme. Interestingly, the transcripts for these genes were the most abundant in the three after chemotherapy tumor samples that clustered apart from their before counterparts (i.e. Norway 47, 61, and 101). These three tumors, all of which had

20   responded to the chemotherapy, were thus notable not only for an overall gene expression pattern resembling that of normal breast tissue, but also, for a particularly large population of macrophages, perhaps representing a secondary response to tumor necrosis.

(g) Basal and Luminal Epithelial Cells of the Mammary Duct, and Their Malignant

25   Counterparts: Two distinct kinds of epithelial cells are found in the adult human mammary gland, basal (and/or myoepithelial cells) and luminal epithelial cells[18,40]. These two cell types are conveniently distinguished immunohistochemically; basal epithelial cells can be stained with antibodies to keratin 5/6 (Figure 3c), while luminal epithelial cells stain with antibodies against keratins 8/18 (Figure 3c). Many genes

30   were expressed by one of these two cell lines, but not by the other. The gene expression subsets characteristic of basal epithelial cells included several genes that have previously been shown to play important roles in this cell type, e.g., keratin 5,

keratin 17, integrin-□4 and laminin[18]. The gene expression subset characteristic of luminal cells was anchored by the previously noted subset of transcription factors that included the estrogen receptor gene.

5   Example 8

Classification of Breast Tumors Using an Optimized Set of Genes Showing
Differential Expression Between Tumors

10   Methods and Rationale

As described in Examples 6 and 7, analysis of genes that are differentially expressed in breast tumor samples provides an indication of the relatedness of the samples and allows identification of samples taken from the same tumor or members of a tumor/metastasis pair. Such analysis further provides insight into specific tumor

15   properties such as variation in growth rate, activity of specific signaling pathways, and the cellular composition of the tumors. The subset of genes analyzed in Examples 6 and 7 was selected solely based upon the fact that genes in the subset were differentially expressed among the experimental samples. Recognizing that the choice of genes whose expression levels provide the basis for the ordering of the

20   tumor samples determines which phenotypic relationships among the tumors are reflected in the clustering patterns, applicants devised methods for selecting subsets of genes optimized to reflect phenotypic relationships among the tumors.

(i) Selection of an intrinsic gene subset

25   The rationale behind the first optimized gene subset was Applicants' recognition that specific features of a gene expression pattern that are to be used as the basis for classifying tumors should typify that tumor; that is, these features should be similar in any sample taken from the same tumor, and they should vary among different tumors. The 22 pairs of independent samples taken from 22 different tumors

30   provided an opportunity for the selection of genes that fulfill these criteria. To select a set of genes whose variation in expression optimally represented differences between tumors rather than just differences between tumor samples, a "within-

between" score was assigned to each gene equal to the mean effect of the gene on the pairwise correlation coefficients of the 22 matched tumor pairs less the mean effect of the gene on the remaining 210 tumor-tumor pairwise correlation coefficients. The "effect" of a gene on a pairwise correlation was defined as the difference in the

5   correlation coefficient with and without data for the gene included. Higher "within-between" scores indicated that the gene had a good tendency to group together paired samples.

The 496 genes with a score one standard deviation above the mean score were selected and defined as the "intrinsic" gene subset. To confirm the existence of an

10   "intrinsic" set of genes and to verify that the "within-between" score identified these genes, the predictive quality of the score was examined using a type of "leave-one-out" cross-validation analysis. The entire analysis was repeated 22 times, each with one of the 22 matched pairs completely removed from the analysis. If an "intrinsic" set of genes existed, and if the "within-between" score successfully identified these

15   genes, it was expected that the genes with high scores in each reduced dataset would produce relatively high correlations in the excluded pair. When the genes were sorted based on their "within-between" score in each reduced dataset, the correlation coefficient of the excluded matched pair in sliding windows of 250 genes increased progressively with increasing "within-between" score for nearly all of the matched

20   pairs, while no such increase was found when randomly matched pairs were used.

The clustering method was used as described above to cluster the experimental samples based on the gene expression patterns of the 496 genes included in the "intrinsic" gene subset.

25   (ii) Selection of an "epithelial-enriched" gene subset

A second optimized gene subset (called the "epithelial-enriched" gene subset) was selected consisting of 374 genes that Applicants considered likely to be expressed primarily by normal or malignant breast epithelial cells. The rationale for this gene subset is that each of the tumors was ultimately caused by alterations in breast

30   epithelial cells. The seven individual subsets of genes that were chosen to form the "epithelial-enriched" gene subset were selected from the 1753 gene cluster diagram.

The actual groups of genes chosen are listed in Table 7. These seven subsets of genes included:

1) A subset that was very highly expressed in the cultured basal cell lines, along with some of the other breast derived cell lines including Hs578T and BT-549;

5   2) A subset that was expressed in all of the cultured epithelial cell lines (both basal and luminal);

3) A subset of genes centered around the high level of expression of *Erb-B2*;

4) A subset of genes that contained genes known to be important for tumor biology (e.g., the urokinase receptor);

10   5) A subset that contained genes that were most highly expressed in the basal-like tumors;

6) A subset of genes highly expressed in some of the luminal-like tumors;

7) A subset of genes that was primarily expressed in the four breast carcinoma derived cell lines and/or in many of the luminal-like tumors.

15

The clustering method was used as described above to cluster the experimental samples based on the gene expression patterns of the 374 genes included in the "epithelial-enriched" gene set.

To confirm the results of the clustering analysis described below, a "weighted

20   voting"method was applied to the data as described in Golub, T.R., *et al.*, *Science*, 286, 531-537, 1999.

Results

The 496 genes included in the "intrinsic" gene set are identified in Table 6.

25   Two large branches were apparent in the tumor dendrogram that resulted from analysis based on this gene set, and within each of these two branches, smaller branches were identified for which common biological themes could be inferred. The branches are colored accordingly (basal-like = ORANGE, *Erb-B2* positive = PINK, normal breast-like = GREEN, and luminal epithelial-like = BLUE). Seventeen of the

30   20 before and after doxorubicin pairs (indicated with suffixes BE and AF following the numerical identifier for each tumor) were matched together on terminal dendrogram branches (red branches), as were both of the tumor/lymph node

metastasis pairs (blue branches). The small black bars beneath the dendrogram identify the 17 pairs that were correctly matched by this hierarchical clustering, while the larger green bars identify the positions of the three pairs that were not matched by the clustering. It is noted that the after-chemotherapy sample in each of these three

5   sample pairs was clustered in a branch with normal breast tissue samples. Thus as for the 1753 gene set described in Examples 6 and 7, the intrinsic gene subset correctly identified independent tumor samples from the same tumor as related to each other. Despite the potential confounding effects of an interval of 16 weeks, independent surgical procedures and cytotoxic chemotherapy, the independent samples taken from

10   the same tumor were in most cases recognizably more similar to each other in their overall pattern of gene expression than either was to any of the other samples. In addition, samples taken from a primary tumor and a metastasis from the same tumor could be recognized as closely related to one another. Thus in most cases independent samples from the same tumor were recognizable as such solely on the basis of gene

15   expression patterns. This implies that the patterns of gene expression are homogeneous and stable in each breast tumor and yet sufficiently diverse between tumors so that they can be viewed as molecular portraits of each tumor.

The 374 genes included in the "epithelial-enriched" subset are listed in Table 8. Figure 2 presents a comparison of tumor dendrograms representing the results of

20   hierarchical clustering of experimental samples using the "intrinsic" gene set and the dendrogram obtained by clustering using the "epithelial-enriched" gene set. The dendrograms are colored according to the clustering patterns obtained using the "intrinsic" gene set. Only two tumors (identified by the colored arrows) were placed in significantly different groups when the clustering was based on expression of the

25   "epithelial-enriched" gene set instead of the "intrinsic" gene set.

The overall architecture of the two dendrograms representing the clustering of breast tumor samples using these two alternative gene sets was very similar, with only two tumor pairs (i.e. Norway 14 and 26) materially changing position (Figure 2). Thus, the classifications derived from the "intrinsic" gene set are consistent with the

30   results using the "epithelial-enriched" gene set, even though the two sets shared only 25% of their genes.

A consistent division of the tumor samples into two subgroups was a striking

feature of the dendrograms produced by both gene sets. Application of the "weighted

voting" method of Golub recapitulated the sorting of the tissue samples between these

two subgroups for all but one of the 65 samples, thus confirming the robustness of the

5   division.

Example 9

Identification of Breast Tumor Subgroups Based on Optimized Gene Sets

10   Several groups of tumors that shared pervasive similarities in their expression

patterns could be identified by cluster analysis; the dendrograms in Figure 2 are color-

coded to highlight these subgroups. Characteristic features of the expression patterns,

or the membership, of each highlighted group also suggested biological

interpretations. These data confirm the ability of the clustering method to divide

15   breast tumors into meaningful subgroups when applied using the "intrinsic" and

"epithelial-enriched" gene subsets. Specific subgroups are discussed below and are

named according to correlations between the genes expressed at high levels in the

tumors and genes known to be expressed in particular cell types.

Luminal Epithelial Cell Pattern: As described above, the major distinction was

20   between a large group of tumors (identified by blue letters and dendrogram branches)

and a second large group that included all of the other tumor subtypes and the normal

breast samples (highlighted in other colors). The tumors in this "blue" group were

characterized by relatively high levels of expression of many genes known to be

expressed by the luminal epithelial cells of the normal mammary duct, notably

25   including the estrogen and prolactin receptors. This connection was further

corroborated using immunohistochemical analysis of breast tumor sections using

antibodies against the luminal cell keratins 8/18, which stained the carcinoma cells in

tumor specimens in this "blue" branch as shown, for example, in Figure 3f. With one

exception, none of the tumors in this group expressed Erb-B2 at high levels. An

30   estrogen receptor-positive phenotype is known to be associated with a relatively

favorable prognosis [30, 31], while Erb-B2 expression is believed to contribute to

tumorogenesis.

Normal Breast Tissue Pattern: Several tumors, including two "before and after" pairs and the single fibroadenoma tested (displayed in green), were clustered in a group of samples that contained all three of the normal breast specimens. The "normal breast" gene expression pattern was typified by a relatively high level of expression of genes

5   characteristic of basal epithelial cells and adipose cells, and relatively low levels of expression of genes characteristic of luminal epithelial cells.

Basal Epithelial Cell Pattern: Many of the genes characteristic of basal epithelial cells were highly expressed in a group of six tumors (New York 2 and 3, Stanford 14 and 23, and Norway 41 and 109, indicated in orange in the dendrogram, that were

10   clustered based on pervasive similarities in their gene expression patterns. To corroborate the "basal cell-like" characteristics of these tumors, immunohistochemistry was performed using antibodies against keratins 5/6, 8/18, and 17. All six of these tumors showed staining for either keratins 5/6 and/or 17 (basal cell keratins), and no staining for keratins 8/18 (See Figure 3e.) Notably, these six tumors

15   also failed to express the estrogen receptor and most of the other genes that were usually co-expressed with it. Approximately 90% of breast tumors are suggested to have characteristics of luminal epithelial cells, while the characteristics of the remaining 10% are less well defined[18]. Breast tumors that stain positive for basal cell keratins may account for 3-15% of all breast tumors [41-46].

20   The incidence among the tumor samples described herein was 15% (6/40). Many of the tumors that stained positive for basal cell keratins only showed staining in a fraction of the tumor cells, and neither basal nor luminal keratins could be detected in any of the other remaining tumor cells (Figure 3e).

25   Erb-B2 Positive: As mentioned above, overexpression of the Erb-B2 oncogene was associated with a high level of expression of a specific set of genes, almost all of which map to the Erb-B2 region of chromosome 17[33]. A clustered group of tumors was identified that was partially characterized by the high level of expression of this subset of genes (Stanford 2 and Norway 47, 53, 57 and 101). These tumors showed

30   low levels of expression of the estrogen receptor[48,49] and almost all of the other genes associated with estrogen receptor expression, a trait they share with the "basal-like" tumors, and which may contribute to the poor prognosis associated with these two

84

subtypes of breast tumors[41,43,49,50]; in addition, both the basal-like and *Erb-B2* positive tumors also show many *p53* sequence mutations (see Table 5).

Example 10

Producing Antibodies to Basal Marker Polypeptides and Cytokeratin 17

This example describes the generation of polyclonal antibodies that bind to cytokeratin 17 and the generation of polyclonal antibodies that bind to the polypeptides encoded by the three basal marker genes described herein, i.e., cadherin3, matrix metalloproteinase 14, and cadherin EGF LAG seven-pass G-type receptor 2 : The example further describes affinity purification of the antibodies.

Materials

- Anisole (Cat. No. A4405, Sigma)
- 2,2'-azino-di-(3-ethyl-benzthiazoline-sulfonic acid) (ABTS) (Cat. No. A6499, Molecular Probes Eugene, OR)
- Activated Maleimide Keyhole Limpet Cyanin (Cat. No. 77106, Pierce Chemical Co. Rockford, IL)
- Biotin (Cat. No. B2643, Sigma)
- Boric acid (Cat. No. B0252, Sigma)
- Sepharose 4b (Cat. No. 17-0120-01, LKB/Pharmacia, Uppsala, Sweden)
- Bovine Serum Albumin (LP) (Cat. No. 100 350, Boehringer Mannheim, Indianapolis, IN)
- Cyanogen bromide (Cat. No. C6388 Sigma, St. Louis, MO)
- Dialysis tubing Spectra/Por Membrane MWCO: 6-8,000 (Cat. No. 132 665, Spectrum Industries Inc., Laguna Hills, CA)
- Dimethyl formamide (DMF) (Cat. No. 22705-6, Aldrich Chemical Company, Milwaukee, WI)
- DIC (Cat. No. BP 592-500, Fisher)
- Ethanedithiol (Cat. No. 39,802-0, Aldrich Chemicals, Milwaukee, WI)
- Ether (Cat. No. TX 1275-3, EM Sciences)
- Ethylenediaminetetraacetatic acid (EDTA)(Cat No. BP 120-1, Fisher Scientific, Springfield, NJ)

- 1-ethyl-3-(3'dimethylaminopropyl)-carbodiimide, HCL (EDC) (Cat No. 341-006, Calbiochem, San Diego, CA)
- Freund's Adjuvant, complete (Cat. No. M-0638-50B, Lee Laboratories, Grayson, GA)

5
- Freund's Adjuvant, incomplete (Cat. No. M0639-50B, Lee Laboratories)
- Fritted chromatography columns (Column part No. 12131011; Frit: Part No. 12131029, Varian Sample Preparation Products, Harbor City, CA)
- Gelatin from Bovine Skin (Cat. No. G9382, Sigma)
- Glycine (Cat. No. BP381-5, Fisher)

10
- Goat anti-rabbit IgG, biotinylated (Cat No. A 0418, Sigma)
- HOBt (Cat. No. 01-62-0008, Calbiochem-Novabiochem)
- Horseradish peroxidase (HRP) (Cat. No. 814 393, Boehringer Mannheim)
- HRP-Streptavidin (Cat. No. S 5512, Sigma)
- Hydrochloric Acid (Cat No. 71445-500, Fisher)

15
- Hydrogen Peroxide 30% w/w (Cat. No. H1009, Sigma)
- Methanol (Cat. No. A412-20, Fisher)
- Microtiter plates, 96 well (Cat. No. 2595, Corning-Costar Pleasanton, CA)
- N-□-Fmoc protected amino acids available from Calbiochem-Novabiochem, San Diego, CA. See 1997-1998 catalog pages 1-45.

20
- N-□-Fmoc protected amino acids attached to Wang Resin available from Calbiochem-Novabiochem. See 1997-1998 catalog pages 161-164.
- NMP (Cat. No. CAS 872-50-4, Burdick and Jackson, Muskegon, MI)
- Peptide (Synthesized by Research Genetics, Inc. Details given below)
- Piperidine (Cat. No. 80640, Fluka, available through Sigma)

25
- Sodium Bicarbonate (Cat. No. BP328-1, Fisher)
- Sodium Borate (Cat. No. B9876, Sigma)
- Sodium Carbonate (Cat. No. BP357-1, Fisher)
- Sodium Chloride (Cat. No. BP 358-10, Fisher)
- Sodium Hydroxide (Cat. No. SS 255-1, Fisher)

30
- Streptavidin (Cat. No. 1 520, Boehringer Mannheim)
- Thioanisole (Cat. No. T-2765, Sigma)
- Trifluoroacetic acid (Cat. No. TX 1275-3, EM Sciences)

- Tween-20 (Cat. No. BP 337-500, Fisher)

- Wetbox-(Rubbermaid Rectangular Servin' Saver™ Part No. 3862 Wooster, OH)

Solutions

5   • BBS - Borate Buffered Saline with EDTA dissolved in distilled water (pH 8.2 to 8.4 with HCl or NaOH)

     -25 mM Sodium borate (Borax)

     -100 mM Boric Acid

     -75 mM NaCl

10   -5 mM EDTA

- 0.1 N HCl in saline

     -concentrated HCl (8.3 mL/0.917 L distilled water)

     -0.154 M NaCl

- Glycine (pH 2.0 and pH 3.0) dissolved in distilled water and adjusted to the

15   desired pH.

     -0.1 M glycine

     -0.154 M NaCl

- 5X Borate 1X Sodium Chloride dissolved in distilled water.

     -0.11 M NaCl

20   -60 mM Sodium Borate

     -250 mM Boric Acid

- Substrate Buffer in distilled water adjusted to pH 4.0 with sodium hydroxide:

     -50 to 100 mM Citric Acid

25   Peptide Synthesis Solutions

- AA solution: HOBt is dissolved in NMP (8.8 grams HOBt to 1 liter NMP). Fmoc-N-a-amino at a concentration at .53 M.

- DIC solution: 1 part DIC to 3 parts NMP.

- Deprotecting solution: 1 part Piperidine to 3 parts DMF

30   • Reagent R: 2 parts anisole, 3 parts ethanedithiol, 5 parts thioanisole, 90 parts trifluoroacetic acid.

Equipment

- MRX Plate Reader (Dynatech Inc., Chantilly, VA)
- Hamilton Eclipse (Hamilton Instruments, Reno, NV)
- Beckman TJ-6 Centrifuge, Refrigerated (Model No. TJ-6, Beckman Instruments,

5   Fullerton, CA)

- Chart Recorder (Recorder 1 Part No. 18-1001-40, Pharmacia LKB Biotechnology)
- UV Monitor (Uvicord SII Part No. 18-1004-50, Pharmacia LKB Biotechnology)
- Amicon Stirred Cell Concentrator (Model 8400, Amicon Inc., Beverly, MA)
- 30 kD MW cut-off filter (Cat. No. YM-30 Membranes Cat. No. 13742, Amicon

10   Inc., Beverly, MA)

- Multi-channel Automated Pipettor (Cat. No. 4880, Corning Costar Inc.,

    Cambridge, MA)

- pH Meter Corning 240 (Corning Science Products, Corning Glassworks, Corning,

NY)

15 • ACT396 peptide synthesizer (Advanced ChemTech, Louisville, KY)

- Vacuum dryer (Box is from Labconco, Kansas City, MO; Pump is from Alcatel,

    Laurel MD).

- Lyophilizer (Unitop 600sl in tandem with Freezemobile 12, both from Virtis,

    Gardiner, NY)

20

Methods

        Peptides were selected using the program Omiga ™1.1 (Oxford Molecular

Group, Inc., 2105 So. Bascom Ave., Suite 200, Campbell, CA 95008) using the

Hopp/Woods method, which is described in Hopp TP, Woods KR, *Mol Immunol,*

25   Apr;20(4):483-9 A computer program for predicting protein antigenic determinants,

1983, and Hopp TP and Woods KR, *Proc. Nat. Acad. Sci.* U.S.A. 78, 3824-3828,

1981. Preferred peptide sequences displayed minimal homology with known

proteins. Three peptide sequences were selected for each polypeptide. The sequences

were as follows:

30

Peptides for antibodies that bind to cadherin3 (GenBank accession number

NP_001784):

RAVFREAEVTLEAGGAEQE (SEQ ID NO:4)

QEPALFSTDNDDFTVRN (SEQ ID NO:5)

QKYEAHVPENAVGHE (SEQ ID NO:6)

5

Peptides for antibodies that bind to matrix metalloproteinase 14 (GenBank accession number NP_004986):

10　　AYIREGHEKQADIMIFFAE (SEQ ID NO:7)

DEASLEPGYPKHIKELGR (SEQ ID NO:8)

RGSFMGSDEVFTYFYK (SEQ ID NO:9)

15　　Peptides for antibodies that bind to anti-cadherin EGF LAG seven-pass G-type receptor 2 (GenBank accession number NP_001399):

QASSLRLEPGRANDGDWH (SEQ ID NO:10)

ELKGFAERLQRNESGLDSGR (SEQ ID NO:11)

20　　RSGKSQPSYIPFLLREE (SEQ ID NO:12)

Peptides for antibodies that bind to anti-cytokeratin17:

25　　KKEPVTTRQVRTIVEE (SEQ ID NO:13)

QDGKVISSREQVHQTTR (SEQ ID NO:14)

SSSIKGSSGLGGGSS (SEQ ID NO:15)

Synthesis of Peptides

30　　Incubate: Resin was immersed in appropriate solution. All incubation steps occured with mixing.

Wash: Added 2 mls. DMF, incubated 5 minutes and drained.

Wash Cycle: Five washes.

Machine Synthesis

The sequence of the desired peptide was provided to the peptide synthesizer. The C-

5   terminal residue was determined and the appropriate Wang Resin was attached to the

reaction vessel. The peptides were synthesized C-terminus to N-terminus by adding

one amino acid at a time using a synthesis cycle. Which amino acid is added was

controlled by the peptide synthesizer, which looks to sequence of the peptide entered

into its database.

10

Step 1 – Resin Swelling: Added 2 mL DMF, incubated 30 minutes, drained DMF.

Step 2 – Synthesis cycle

        2a – Deprotection: 1 mL deprotecting solution was added to the reaction

            vessel and incubated for 20 minutes.

15   2b – Wash Cycle

        2c – Coupling: 750 mL of amino acid solution and 250 mL of DIC solution

            were added to the reaction vessel. The reaction vessel was incubated for

            thirty minutes and washed once. The coupling step was repeated once.

        2d – Wash Cycle

20 Step 2 was repeated over the length of the peptide. The amino acid solution changed

as the sequence listed in peptide synthesizer dictated.

Step 3 – Final Deprotection: Steps 2a and 2b were performed one last time.

Resins were deswelled in methanol—rinsed twice in 5 mL methanol, incubated 5

25 minutes in 5 mL methanol, rinsed in 5 mL methanol—and then vacuum dried.

Peptide was removed from the resin by incubating 2 hours in reagent R and then

precipitated into ether. Peptide was washed in ether and then vacuum dried. Peptide

was resolubilized in diH20, frozen, and lyophilized overnight.

30

Conjugation of Peptide with Keyhole Limpet Hemocyanin

Peptide (6 mg) was dissolved in PBS (6 mL) and mixed with 6 mg of maleiimide

activated KLH carrier in 6 mL of PBS for a total volume of 12 mL. The entire
solution was mixed for two hours, dialyzed in 1L PBS, and lyophilized.

Immunization of Rabbits

5   Two New Zealand White Rabbits were injected with 250 μg keyhole limpet
hemocyanin (KLH) conjugated peptide in an equal volume of complete Freund's
adjuvant and saline in a total volume of 1 mL. Antigens (KLH-Peptide, 100 μg each)
in an equal volume of incomplete Freund's Adjuvant and saline were injected into
three to four subcutaneous dorsal sites for a total volume of 1 mL two, four, and six
10   weeks after the first immunization. The three peptides were injected together.

The immunization schedule was as follows:

Day 0	Pre-immune bleed, primary immunization
Day 15	1st Boost
Day 27	1st Bleed
Day 44	2nd Boost
Day 57	2nd Bleed and 3rd Boost
Day 69	3rd Bleed
Day 84	4th boost
Day 98	4th bleed

15   The Collection of Rabbit Serum

The rabbits were bled (30 to 50 mL) from the auricular artery. The blood was allowed
to clot at room temperature for 15 minutes and the serum was separated from the clot
using an IEC DPR-6000 centrifuge at 5000 x g. Cell-free serum was decanted gently
into a clean test tube and stored at -20°C for affinity purification.

20

Determination of Antibody Titer

All solutions with the exception of wash solution were added by the Hamilton
Eclipse, a liquid handling dispenser. The antibody titer was determined in the rabbits
using an ELISA assay with peptide on the solid phase. Flexible high binding ELISA

plates were passively coated with peptide diluted in BBS (100 µL, 1 µg/well) and the
plate was incubated at 4°C in a wetbox overnight (air-tight container with moistened
cotton balls). The plates were emptied and then washed three times with BBS
containing 0.1% Tween-20 (BBS-TW) by repeated filling and emptying using a semi-
5   automated plate washer. The plates were blocked by completely filling each well with
BBS-TW containing 1% BSA and 0.1% gelatin (BBS-TW-BG) and incubating for 2
hours at room temperature. The plates were emptied and sera of both pre- and post-
immune serum were added to wells. The first well contained sera at 1:50 in BBS.
The sera were then serially titrated eleven more times across the plate at a ratio of 1:1
10   for a final (twelfth) dilution of 1:204,800. The plates were incubated overnight at
4°C. The plates were emptied and washed three times as described.

Biotinylated goat anti-rabbit IgG (100 µL) was added to each microtiter plate test well
and incubated for four hours at room temperature. The plates were emptied and
15   washed three times. Horseradish peroxidase-conjugated Streptavidin (100 µL diluted
1:10,000 in BBS-TW-BG) was added to each well and incubated for two hours at
room temperature. The plates were emptied and washed three times. The ABTS was
prepared fresh from stock by combining 10 mL of citrate buffer (0.1 M at pH 4.0), 0.2
mL of the stock solution (15 mg/mL in water) and 10 µL of 30% H_2O_2. The ABTS
20   solution (100µL) was added to each well and incubated at room temperature. The
plates were read at 414 λ, 20 minutes following the addition of substrate.

Preparation of the Peptide Affinity Purification Column:

The affinity column was prepared by conjugating 5 mg of peptide to 10 mL of
25   cyanogen bromide-activated Sepharose 4B, and 5 mg of peptide to hydrazine-
Sepharose 4B. Briefly, 100 uL of DMF was added to peptide (5 mg) and the mixture
was vortexed until the contents were completely wetted. Water was then added (900
µL) and the contents were vortexed until the peptide dissolved. Half of the dissolved
peptide (500 µL) was added to separate tubes containing 10 mL of cyanogen-bromide
30   activated sepharose 4B in 0.1 mL of borate buffered saline at pH 8.4 (BBS), and 10
mL of hydrazine-Sepharose 4B in 0.1 M carbonate buffer adjusted to pH 4.5 using
excess EDC in citrate buffer pH 6.0. The conjugation reactions were allowed to

proceed overnight at room temperature. The conjugated sepharose was pooled and
loaded onto fritted columns, washed with 10 mL of BBS, blocked with 10 mL of 1 M
glycine, and washed with 10 mL 0.1 M glycine adjusted to pH 2.5 with HCl and re-
neutralized in BBS. The column was washed with enough volume for the optical

5   density at 280λ to reach baseline.

The Affinity Purification of Antibodies

The peptide affinity column was attached to a UV monitor and chart recorder.

10·   The titered rabbit antiserum was thawed and pooled. The serum was diluted with one
volume of BBS and allowed to flow through the columns at 10 mL per minute. The
non-peptide immunoglobulins and other proteins were washed from the column with
excess BBS until the optical density at 280 λ reached baseline. The columns were
disconnected and the affinity purified column was eluted using a stepwise pH gradient

15   from pH 7.0 to pH 1.0. The elution was monitored at 280 nM, and fractions
containing antibody (pH 3.0 to pH 1.0) were collected directly into excess 0.5 M
BBS. Excess buffer (0.5 M BBS) in the collection tubes served to neutralize the
antibodies collected in the acidic fractions of the pH gradient.

20   The entire procedure was repeated with "depleted" serum to ensure maximal recovery
of antibodies. The eluted material was concentrated using a stirred cell apparatus and
a membrane with a molecular weight cutoff of 30 kD. The concentration of the final
preparation was determined using an optical density reading at 280 nM. The
concentration was determined using the following formula: mg/mL = OD_{280}/1.4.

25

Example 11

SDS-PAGE and Immunoblot Analysis of Basal Marker Polypeptides

To investigate the expression pattern of cadherin3, matrix metalloproteinase

30   14, and cadherin EGF LAG seven-pass G-type receptor 2 , extracts were made from a
variety of different cell lines and subjected to SDS-PAGE followed by

93

immunoblotting according to the protocol below, using affinity purified polyclonal antibody to BSTP-ECG1 prepared as described in Example 10.

<u>Materials</u>

- Acetic acid, Glacial (Cat. No. A38ᶜ-212, Fisher)

5
- Acrylamide (Cat. No. A-3553, Sigma)

- Anti-Rabbit IgG (H&L) (Cat. No. 31460ZZ, Pierce)

- Bis-acrylamide (Cat. No. M-7279, Sigma)

- Blotting paper (Cat. No. 170-3960, Bio-Rad, Hercules, CA)

- Bovine Serum Albumin (LP) (Cat. No. 100-350, Boehringer Mannheim,

10   Indianapolis, IN)

- Brilliant Blue R-250 (Cat. No. BP101-25, Fisher)

- Complete™ Mini (Cat. No. 1836153, Boehringer Mannheim)

- ECL Western Blotting Detection Reagents (Cat. No. RPN2106, Amersham Pharmacia Biotech, Piscataway, NJ)

15
- Ethyl alcohol (AAPER Alcohol and Paper Chemical Co., Shelbyville, KY)

- Gelplate Clean (Cat. No. 786-140RF, Geno Technology, Inc., St. Louis)

- Gelatin (Cat. No. G-2500, Sigma)

- Glycerol (Cat. No. BP229-1, Fisher)

- Glycine (Cat. No. G-8898, Sigma)

20
- Hybond ECL (Cat. No. RPN303D, Amersham Pharmacia Biotech)

- Lauryl Sulfate (SDS) (Cat. No. L-3771, Sigma)

- Methanol (Cat. No. BP1105-4, Fisher)

- M-Per (Cat. No. 78501, Pierce, Rockford, IL)

- Nalgene bottle top filters (Cat. No. 09-740-62B, Fisher)

25
- Nonfat dry milk (Kroger Co., Cincinnati, OH)

- Ponceau-S (Cat. No. P-07170, Sigma)

- Potassium phosphate (Cat. No. P-0662, Sigma)

- 2X SDS gel loading buffer (Cat. No. 750006, Research Genetics, Huntsville, AL)

- Size markers (Cat. No. M-3913, M-4038, M-3788, Sigma)

30
- Sodium azide (Cat. No. S2271-25, Fish)

- Sodium chloride (Cat. No. S271-3, Fisher)

- Sodium phosphate, Dibasic, Anhydrous (Cat. No. BP332-1, Fisher)

- t-amyl alcohol (Cat. No. A-16852, Sigma)
- TEMED (Cat. No. T-9281, Sigma)
- Trizma® Base (Cat. No. T-6066, Sigma)
- Tween-20 (Cat. No. BP337-500, Fisher)

5

Solutions

- PBS – Phosphate Buffered Saline dissolved in distilled water

  -136 mM NaCl

  -2.7 mM KCl

10   -10.1 mM Na_2HPO_4

  -1.8 mM KH_2PO_4

- Acrylamide/Bis (30% T, 2.67% C) dissolved in distilled water

  -4.1 M acrylamide

  -51.9 mM N,N'-

15 • 1.5 M Tris-HCl (pH 8.8) dissolved in distilled water

- 0.5 M Tris-HCl (pH 6.8) dissolved in distilled water

- 10% SDS – dissolve 10 grams SDS in 100 mls distilled water

- Running Buffer

  -24.8 mM Tris base

20   -191.9 mM glycine

  -3.5 mM SDS

- Towbin transfer buffer (pH 8.3) dissolved in distilled water

  -20% methanol

  -25 mM Tris

25   -192 mM glycine

- Equilibrating buffer for gel drying, mixed in distilled water

  -20% ethanol

  -10% glycerol

- Gel staining solution dissolved in distilled water

30   -0.3 mM Coomassie brilliant blue R-250

  -40% methanol

  -7% glacial acetic acid

- Gel destaining solution mixed in distilled water

  -25% methanol

  -7% glacial acetic acid

- 10% Tween®20 in PBS

5   - 5% Nonfat dry milk in PBS

- 0.2% BSA Blocking Buffer dissolved in PBS

  -0.2% BSA

  -0.1% gelatin

  -0.05% Tween®20

10   - Wash Buffer

  -0.05% Tween®20

  -1X PBS

Equipment

- Microcentrifuge (Model 5415, Eppendorf)

15   - Power Pak 200 (Cat. No. 165-5052, Bio-Rad)

- Power Pak 3000 (Cat. No. 165-5056, Bio-Rad)

- Protean II xi Cell (Cat. No. 165-1813, Bio-Rad)

- Recirculating chiller (Cat. No. CFT33D115V, Neslab Instruments, Inc.,

  Portsmouth, NH)

20   - 20-Well comb (Cat. No. 165-1867, Bio-Rad)

- pH Meter Corning 240 (Corning Science Products, Corning Glasswares, Corning,

  NY)

- Air Cadet vacuum pump (Cat. No. P-07530-50, Cole-Palmer Instruments Co.,

  Chicago, IL)

25   - Tissue Tearor tissue homogenizer (Cat. No. 985370-07, BioSpec Products Inc.,

  Bartletsville, OK)

Methods

Sample Preparation

30   The following cell lines were used: 184B5, MCF7, OVCAR3, UACC62,

HepG2, Colo205, UACC62, JURKAT, N-TERA2, MOLT4, Sw872. These cell lines

are well known in the art. Descriptions of these cell lines are provided in Table 3, in

Perou, et al., Molecular portraits of human breast tumours, *Nature*, 406(6797):747-52, 2000, in Ross, D. T. et al. Systematic Variation in Gene Expression Patterns in Human Cancer Cell Lines. Nature Genetics, 24(3):227-35, 2000, and at the American Type Culture Collection Web site: http://www.atcc.org. Cell lines were maintained

5   under standard growth conditions and in standard tissue culture media as appropriate for the particular cell line. Cells were collected according to standard techniques (e.g., trypsinization in the case of adherent cells), and the resulting cell suspension was prepared as follows:

-The cell suspension was pelleted by centrifugation at 3000 RPM for 10 minutes, and

10   the supernatant was discarded.

-The pellet was washed with 1ml PBS, centrifuged at 10000 RPM for 10 minutes, and the supernatant was discarded.

-An appropriate volume of M-Per™ Reagent was added to the cell pellet and mixed gently for 10 minutes in an ice bath. The mixture was centrifuged at 13200 RPM for

15   15 minutes, and the supernatant was saved.

The protein concentration in the supernatant was measured according to standard techniques.

All samples were mixed at 1:1 with gel loading buffer and boiled for 5 minutes before loading.

20

SDS PAGE

Standard SDS-PAGE stacking and running gels were prepared and placed in an electrophoresis apparatus. After filling the upper and lower chambers with running buffers the samples (60 □g/lane) were loaded. The inner core was placed in the lower

25   chamber and the lid placed on top. The apparatus was connected to the power supply and recirculating system. The temperature setting was10°C. The stacking gel was run at 14mA per gel for 1 hour. The separating gel was run at 0.58mA per gel per hour for 16 hours.

30   Transfer to nitrocellulose

After electrophoresis was complete, the gel was equilibrated in Towbin Buffer for 15-30 minutes. The assembly for transfer was as follows:

cathode

pre-soaked blotting paper

gel

pre-wetted nitrocellulose

5   pre-soaked blotting paper

anode

The transfer was performed at 20V for 25 minutes, then 25V for 20 minutes. After

the transfer was complete, the gel was stained with Coomassie and the blot was

stained with Ponceau-S.

10

Western Blotting

Primary and secondary antibodies

All primary and secondary antibodies were diluted in 0.2% BSA blocking buffer. All

incubation steps were done with gentle mixing.

15   Blots were blocked in 5% milk overnight at room temperature. The blots were rinsed

with wash buffer before adding the primary antibody and incubating for two hours at

room temperature. The primary antibodies were used at titers of 1:200, 1:500, and

1:1000 for anti-matrix metalloproteinase 14 and anti-cadherin EGF LAG seven-pass

G-type receptor 2 and at 1:100 for anti-cadherin3.

20   One wash cycle was performed. One wash cycle consisted of:

Wash 5 min, rinse

Wash 5 min, rinse

Wash 10 min, rinse

Wash 5 min, rinse

25   Wash 5 min, rinse

The secondary antibody was added and incubated for one hour at room temperature.

One wash cycle was then performed.

Peptide Block

30   As a control to demonstrate the specificity of the antibody, in some experiments equal

amounts (w/w) of peptide and antibody were added to 1/10 of the final volume of

blocking buffer and incubated overnight at 4°C. The volume of blocking buffer was

then brought up to the final volume, and the membrane was incubated for an additional two hours at room temperature.

Developing

5   The blots were placed in a Ziploc® bag. Equal volumes of ECL western blotting detection reagents were mixed and distributed evenly over the blots. The blots were placed in an autoradiography cassette, covered with a piece of film, and exposed.

Results

10   Figure 4A shows a Western blot demonstrating expression of the cadherin3 polypeptide in various cell lines. The lane order is, from left to right: MCF-7, Colo205, UACC62, JURKAT, HEPG2, N-TERA2, MOLT4, Sw872. The primary antibody was used at a dilution of 1:100.

          Figure 4B shows a Western blot demonstrating expression of the matrix
15   metalloproteinase 14 polypeptide in various cell lines. The lane order is, from left to right: 184B5, MCF7, OVCAR3, UACC62, HepG2. The three images present identical blots in which the primary antibody was used at dilutions of 1:200 (left), 1:500 (middle), and 1:1000 (right).

          Figure 4C shows a Western blot demonstrating expression of the cadherin
20   EGF LAG seven-pass G-type receptor 2 polypeptide in various cell lines. The lane order is, from left to right: 184B5, MCF7, OVCAR3, UACC62, HepG2. The three images present identical blots in which the primary antibody was used at dilutions of 1:200 (left), 1:500 (middle), and 1:1000 (right).

          For all three antibodies, the Western blots demonstrated that the antibodies
25   bind to a polypeptide of the expected size. All of the basal marker polypeptides are expressed in a range of different cell types. While not wishing to be bound by any theory, inventors postulate that basal cells in tissues other than breast may express the basal marker genes, which may make them useful for identification of basal tumor subclasses for tumors other than breast tumors.

30

Example 12

Immunohistochemical Staining of Breast Tumor Arrays with Antibodies to

Cytokeratin 17 Demonstrates that Cytokeratin 17 Expression Correlates with Poor

Outcome

Materials and Methods

5   Tissue arrays.

A total of 611 different paraffin embedded breast carcinoma samples were

identified in the files in the Department of Pathology at the University of Basel,

Women's hospital Rheinfelden, and the Kreiskrankenhaus Lorrach. The specimens

were obtained from patients who underwent surgery in the period between 1985 and

10   1994. The histologic parameters for all cases were reviewed by a single pathologist

(JT) and the histologic type and grade was determined for each case according to

Elston and Ellis Elston CW, Ellis IO: Pathological prognostic factors in breast cancer.

I. The value of histological grade in breast cancer: experience from a large study with

long-term follow-up. *Histopathology* 1991, 19:403-10.

15   Follow-up was obtained for 553 cases and ranged from 1 to 151 months with a

mean of 65.9 months. The use of these specimens and data for research purposes was

approved by the Ethics Committee of the Basel University Hospital. Tissue arrays

were constructed by obtaining 0.6 mm diameter tissue cores from each tumor and

placing these cores in a new paraffin block in rows and columns as described in

20   Kononen J, Bubendorf L, Kallioniemi A, Barlund M, Schraml P, Leighton S, Torhorst

J, Mihatsch MJ, Sauter G, Kallioniemi OP: Tissue microarrays for high-throughput

molecular profiling of tumor specimens [see comments]. *Nat Med* 1998, 4:844-7 and

in Schraml P, Kononen J, Bubendorf L, Moch H, Bissig H, Nocito A, Mihatsch MJ,

Kallioniemi OP, Sauter G: Tissue microarrays for gene amplification surveys in many

25   different tumor types. *Clin Cancer Res* 1999, 5:1966-75.

Each of the 611 cases was sampled twice, once from the center of the tumor,

and once from the periphery of the mass. Cores taken from the central area from each

case were combined in one array and cores taken from the periphery of the tumor

were combined in the other array.

30

Immunohistochemistry and scoring.

Double staining of normal breast epithelium in conventional paraffin sections

was performed by first staining lumenal cells with CAM5.2 using alkaline

phosphatase/fast blue staining and subsequently staining basal cells with CK17 using

horse radish peroxidase/DAB staining.

Sections of arrays were stained with monoclonal antibodies specific for

5   cytokeratin 17 (DAKO, clone E3, dilution 1:10) and cytokeratin 5/6 (Boehringer

Mannheim, dilution 1:10) after antigen retrieval by microwaving in citrate buffer.

Note that the anti-cytokeratin 5/6 antibody used herein detects both cytokeratins 5 and

6.   However, cytokeratin 5 is likely to be the major antigen recognized by this

antibody in breast basal cells. Staining results were scored as follows: 1 = invasive

10   tumor cells present in tissue core and no staining seen; 2 = invasive tumor cells

present and weak staining; 3 = invasive tumor cells present with strong staining. Only

those cores containing tissue consistent with a diagnosis of invasive carcinoma were

included in the outcome analysis. Cases that either had no tissue present on the array

sections or cases in which the material sampled consisted of fat, fibrosis, normal

15   breast glands, or in-situ carcinoma only, were omitted from further analysis.

Cytokeratins often showed only focal staining of tumor cells within the tissue array

cores or conventional paraffin sections. To account for the focal expression of CK17

and CK5/6, each of the 612 breast tumors was analyzed 4 times: with anti-CK17 and

anti-CK5/6 antibody on the "central sample" array, and with anti-CK17 and anti-

20   CK5/6 antibody on the "peripheral sample" array. A breast tumor sample was scored

as staining positive for the keratins if infiltrating carcinoma in one or more of the

cores from that sample reacted with either of the antibodies.

To aid in recognizing infiltrating carcinoma in the core samples, sections of

each array were also stained with an anti-cytokeratin antibody mix reacting with

25   cytokeratins 8 and 18 (CAM5.2, Becton & Dickinson, dilution 1:20) after antigen

unmasking by trypsin digestion to highlight invasive carcinoma cells.

Statistical analysis

Univariate survival analysis based upon gene expression defined subgroups of

30   patients was performed by Kaplan-Meier statistics using WinSTAT software

(www.winstat.com). Subsequent multivariate analyses were performed using Cox's

proportional hazards model for survival data (Cox: Regression models and life tables.

Journal Royal Statistical Society 1972, 74:187-220).

<u>Results</u>

<u>Basal keratin staining in normal breast and breast carcinoma.</u>

5   In normal breast, antibodies that bind to cytokeratin17 (CK17) and cytokeratin

5/6 (CK5/6) stain the basal layer of breast glandular epithelium while antibodies that

bind to cytokeratins 8 and 18 stain lumenal cells (figures 3C and 3D). Whole paraffin

sections of breast carcinoma showed that cytokeratin 17 and 5/6 expression in paraffin

embedded tissue when present was focal (Figures 3E and 3F) with often less than 10%

10   of tumor cells reacting. In an attempt to study further the focal reactivity of the

monoclonal antibodies against the basal type cytokeratins, and to attempt to improve

the reliability of this test, rabbit antisera against CK17 were raised as described in

Example 12. This serum was tested on a separate tissue array with over 300 hundred

breast samples. The antiserum and the monoclonal antibody against CK17 showed

15   highly similar reactivity with epithelial cells in the breast cores. Both reagents stained

the same fraction of tumor cells suggesting that neither is a significantly better

reagent. These results suggest that the focal reactivity seen with monoclonal anti-

CK17 was not due to weak reactivity of the monoclonal antibody but indicates that

within a tumor only a subset of tumor cells express these basal keratins, reinforcing

20   the need for alternative basal markers.

<u>Basal keratin staining on breast carcinoma tissue arrays.</u>

        Since the size of sample examined in tissue array cores is significantly smaller

than on conventional samples, there was a concern that the focal reactivity of basal

25   type cytokeratins might cause positive tumors to be missed. We decided to maximize

the chance of detecting basal keratin expression in the breast tumors on the arrays by

staining them with monoclonal antibodies directed at CK5/6 and CK17 and by

examining arrays made with cores taken from central and peripheral areas of the

tumors. By combining the results from the "central" array and the "peripheral" array,

30   532 tumors were available for CK17 analysis, 535 were available for CK5/6 analysis,

and 564 were available for either CK17 or CK5/6. The remainder of the tumors

represented on the arrays were either lost in transfer during sectioning of the tissue

arrays block, or showed no convincing invasive carcinoma on the core section. Of the cases available for scoring, 75 and 63 tumors scored positive (either weak or strongly) for CK17 and CK5/6, respectively. By combining the results from the stains for CK17 and CK5/6, 90 cases (16%) out of the 564 tumors examined reacted with either CK17

5   and/or CK5/6. Follow-up data were available for 505 of the 564 cases on which CK staining data was obtained. The follow-up period ranged from 1 to 151 months with a mean of 66.1 months.

Kaplan-Meier survival analysis on all patients with follow-up showed that the absence of cytokeratin 17 and cytokeratin 5 is associated with a significantly better

10   prognosis than the presence of either of these cytokeratins (figure 5A, p=0.012). In the group of 229 patients with known lymph node metastases, the expression of CK17 and CK5/6 had no predictive value. In contrast, in the group of 245 patients without lymph node metastases, CK17 and/or CK5/6 expression was significantly associated with shorter survival (figure 5B, p=0.006). The percentage of basal keratin positive

15   tumors was similar in patients with and without lymph node metastases. Multivariate analysis on all patients taken together showed that the prognostic association of basal cytokeratin expression with poor outcome was not independent from tumor size, LN status and histologic grade. However when analyzed on LN-negative tumors alone, the expression of basal cytokeratins is not only a statistically significant

20   prognosticator, but is also independent of tumor size, tumor grade, her2neu status, ER status, and GATA3 status. The results clearly demonstrate the utility of cytokeratin17 as a marker for a subclass of tumors with a poor clinical outcome while also highlighting the difficulties associated with use of anti-cytokeratin17 antibodies.

25   Her2neu, estrogen receptor and GATA-3 staining on breast carcinoma arrays

To further confirm the accuracy of correlations between immunohistochemistry results and clinical data obtained using tissue arrays, sections of the arrays made with peripheral cores were stained for a variety of other proteins known or suspected to be associated with a good or a poor clinical outcome, for

30   example estrogen receptor and Her2neu. As expected, expression of estrogen receptors was associated with a better clinical outcome. This finding was independent of BRE grade, LN status and size. In contrast, Her2neu expression was associated

with a poor prognosis. These results are compatible with published data and are similar to those of two additional studies performed on the same breast tumor arrays. (Bucher C, Torhorst J, Kononen J, Haas P, Schraml L, Bubendorf L, Zuber M, Kochli OR, Mross F, Dieterich H, Askaa J, Godtfredsen SE, Seelig S, Moch H, Mihatsch M,

5.   Kallioniemi O, Sauter G: Prognostic significance of HER-2 amplification and overexpression in breast cancer: Methodological comparison of fluorescence *in situ* hybridization and immunohistochemistry using tissue microarrays of 611 primary breast cancers. in press, 2001; Torhorst J, Bucher C, Kononen J, Haas P, Zuber M, Kochli OR, Mross F, Dieterich H, Moch H, Mihatsch M, Kallioniemi O, Sauter G:

10   Tissue microarrays for rapid linking of molecular changes to clinical endpoints. in press. 2001)

Sections of the arrays were also stained for GATA-binding protein 3, an antigen thought to be co-expressed with estrogen receptors on the mRNA and protein level (Hoch RV, Thompson DA, Baker RJ, Weigel RJ: GATA-3 is expressed in

15   association with estrogen receptor in breast cancer. *International Journal of Cancer* 1999, 84:122-8). The expression for GATA-3 was associated with a good clinical outcome and had a high correlation (Chi-square=720.3 on 9 degrees of freedom) with estrogen receptor expression. The staining results for estrogen receptor, GATA-3 and her2neu confirm findings from prior studies, and also function as an independent

20   validation of tissue array-based studies.

Tissue arrays present a number of advantages for tumor analysis. Analysis of large numbers of tissue sections using conventional techniques is laborious and expensive. An added disadvantage is that slides are stained in different batches, which can introduce variation in staining intensity. In addition, the analysis of large number

25   of conventional glass slides makes comparisons between tumor samples difficult. Many of these problems are circumvented by the new technique of tissue arrays. This approach allows the efficient analysis of antibody reactivity on large numbers of tumors that are stained together on the same slide.

The tissue array studies reported here allowed separation of the patients groups

30   into patients with lymph node metastasis and those without. In patients with metastatic disease to the lymph nodes, the expression of the basal cytokeratins was not associated with a significant difference in clinical outcome. However, in lymph node

negative patients the reactivity for these markers was associated with a poor prognosis independent of tumor size, tumor grade, or immunostain reactivity for ER, her2neu or GATA3. While not wishing to be bound by any theory, taken together with the gene array data, these findings support the idea that anti-cytokeratin antibodies may

5   identify a different type of tumor rather than just another prognostic marker and suggest the possibility that these tumors are derived from basal cells and not from lumenal cells.

Due to the focal and often weak reactivity of monoclonal antibodies against basal type keratins, the interpretation of staining results for these markers can be

10   difficult. The intensity of staining with these markers is not comparable with other markers currently used in diagnosis of breast carcinoma, such as estrogen receptor and her2neu, a feature that prevents their use in clinical settings. We attempted to generate new reagents in the hope that they would have more robust IHC staining characteristics. Analysis of over 300 breast carcinoma samples in a separate array

15   showed that the number of cells and the pattern of focal reactivity for the antiserum against CK17 and the intensity of staining were similar to that seen with the monoclonal antibodies. This indicates that the basal keratins are indeed only focally expressed and that the low numbers of cells stained with antibodies is not due to a weak reactivity of the monoclonal antibodies with the protein.

20   The studies presented here show that basal epithelial cytokeratin positive tumors occur with a significant frequency (>10%) and are associated with a poor prognosis. Patients with metastatic breast carcinoma to the axillary lymph nodes are at high risk for recurrence and most receive adjuvant therapy. The situation for node negative patients is less clear; depending on the size and grade of the tumor, the

25   reported recurrence rate varies between 5-30%. In lymph node negative patients, the clinical decision whether to give or withhold systemic therapy thus is a difficult one and hence it is in this group of patients that the need for new prognostic markers is the greatest. The relative size of this group of patients is also expected to increase, due to continuing advances in screening and diagnostic techniques that identify increasingly

30   smaller breast tumors. Most of these smaller tumors have not metastasized to the "sentinel" lymph node. This group of patients, therefore, has to make a difficult choice between a variety of additional therapies, such as: lumpectomy, mastectomy,

chemotherapy, radiation therapy, or hormonal therapy in the absence of reliable

guidance from pathologic characteristics of their tumor. The cytokeratins 17 and 5/6

appear to detect a subcategory of tumors that behave poorly and may help in treatment

decisions for node-negative breast carcinoma patients. These results suggest that

5   patients that present with basal epithelial cytokeratin expressing tumors may be

candidates for more aggressive treatment procedures and also for alternate therapies

directed against tumors with this particular biology.

Example 13

10

Immunohistochemical Staining of Normal Breast and Breast Tumor Samples in

Tissue Arrays with Antibodies to Basal Marker Polypeptides

Materials and Methods

Tissue arrays including normal breast and breast tumor samples were prepared

15   as described in Example 12. Monoclonal antibody to cytokeratin 5/6 (Boeringer

Mannheim, Inc.) and polyclonal, affinity purified, anti-peptide antibodies to

cadherin3, cadherin EGF LAG seven-pass G-type receptor 2, and matrix

metalloproteinase 14 prepared as described in Example 10 were used to perform

immunohistochemical staining using the DAKO Envision+, Peroxidase IHC kit

20   (DAKO Corp., Carpenteria, CA) with DAB substrate according to the manufacturer's

instructions.

Results

Figure 6 shows antibody staining of normal breast tissue cores. Figure 6A

25   shows staining with anti-cytokeratin 5/6 monoclonal antibody (ck5/6). Figures 6B,

6C, and 6D show staining with anti-cadherin 3 polyclonal antibody (s0158), anti-EGF

LAG seven-pass G-type receptor 2 polyclonal antibody (s0137), and anti-

metalloproteinase 14 polyclonal antibody (s0144), respectively, on sections from a

core derived from the same patient. The brown areas represent prominent staining of

30   the basal layer in the two-cell layered epithelium lining the mammary gland lumen.

These results confirm that the staining pattern of antibodies to the basal marker

polypeptides identified herein is comparable to that of antibodies to cytokeratin 17 in

terms of the cell type stained and the ability to distinguish between basal and luminal cells in the normal mammary gland.

        Figure 7 shows antibody staining of breast cancer tissue cores. Figure 7A shows antibody staining with anti-cytokeratin 5/6 monoclonal antibody (cd5/6).

5   Figures 7B and 7C show staining with anti-EGF LAG seven-pass G-type receptor 2 polyclonal antibody (s0137) and anti-cadherin 3 polyclonal antibody (s0158), respectively. The brown areas represent prominent staining of the epithelial cells within tumor tissue. Note the loss of normal breast glandular architecture consistent with the diagnosis of carcinoma.

10

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1   CLAIMS

2

3   We claim:

4

5   1. A method of classifying a tumor comprising the steps of:

6   providing a tumor sample;

7   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

8   NO:1 in the sample; and

9   classifying the tumor as belonging to a tumor subclass based on the results of

10   the detecting step.

11

12   2. A method of classifying a tumor comprising the steps of:

13   providing a tumor sample;

14   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

15   NO:2 in the sample; and

16   classifying the tumor as belonging to a tumor subclass based on the results of

17   the detecting step.

18

19   3. A method of classifying a tumor comprising the steps of:

20   providing a tumor sample;

21   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

22   NO:3 in the sample; and

23   classifying the tumor as belonging to a tumor subclass based on the results of

24   the detecting step.

25

26   4. A method of classifying a tumor comprising the steps of:

27   providing a tumor sample;

28   detecting expression or activity of at least two genes selected from the group

29   consisting of: a gene encoding the polypeptide of SEQ ID NO:1, SEQ ID NO:2, and

30   SEQ ID NO:3 in the sample; and

31   classifying the tumor as belonging to a tumor subclass based on the results of

32   the detecting step.

1

2   5. The method of any of claims 1, 2, 3, or 4, wherein the detecting step comprises

3   detecting the polypeptide or polypeptides.

4

5   6. The method of claim 5, wherein the polypeptide is detected by performing

6   immunohistochemical analysis on the sample using an antibody that specifically binds

7   to the polypeptide.

8

9   6a. The method of claim 5, wherein the polypeptide is detected by performing an

10   ELISA assay using an antibody that specifically binds to the polypeptide.

11

12   6b. The method of claim 5, wherein the polypeptide is detected using an antibody

13   array comprising an antibody that specifically binds to the polypeptide.

14

15   6c. The method of claim 5, wherein the detecting step comprises:

16   detecting modification of a substrate by the polypeptide.

17

18   7. The method of any of claims 1, 2, 3, or 4, wherein classifying a tumor comprises:

19   stratifying a subject having the tumor for a clinical trial.

20

21   8. The method of claim 7, wherein the tumor is a breast tumor.

22

23   9. The method of any of claims 1, 2, 3, or 4, wherein the tumor is a breast tumor and

24   the tumor subclass is a basal tumor subclass.

25

26   1a. The method of claim 1, further comprising:

27   providing diagnostic, prognostic, or predictive information based on the

28   classifying step.

29

30   2a. The method of claim 2, further comprising:

31   providing diagnostic, prognostic, or predictive information based on the

32   classifying step.

1

2   3a. The method of claim 3, further comprising:

3   providing diagnostic, prognostic, or predictive information based on the

4   classifying step.

5

6   4a. The method of claim 4, further comprising:

7   providing diagnostic, prognostic, or predictive information based on the

8   classifying step.

9

10   5a. The method of claim 5, further comprising:

11   providing diagnostic, prognostic, or predictive information based on the

12   classifying step.

13

14   6aa. The method of claim 5a, wherein the polypeptide is detected by performing

15   immunohistochemical analysis on the sample using an antibody that specifically binds

16   to the polypeptide.

17

18   6ab. The method of claim 5a, wherein the polypeptide is detected by performing an

19   ELISA assay using an antibody that specifically binds to the polypeptide.

20

21   6ac. The method of claim 5a, wherein the polypeptide is detected using an antibody

22   array comprising an antibody that specifically binds to the polypeptide.

23

24   6ad. The method of claim 5a, wherein the detecting step comprises:

25   detecting modification of a substrate by the polypeptide.

26

27   9a. The method of any of claims 1a, 2a, 3a, or 4a, wherein the tumor is a breast tumor

28   and the tumor subclass is a basal tumor subclass.

29

30   1g. The method of claim 1, further comprising:

31   selecting a treatment based on the classifying step.

32

1   2g. The method of claim 2, further comprising:

2   selecting a treatment based on the classifying step.

3

4   3g. The method of claim 3, further comprising:

5   selecting a treatment based on the classifying step.

6

7   4g. The method of claim 4, further comprising:

8   selecting a treatment based on the classifying step.

9

10 5g. The method of claim 5, further comprising:

11   selecting a treatment based on the classifying step.

12

13 6ag. The method of claim 5g, wherein the polypeptide is detected by performing

14 immunohistochemical analysis on the sample using an antibody that specifically binds

15 to the polypeptide.

16

17 6bg. The method of claim 5g, wherein the polypeptide is detected by performing an

18 ELISA assay using an antibody that specifically binds to the polypeptide.

19

20 6cg. The method of claim 5g, wherein the polypeptide is detected using an antibody

21 array comprising an antibody that specifically binds to the polypeptide.

22

23 6dg. The method of claim 5g, wherein the detecting step comprises:

24   detecting modification of a substrate by the polypeptide.

25

26 9g. The method of any of claims 1g, 2g, 3g, or 4g, wherein the tumor is a breast tumor

27 and the tumor subclass is a basal tumor subclass.

28

29 1m. A method of testing a subject comprising the steps of:

30   providing a sample isolated from a subject;

31   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

32 NO:1 in the sample; and

1   providing diagnostic, prognostic, or predictive information based on the

2   detecting step.

3

4   2m. A method of testing a subject comprising the steps of:

5   providing a sample isolated from a subject;

6   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

7   NO:2 in the sample; and

8   providing diagnostic, prognostic, or predictive information based on the

9   detecting step.

10

11   3m. A method of testing a subject comprising the steps of:

12   providing a sample isolated from a subject;

13   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

14   NO:3 in the sample; and

15   providing diagnostic, prognostic, or predictive information based on the

16   detecting step.

17

18   4m. A method of testing a subject comprising the steps of:

19   providing a sample isolated from the subject;

20   detecting expression or activity of at least two genes selected from the group

21   consisting of: a gene encoding the polypeptide of SEQ ID NO:1, SEQ ID NO:2, and

22   SEQ ID NO:3 in the sample; and

23   providing diagnostic, prognostic, or predictive information based on the

24   detecting step.

25

26   5m. The method of any of claims 1m, 2m, 3m, or 4m, wherein the detecting step

27   comprises detecting the polypeptide or polypeptides.

28

29   6m. The method of claim 5m, wherein the polypeptide is detected by performing

30   immunohistochemical analysis on the sample using an antibody that specifically binds

31   to the polypeptide.

32

1 6ma. The method of claim 5m, wherein the polypeptide is detected by performing an

2 ELISA assay using an antibody that specifically binds to the polypeptide.

3

4 6mb. The method of claim 5m, wherein the polypeptide is detected using an antibody

5 array comprising an antibody that specifically binds to the polypeptide.

6

7 6mc. The method of claim 5m, wherein the detecting step comprises:

8   detecting modification of a substrate by the polypeptide.

9

10 9m. The method of any of claims 1m, 2m, 3m, or 4m, wherein the sample is selected

11 from the group consisting of:

12   a blood sample, a urine sample, a serum sample, an ascites sample, a saliva

13 sample, a cell, and a portion of tissue.

14

15 10m. The method of any of claims 1m, 2m, 3m, or 4m, wherein the sample is a tumor

16 sample.

17

18 11m. The method of claim 10m, wherein the tumor sample is a breast tumor sample.

19

20 1r. A method of testing a subject comprising the steps of:

21   providing a sample isolated from a subject;

22   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

23 NO:1 in the sample; and

24   stratifying the subject for a clinical trial based on the detecting step.

25

26 2r. A method of testing a subject comprising the steps of:

27   providing a sample isolated from a subject;

28   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

29 NO:2 in the sample; and

30   stratifying the subject for a clinical trial based on the detecting step.

31

32 3r. A method of testing a subject comprising the steps of:

1   providing a sample isolated from a subject;

2   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

3   NO:3 in the sample; and

4   stratifying the subject for a clinical trial based on the detecting step.

5

6   4r. A method of testing a subject comprising the steps of:

7   providing a sample isolated from the subject;

8   detecting expression or activity of at least two genes selected from the group

9   consisting of: a gene encoding the polypeptide of SEQ ID NO:1, SEQ ID NO:2, and

10   SEQ ID NO:3 in the sample; and

11   stratifying the subject for a clinical trial based on the detecting step.

12

13   5r. The method of any of claims 1r, 2r, 3r, or 4r, wherein the detecting step comprises

14   detecting the polypeptide or polypeptides.

15

16   6r. The method of claim 5r, wherein the polypeptide is detected by performing

17   immunohistochemical analysis on the sample using an antibody that specifically binds

18   to the polypeptide.

19

20   6ra. The method of claim 5r, wherein the polypeptide is detected by performing an

21   ELISA assay using an antibody that specifically binds to the polypeptide.

22

23   6rb. The method of claim 5r, wherein the polypeptide is detected using an antibody

24   array comprising an antibody that specifically binds to the polypeptide.

25

26   6rc. The method of claim 5r, wherein the detecting step comprises:

27   detecting modification of a substrate by the polypeptide.

28

29   9r. The method of any of claims 1r, 2r, 3r, or 4r, wherein the sample is selected from

30   the group consisting of:

31   a blood sample, a urine sample, a serum sample, an ascites sample, a saliva

32   sample, a cell, and a portion of tissue.

1

2   10r. The method of any of claims 1r, 2r, 3r, or 4r, wherein the sample is a tumor

3   sample.

4

5   11r. The method of claim 10r, wherein the tumor sample is a breast tumor sample.

6

7   1q. A method of testing a subject comprising the steps of:

8   providing a sample isolated from a subject;

9   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

10   NO:1 in the sample; and

11   selecting a treatment based on the detecting step.

12

13   2q. A method of testing a subject comprising the steps of:

14   providing a sample isolated from a subject;

15   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

16   NO:2 in the sample; and

17   selecting a treatment based on the detecting step.

18

19   . 3q. A method of testing a subject comprising the steps of:

20   providing a sample isolated from a subject;

21   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

22   NO:3 in the sample; and

23   selecting a treatment based on the detecting step.

24

25   4q. A method of testing a subject comprising the steps of:

26   providing a sample isolated from the subject;

27   detecting expression or activity of at least two genes selected from the group

28   consisting of: a gene encoding the polypeptide of SEQ ID NO:1, SEQ ID NO:2, and

29   SEQ ID NO:3 in the sample; and

30   selecting a treatment based on the detecting step.

31

1   5q. The method of any of claims 1q, 2q, 3q, or 4q, wherein the detecting step

2   comprises detecting the polypeptide or polypeptides.

3

4   6q. The method of claim 5q, wherein the polypeptide is detected by performing

5   immunohistochemical analysis on the sample using an antibody that specifically binds

6   to the polypeptide.

7

8   6qa. The method of claim 5q, wherein the polypeptide is detected by performing an

9   ELISA assay using an antibody that specifically binds to the polypeptide.

10

11   6qb. The method of claim 5q, wherein the polypeptide is detected using an antibody

12   array comprising an antibody that specifically binds to the polypeptide.

13

14   6qc. The method of claim 5q, wherein the detecting step comprises:

15   detecting modification of a substrate by the polypeptide.

16

17   9q. The method of any of claims 1q, 2q, 3q, or 4q, wherein the sample is selected

18   from the group consisting of:

19   a blood sample, a urine sample, a serum sample, an ascites sample, a saliva

20   sample, a cell, and a portion of tissue.

21

22   10m. The method of any of claims 1m, 2m, 3m, or 4m, wherein the sample is a tumor

23   sample.

24

25   11m. The method of claim 10m, wherein the tumor sample is a breast tumor sample.

26

27   20. An antibody that specifically binds to an epitope found in a polypeptide whose

28   amino acid sequence the amino acid sequence of SEQ ID NO:1, and wherein the

29   antibody recognizes basal cells in normal mammary lactation glands.

30

31   21. The antibody of claim 21, wherein the antibody distinguishes basal cells from

32   luminal cells in normal mammary lactation glands.

1

2   22. The antibody of claim 20, wherein the antibody is a monoclonal antibody.

3

4   23. The antibody of claim 20, wherein the antibody is a polyclonal antibody.

5

6   24. The antibody of claim 20, wherein the antibody recognizes an epitope found in a

7   peptide having an amino acid sequence selected from the group consisting of SEQ ID

8   NO:4, SEQ ID NO:5, and SEQ ID NO:6.

9

10   25. An antibody that specifically binds to an epitope found in a polypeptide whose

11   amino acid sequence comprises the amino acid sequence of SEQ ID NO:2, and

12   wherein the antibody recognizes basal cells in normal mammary lactation glands.

13

14   26. The antibody of claim 25, wherein the antibody distinguishes basal cells from

15   luminal cells in normal mammary lactation glands.

16

17   27. The antibody of claim 25, wherein the antibody is a monoclonal antibody.

18

19   28. The antibody of claim 25, wherein the antibody is a polyclonal antibody.

20

21   29. The antibody of claim 25, wherein the antibody recognizes an epitope found in a

22   peptide having an amino acid sequence selected from the group consisting of SEQ ID

23   NO:7, SEQ ID NO:8, and SEQ ID NO:9.

24

25   30. An antibody that specifically binds to an epitope found in a polypeptide whose

26   amino acid sequence comprises the amino acid sequence of SEQ ID NO:3, and

27   wherein the antibody recognizes basal cells in normal mammary lactation glands.

28

29   31. The antibody of claim 30, wherein the antibody distinguishes basal cells from

30   luminal cells in normal mammary lactation glands.

31

32   32. The antibody of claim 30, wherein the antibody is a monoclonal antibody.

1

2   33. The antibody of claim 30, wherein the antibody is a polyclonal antibody.

3

4   34. The antibody of claim 30, wherein the antibody recognizes an epitope found in a

5   peptide having an amino acid sequence selected from the group consisting of SEQ ID

6   NO:10, SEQ ID NO:11, and SEQ ID NO:12.

7

8   38. A kit for tumor diagnosis comprising:

9   one or more of the antibodies of any of claims 20 through 34;

10   instructions for use of the kit; and

11   a control slide comprising breast tissue samples for testing reagents in the kit.

12

13   40. A method of testing a compound or a combination of compounds for activity

14   against tumors comprising steps of:

15   obtaining or providing tumor samples taken from subjects who have been

16   treated with the compound or combination of compounds, wherein the tumors fall

17   within a tumor subclass;

18   comparing the response rate of tumors that fall within the tumor subclass and

19   have been treated with the compound with the overall response rate of tumors that

20   have been treated with the compound or combination of compounds or with the

21   response rate of tumors that do not fall within the subclass and have been treated with

22   the compound or combination of compounds; and

23   identifying the compound or combination of compounds as having selective

24   activity against tumors in the tumor subclass if the response rate of tumors in the

25   subclass is greater than the overall response rate or the response rate of tumors that do

26   not fall within the subclass.

27

28   41. The method of claim 40, wherein the tumors are breast tumors.

29

30   42. The method of claim 41, wherein the tumor subclass is a basal tumor subclass.

31

1   43. The method of claim 41, wherein the tumors are classified according to the

2   method of any of claims 1, 2, 3, or 4.

3

4   44. The method of claim 41, wherein the tumor subclass is a basal tumor subclass and

5   wherein a tumor is identified as belonging to the tumor subclass based on evidence of

6   expression of one or more basal marker genes in the sample.

7

8   45. The method of claim 44, wherein evidence of expression comprises presence of a

9   protein encoded by a basal marker gene, and wherein the evidence of expression is

10   obtained using an antibody that binds to the protein.

11

12   46. The method of claim 45, wherein the basal marker gene encodes a polypeptide

13   comprising the amino acid sequence of SEQ ID NO:1.

14

15   47. The method of claim 45, wherein the basal marker gene encodes a polypeptide

16   comprising the amino acid sequence of SEQ ID NO:2.

17

18   48. The method of claim 45, wherein the basal marker gene encodes a polypeptide

19   comprising the amino acid sequence of SEQ ID NO:3.

20

21   49. The method of claim 40, wherein the samples are present within a tissue array.

22

23   60. A method of testing a compound or a combination of compounds for activity

24   against tumors comprising steps of:

25   treating subjects in need of treatment for tumors with the compound or

26   combination of compounds;

27   comparing the response rate of tumors that fall within a tumor subclass with

28   the overall response rate of tumors or with the response rate of tumors that do not fall

29   within the subclass; and

30   identifying the compound or combination of compounds as having selective

31   activity against tumors in the tumor subclass if the response rate of tumors in the

1   subclass is greater than the overall response rate or the response rate of tumors that do

2   not fall within the subclass.

3

4   61. The method of claim 60, further comprising the steps of:

5   providing tumor samples from subjects in need of treatment for tumors;

6   determining whether the tumors fall within a tumor subclass; and

7   stratifying the subjects based on the results of the determining step prior to

8   performing the treating step.

9

10   62. The method of claim 60, further comprising the steps of:

11   providing tumor samples from subjects in need of treatment for tumors;

12   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

13   NO:1 in the samples; and

14   stratifying the subjects based on the results of the detecting step prior to

15   performing the the treating step.

16

17   63. The method of claim 60, further comprising the steps of:

18   providing tumor samples from subjects in need of treatment for tumors;

19   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

20   NO:2 in the samples; and

21   stratifying the subjects based on the results of the detecting step prior to

22   performing the treating step.

23

24   64. The method of claim 60, further comprising the steps of:

25   providing tumor samples from subjects in need of treatment for tumors;

26   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

27   NO:3 in the samples; and

28   stratifying the subjects based on the results of the detecting step prior to

29   performing the treating step.

30

31   65. The method of claim 60, further comprising the steps of:

32   providing tumor samples from subjects in need of treatment for tumors;

1   detecting expression or activity of at least two genes, wherein each of the

2   genes encodes a polypeptide whose sequence comprises a sequence selected from the

3   group consisting of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3 in the samples;

4   and

5   stratifying the subjects based on the results of the detecting step prior to

6   performing the treating step.

7

8   80. A method of testing a compound or a combination of compounds for activity

9   against tumors comprising steps of:

10   treating subjects in need of treatment for tumors with the compound or

11   combination of compounds or with an alternate compound, wherein the tumors fall

12   within a tumor subclass;

13   comparing the response rate of tumors treated with the compound or

14   combination of compounds with the response rate of tumors treated with the alternate

15   compound; and

16   identifying the compound or combination of compounds as having superior

17   activity against tumors in the tumor subclass, as compared with the alternate

18   compound, if the response rate of tumors treated with the compound or combination

19   of compounds is greater than the response rate of tumors treated with the alternate

20   compound.

21

22   81. The method of claim 80, further comprising the steps of:

23   providing tumor samples from subjects in need of treatment for tumors;

24   determining whether the tumors fall within a tumor subclass; and

25   stratifying the subjects based on the results of the determining step prior to

26   performing the treating step.

27

28   82. The method of claim 80, further comprising the steps of:

29   providing tumor samples from subjects in need of treatment for tumors;

30   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

31   NO:1 in the samples; and

1   stratifying the subjects based on the results of the detecting step prior to

2   performing the treating step.

3

4   83. The method of claim 80, further comprising the steps of:

5   providing tumor samples from subjects in need of treatment for tumors;

6   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

7   NO:2 in the samples; and

8   stratifying the subjects based on the results of the detecting step prior to

9   performing the treating step.

10

11 84. The method of claim 80, further comprising the steps of:

12   providing tumor samples from subjects in need of treatment for tumors;

13   detecting expression or activity of a gene encoding the polypeptide of SEQ ID

14 NO:3 in the samples; and

15   stratifying the subjects based on the results of the detecting step prior to

16 performing the treating step.

17

18 85. The method of claim 80, further comprising the steps of:

19   providing tumor samples from subjects in need of treatment for tumors;

20   detecting expression or activity of at least two genes, wherein each of the

21 genes encodes a polypeptide whose sequence comprises a sequence selected from the

22 group consisting of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3 in the samples;

23 and

24   stratifying the subjects based on the results of the detecting step prior to

25 performing the treating step.

26

27 86. The method of any of claims 80, 81, 82, 83, 84, or 85, wherein the alternate

28 compound is a compound approved by the U.S. Food and Drug administration for

29 treatment of tumors.

30

31 100. A method of treating a subject comprising steps of:

32   identifying a subject as having a tumor in a basal tumor subclass; and

1   administering a compound identified according to the method of any of claims

2 40, 41, 42, or 45 to the subject.

3

4 101. A method of treating a subject comprising steps of:

5   identifying a subject as having a tumor in a basal tumor subclass; and

6   administering a compound identified according to the method of any of claims

7 60, 61, 62, 63, 64, or 65 to the subject.

8

9 103. A method of treating a subject comprising steps of:

10   identifying a subject as having a tumor in a basal tumor subclass; and

11   administering a compound identified according to the method of any of claims

12 80, 81, 82, 83, 84, or 85 to the subject.

13

14 120. A method of treating a subject comprising steps of:

15   providing a subject in need of treatment for cancer;

16   administering to the subject an antibody that specifically binds to a

17 polypeptide having an amino acid sequence comprising the sequence of SEQ ID

18 NO:1.

19

20 121. A method of treating a subject comprising steps of:

21   providing a subject in need of treatment for a tumor;

22   administering to the subject an antibody that specifically binds to a

23 polypeptide having an amino acid sequence comprising the sequence of SEQ ID

24 NO:2.

25

26 122. A method of treating a subject comprising steps of:

27   providing a subject in need of treatment for a tumor;

28   administering to the subject an antibody that specifically binds to a

29 polypeptide having an amino acid sequence comprising the sequence of SEQ ID

30 NO:3.

31

1   130. The method of any of claims 120, 121, or 122, wherein the tumor is a breast

2   tumor, and wherein the method further comprises the step of:

3   identifying the tumor as belonging to a basal tumor subclass.

4

5   131. The method of any of claims 120, 121, or 122, wherein the antibody is

6   conjugated with a toxic molecule.

7

8   140. A method of treating a subject comprising steps of:

9   providing a subject in need of treatment for cancer;

10   administering to the subject a compound that activates or inhibits a gene that

11   encodes an amino acid having a sequence comprising the sequence of SEQ ID NO:1,

12   or that activates or inhibits an expression product of the gene.

13

14   141. A method of treating a subject comprising steps of:

15   providing a subject in need of treatment for a tumor;

16   administering to the subject a compound that activates or inhibits a gene that

17   encodes an amino acid having a sequence comprising the sequence of SEQ ID NO:2,

18   or that activates or inhibits an expression product of the gene.

19

20   142. A method of treating a subject comprising steps of:

21   providing a subject in need of treatment for a tumor;

22   administering to the subject a compound that activates or inhibits a gene that

23   encodes an amino acid having a sequence comprising the sequence of SEQ ID NO:3,

24   or that activates or inhibits an expression product of the gene.

25

26   150. A composition comprising:

27   two or more compounds identified according to the method of any of claims

28   40, 60, or 80.

29

30   151. A pharmaceutical composition comprising:

31   the composition of claim 150; and

32   a pharmaceutically acceptable carrier.

1

2   160. A composition comprising:

3   a compound identified according to the method of any of claims 40, 60, or 80;

4   a second compound, wherein the second compound is approved by the U.S.

5   Food and Drug administration for the treatment of cancer or has shown potential

6   efficacy against cancer in pre-clinical studies.

7

8   161. A pharmaceutical composition comprising:

9   the composition of claim 160; and

10   a pharmaceutically acceptable carrier.

11

FIGURE 1A

Sequence of cadherin 3 (GenBank accession number NP_001784)

SEQ ID NO:1

MGLPRGPLASLLLLQVCWLQCAASEPCRAVFREAEVTLEAGGAEQEPGQALGK
VFMGCPGQEPALFSTDNDDFTVRNGETVQERRSLKERNPLKIFPSKRILRRHKRD
WVVAPISVPENGKGPFPQRLNQLKSNKDRDTKIFYSITGPGADSPPEGVFAVEKE
TGWLLLNKPLDREEIAKYELFGHAVSENGASVEDPMNISIIVTDQNDHKPKFTQD
TFRGSVLEGVLPGTSVMQVTATDEDDAIYTYNGVVAYSIHSQEPKDPHDLMFTI
HRSTGTISVISSGLDREKVPEYTLTIQATDMDGDGSTTTAVAVVEILDANDNAPM
FDPQKYEAHVPENAVGHEVQRLTVTDLDAPNSPAWRATYLIMGGDDGDHFTITT
HPESNQGILTTRKGLDFEAKNQHTLYVEVTNEAPFVLKLPTSTATIVVHVEDVNE
APVFVPPSKVVEVQEGIPTGEPVCVYTAEDPDKENQKISYRILRDPAGWLAMDPD
SGQVTAVGTLDREDEQFVRNNIYEVMVLAMDNGSPPTTGTGTLLLTLIDVNDHG
PVPEPRQITICNQSPVRHVLNITDKDLSPHTSPFQAQLTDDSDIYWTAEVNEEGDT
VVLSLKKFLKQDTYDVHLSLSDHGNKEQLTVIRATVCDCHGHVETCPGPWKGG
FILPVLGAVLALLFLLLVLLLLVRKKRKIKEPLLLPEDDTRDNVFYYGEEGGGEE
DQDYDITQLHRGLEARPEVVLRNDVAPTIIPTPMYRPRPANPDEIGNFIIENLKAA
NTDPTAPPYDTLLVFDYEGSGSDAASLSSLTSSASDQDQDYDYLNEWGSRFKKL
ADMYGGGEDD

FIGURE 1B

Sequence of matrix metalloproteinase 14 (GenBank accession number NP_004986)

SEQ ID NO:2

MSPAPRPPRCLLLPLLTLGTALASLGSAQSSSFSPEAWLQQYGYLPPGDLRTHTQ
RSPQSLSAAIAAMQKFYGLQVTGKADADTMKAMRRPRCGVPDKFGAEIKANVR
RKRYAIQGLKWQHNEITFCIQNYTPKVGEYATYEAIRKAFRVWESATPLRFREVP
YAYIREGHEKQADIMIFFAEGFHGDSTPFDGEGGFLAHAYFPGPNIGGDTHFDSA
EPWTVRNEDLNGNDIFLVAVHELGHALGLEHSSDPSAIMAPFYQWMDTENFVLP
DDDRRGIQQLYGGESGFPTKMPPQPRTTSRPSVPDKPKNPTYGPNICDGNFDTVA
MLRGEMFVFKERWFWRVRNNQVMDGYPMPIGQFWRGLPASINTAYERKDGKF
VFFKGDKHWVFDEASLEPGYPKHIKELGRGLPTDKIDAALFWMPNGKTYFFRGN
KYYRFNEELRAVDSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFN
NQKLKVEPGYPKSALRDWMGCPSGGRPDEGTEEETEVIIIEVDEEGGGAVSAAA
VVLPVLLLLLVLAVGLAVFFFRRHGTPRRLLYCQRSLLDKV

FIGURE 1C

Sequence of cadherin EGF LAG seven-pass G-type receptor 2 (GenBank accession number NP_001399)

SEQ ID NO:3

MRSPATGVPLPTPPPPLLLLLLLLLLPPPLLGDQVGPCRSLGSRGRGSSGACAPMG
WLCPSSASNLWLYTSRCRDAGTELTGHLVPHHDGLRVWCPESEAHIPLPPAPEG
CPWSCRLLGIGGHLSPQGKLTLPEEHPCLKAPRLRCQSCKLAQAPGLRAGERSPE
ESLGGRRKRNVNTAPQFQPPSYQATVPENQPAGTPVASLRAIDPDEGEAGRLEYT
MDALFDSRSNQFFSLDPVTGAVTTAEELDRETKSTHVFRVTAQDHGMPRRSALA
TLTILVTDTNDHDPVFEQQEYKESLRENLEVGYEVLTVRATDGDAPPNANILYRL
LEGSGGSPSEVFEIDPRSGVIRTRGPVDREEVESYQLTVEASDQGRDPGPRSTTAA
VFLSVEDDNDNAPQFSEKRYVVQVREDVTPGAPVLRVTASDRDKGSNAVVHYSI
MSGNARGQFYLDAQTGALDVVSPLDYETTKEYTLRVRAQDGGRPPLSNVSGLV
TVQVLDINDNAPIFVSTPFQATVLESVPLGYLVLHVQAIDADAGDNARLEYRLAG
VGHDFPFTINNGTGWISVAAELDREEVDFYSFGVEARDHGTPALTASASVSVTVL
DVNDNNPTFTQPEYTVRLNEDAAVGTSVVTVSAVDRDAHSVITYQITSGNTRNR
FSITSQSGGGLVSLALPLDYKLERQYVLAVTASDGTRQDTAQIVVNVTDANTHRP
VFQSSHYTVNVNEDRPAGTTVVLISATDEDTGENARITYFMEDSIPQFRIDADTG
AVTTQAELDYEDQVSYTLAITARDNGIPQKSDTTYLEILVNDVNDNAPQFLRDSY
QGSVYEDVPPFTSVLQISATDRDSGLNGRVFYTFQGGDDGDGDFIVESTSGIVRT
LRRLDRENVAQYVLRAYAVDKGMPPARTPMEVTVTVLDVNDNPPVFEQDEFDV
FVEENSPIGLAVARVTATDPDEGTNAQIMYQIVEGNIPEVFQLDIFSGELTALVDL
DYEDRPEYVLVIQATSAPLVSRATVHVRLLDRNDNPPVLGNFEILFNNYVTNRSS
SFPGGAIGRVPAHDPDISDSLTYSFERGNELSLVLLNASTGELKLSRALDNNRPLE
AIMSVLVSDGVHSVTAQCALRVTITDEMLTHSITLRLEDMSPERFLSPLLGLFIQA
VAATLATPPDHVVVFNVQRDTDAPGGHILNVSLSVGQPPGPGGGPPFLPSEDLQE
RLYLNRSLLTAISAQRVLPFDDNICLREPCENYMRCVSVLRFDSSAPFIASSSVLFR
PIHPVGGLRCRCPPGFTGDYCETEVDLCYSRPCGPHGRCRSREGGYTCLCRDGYT
GEHCEVSARSGRCTPGVCKNGGTCVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP
AHSFITFRGLRQRFHFTLALSFATKERDGLLLYNGRFNEKHDFVALEVIQEQVQL
TFSAGESTTTVSPFVPGGVSDGQWHTVQLKYYNKPLLGQTGLPQGPSEQKVAVV
TVDGCDTGVALRFGSVLGNYSCAAQGTQGGSKKSLDLTGPLLLGGVPDLPESFP
VRMRQFVGCMRNLQVDSRHIDMADFIANNGTVPGCPAKKNVCDSNTCHNGGT
CVNQWDAFSCECPLGFGGKSCAQEMANPQHFLGSSLVAWHGLSLPISQPWYLSL
MFRTRQADGVLLQAITRGRSTITLQLREGHVMLSVEGTGLQASSLRLEPGRAND
GDWHHAQLALGASGGPGHAILSFDYGQQRAEGNLGPRLHGLHLSNITVGGIPGP
AGGVARGFRGCLQGVRVSDTPEGVNSLDPSHGESINVEQGCSLPDPCDSNPCPA
NSYCSNDWDSYSCSCDPGYYGDNCTNVCDLNPCEHQSVCTRKPSAPHGYTCEC
PPNYLGPYCETRIDQPCPRGWWGHPTCGPCNCDVSKGFDPDCNKTSGECHCKEN
HYRPPGSPTCLLCDCYPTGSLSRVCDPEDGQCPCKPGVIGRQCDRCDNPFAEVTT
NGCEVNYDSCPRAIEAGIWWPRTRFGLPAAAPCPKGSFGTAVRHCDEHRGWLPP
NLFNCTSITFSELKGFAERLQRNESGLDSGRSQQLALLLRNATQHTAGYFGSDVK
VAYQLATRLLAHESTQRGFGLSATQDVHFTENLLRVGSALLDTANKRHWELIQQ

TEGGTAWLLQHYEAYASALAQNMRHTYLSPFTIVTPNIVISVVRLDKGNFAGAK
LPRYEALRGEQPPDLETTVILPESVFRETPPVVRPAGPGEAQEPEELARRQRRHPE
LSQGEAVASVIIYRTLAGLLPHNYDPDKRSLRVPKRPIINTPVVSISVHDDEELLPR
ALDKPVTVQFRLLETEERTKPICVFWNHSILVSGTGGWSARGCEVVFRNESHVSC
QCNHMTSFAVLMDVSRRENGEILPLKTLTYVALGVTLAALLLTFFFLTLLRILRS
NQHGIRRNLTAALGLAQLVFLLGINQADLPFACTVIAILLHFLYLCTFSWALLEAL
HLYRALTEVRDVNTGPMRFYYMLGWGVPAFITGLAVGLDPEGYGNPDFCWLSI
YDTLIWSFAGPVAFAVSMSVFLYILAARASCAAQRQGFEKKGPVSGLQPSFAVLL
LLSATWLLALLSVNSDTLLFHYLFATCNCIQGPFIFLSYVVLSKEVRKALKLACSR
KPSPDPALTTKSTLTSSYNCPSPYADGRLYQPYGDSAGSLHSTSRSGKSQPSYIPF
LLREESALNPGQGPPGLGDPGSLFLEGQDQQHDPDTDSDSDLSLEDDQSGSYAST
HSSDSEEEEEEEEEEAAFPGEQGWDSLLGPGAERLPLHSTPKDGGPGPGKAPWPG
DFGTTAKESSGNGAPEERLRENGDALSREGSLGPLPGSSAQPHKGILKKKCLPTIS
EKSSLLRLPLEQCTGSSRGSSASEGSRGGPPPRPPPRQSLQEQLNGVMPIAMSIKA
GTVDEDSSGSEFLFFNFLH

Figure 1D

Peptides for antibodies that bind to cadherin3 (GenBank accession number NP_001784):

RAVFREAEVTLEAGGAEQE (SEQ ID NO:4)

QEPALFSTDNDDFTVRN (SEQ ID NO:5)

QKYEAHVPENAVGHE (SEQ ID NO:6)

Peptides for antibodies that bind to matrix metalloproteinase 14 (GenBank accession number NP_004986):

AYIREGHEKQADIMIFFAE (SEQ ID NO:7)

DEASLEPGYPKHIKELGR (SEQ ID NO:8)

RGSFMGSDEVFTYFYK (SEQ ID NO:9)

Peptides for antibodies that bind to anti-cadherin EGF LAG seven-pass G-type receptor 2 (GenBank accession number NP_001399):

QASSLRLEPGRANDGDWH (SEQ ID NO:10)

ELKGFAERLQRNESGLDSGR (SEQ ID NO:11)

RSGKSQPSYIPFLLREE (SEQ ID NO:12)

Peptides for antibodies that bind to anti-cytokeratin17:

KKEPVTTRQVRTIVEE (SEQ ID NO:13)

QDGKVISSREQVHQTTR (SEQ ID NO:14)

SSSIKGSSGLGGGSS (SEQ ID NO:15)

3294483_1.DOC

FIGURE 2

Intrinsic Gene Subset
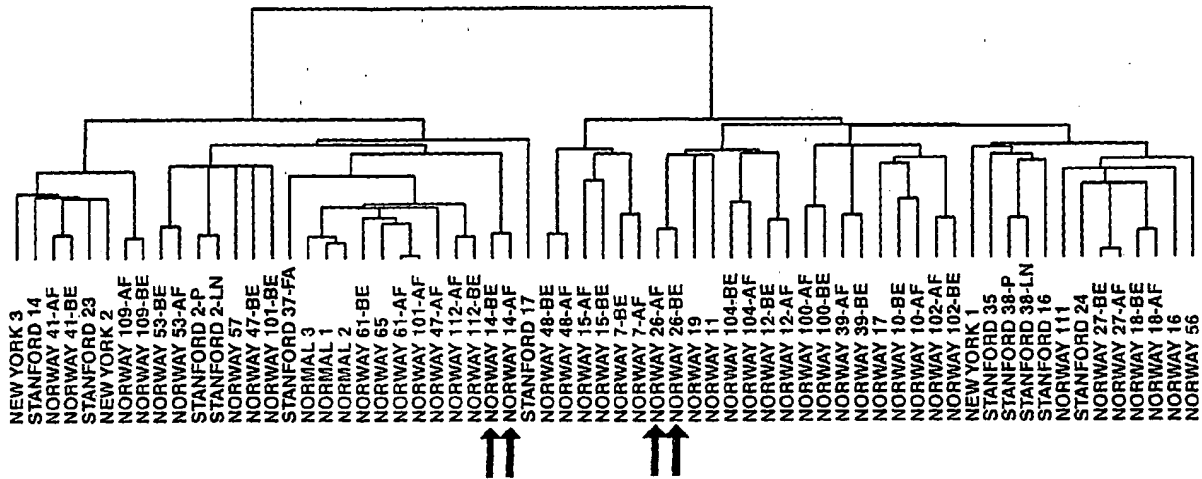
Epithelial-Enriched Gene Subset
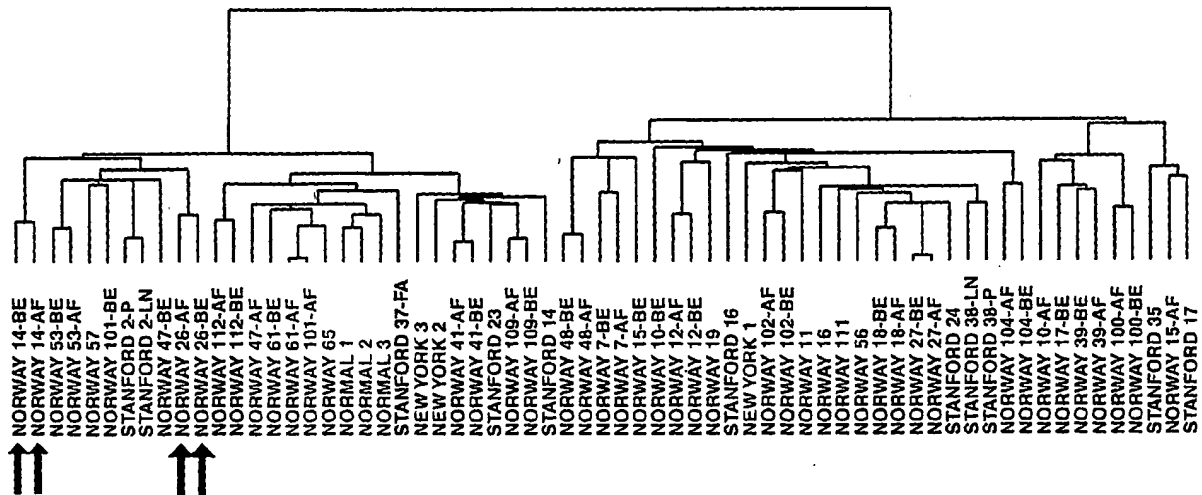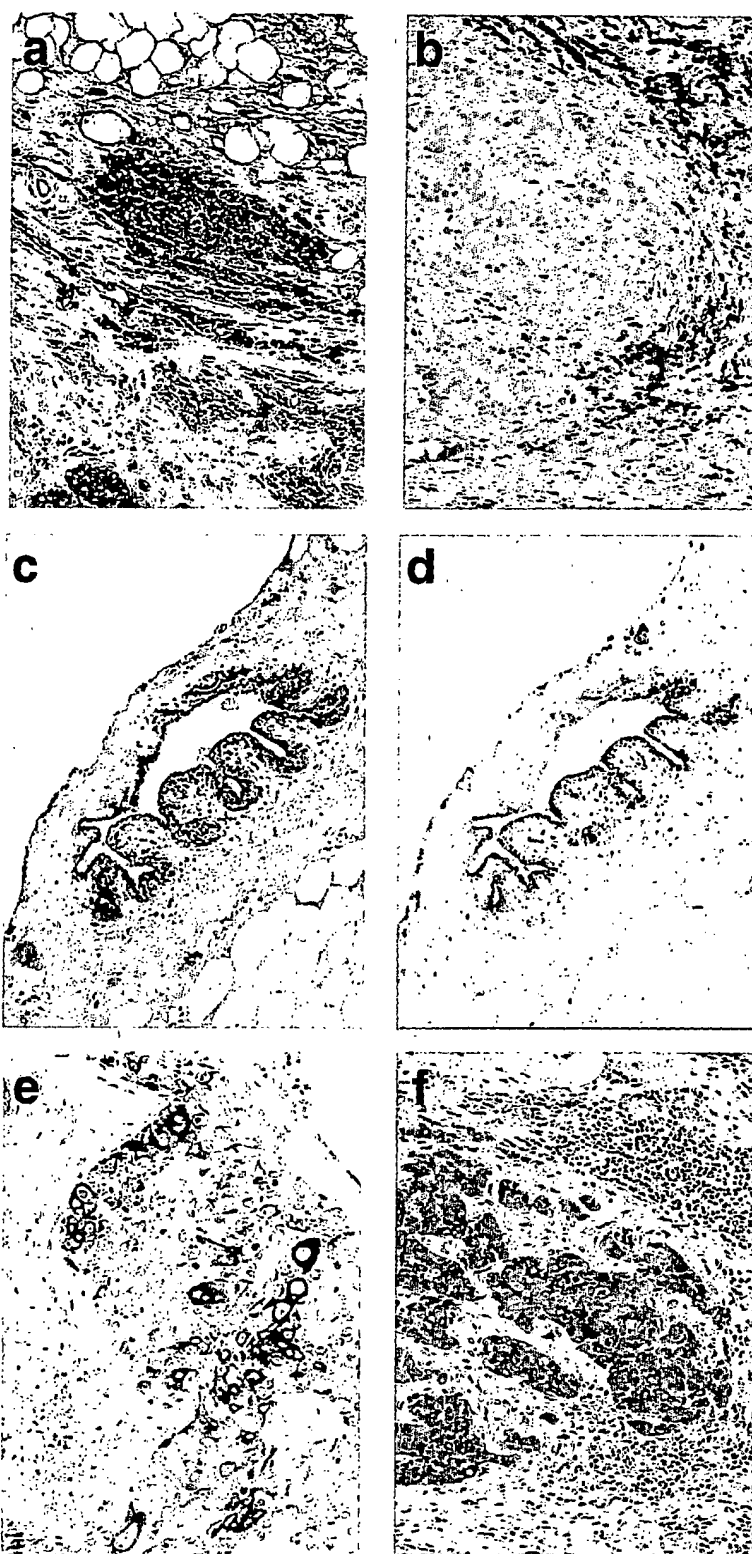
Figure 3
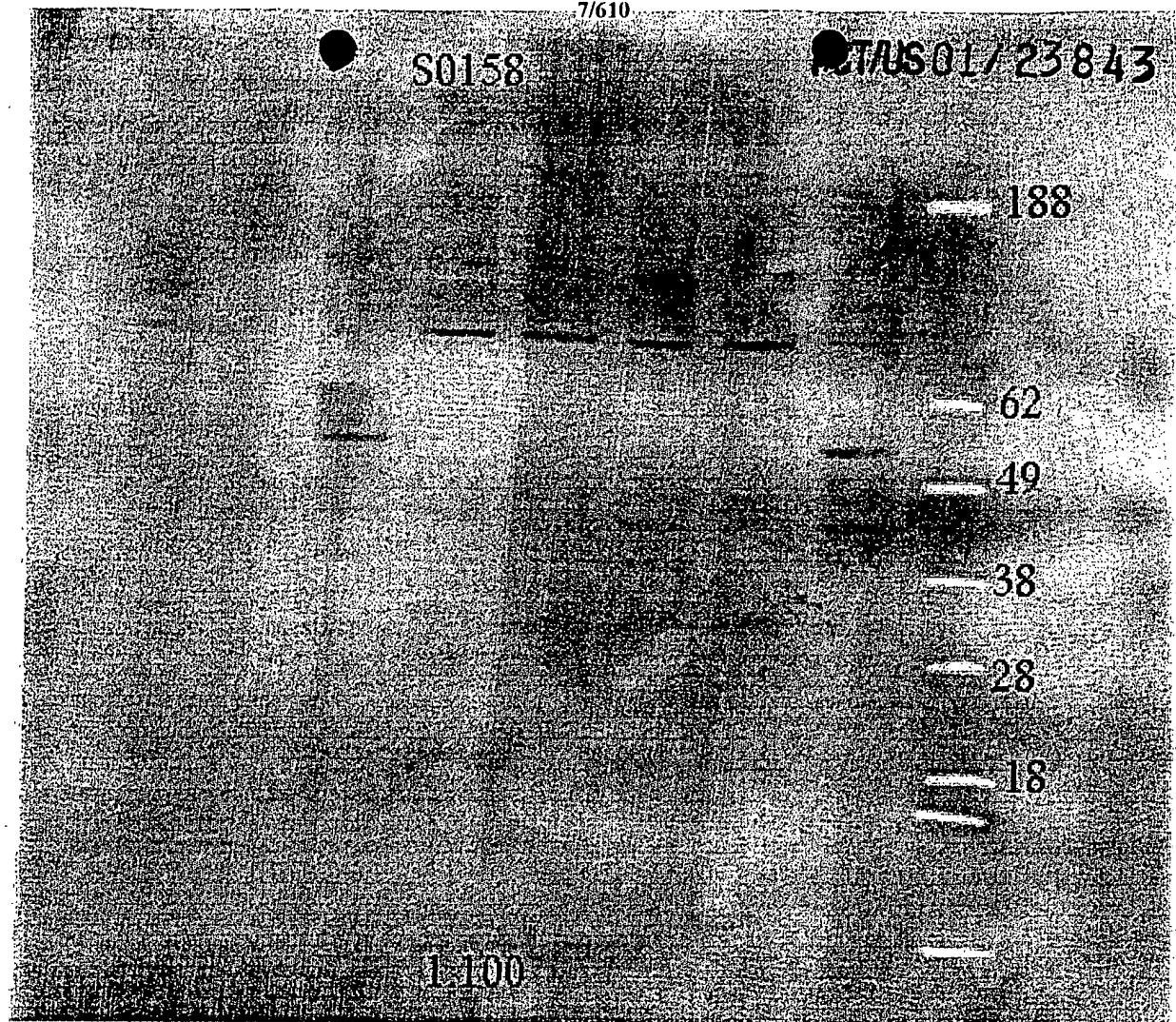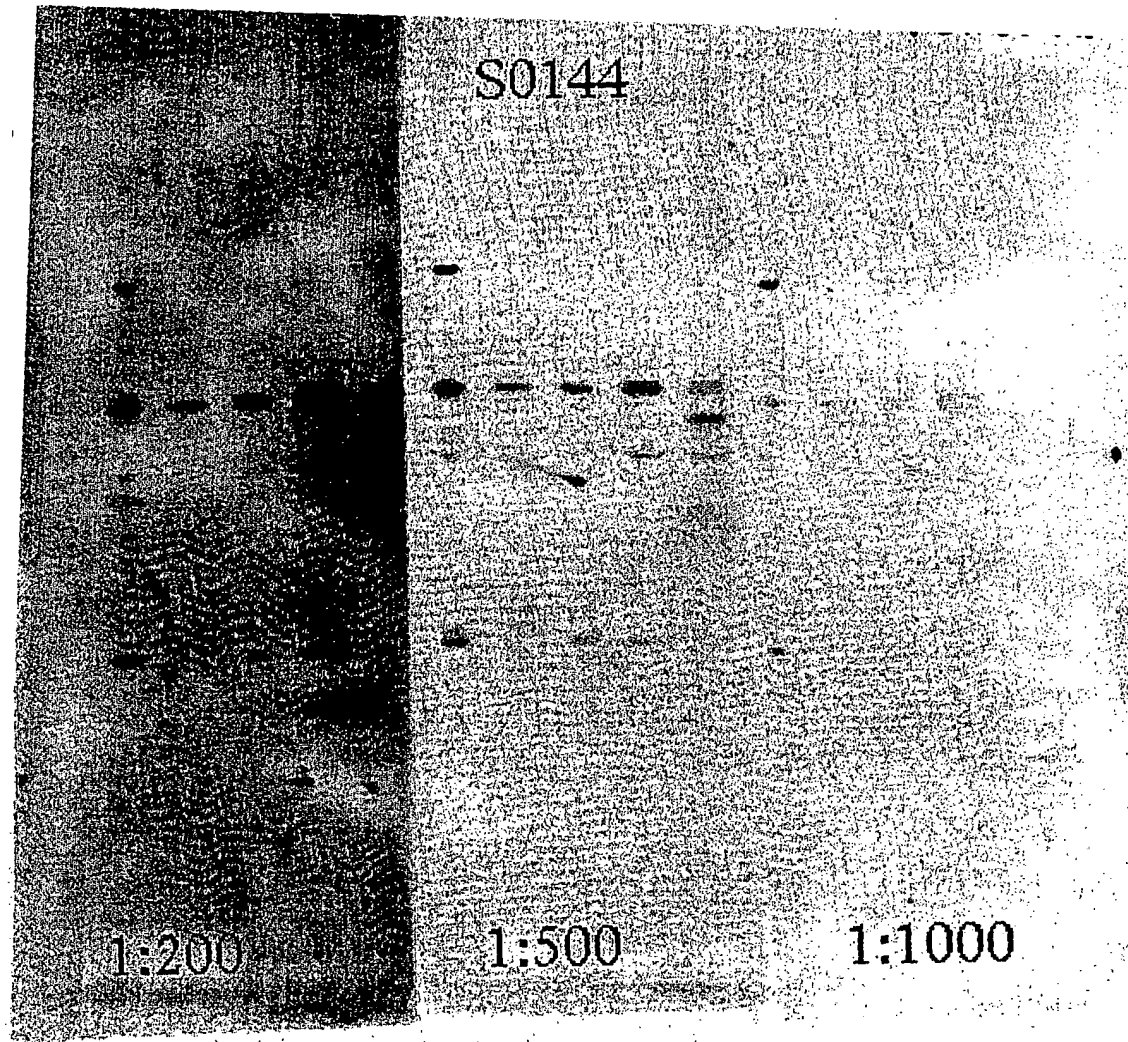
FIGURE 4A

FIGURE 4B
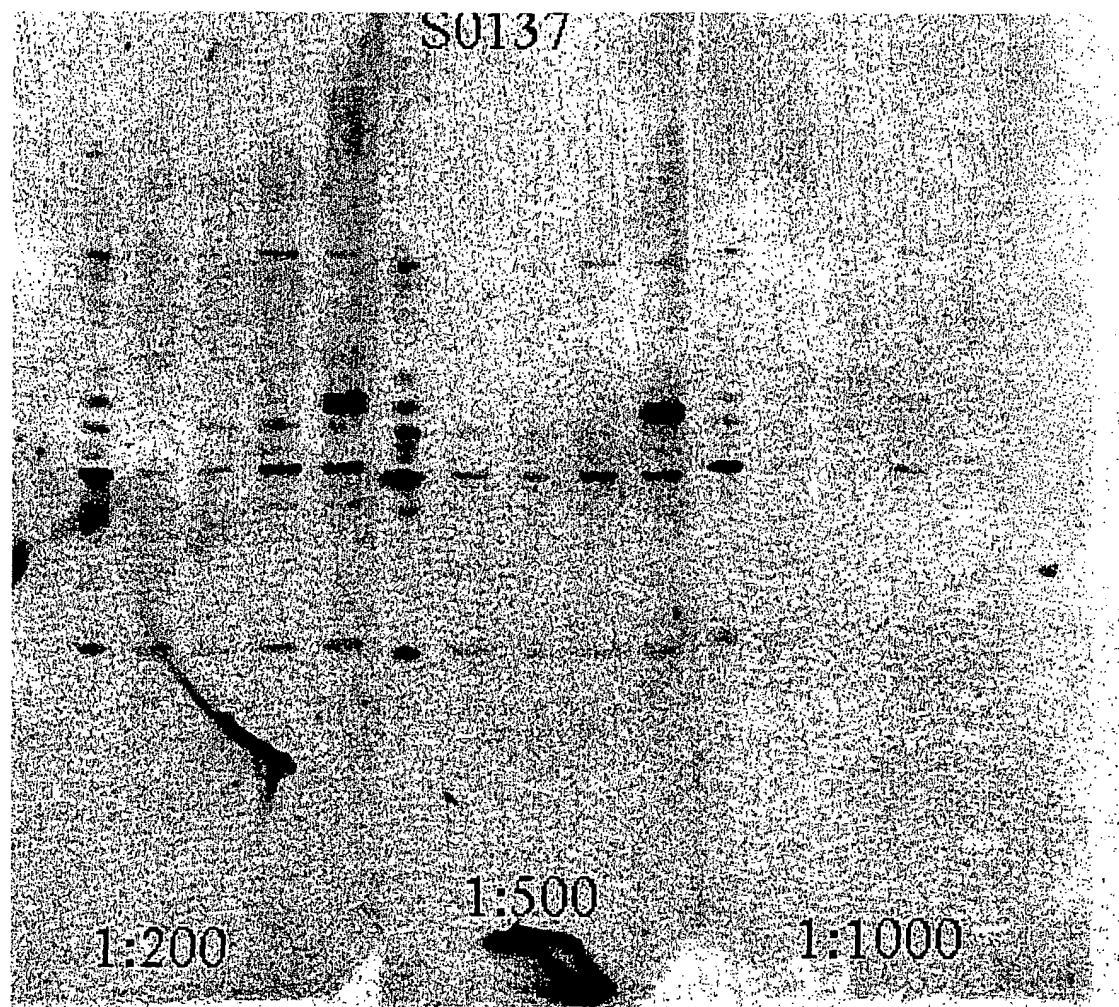
FIGURE 4C

Figure 5A
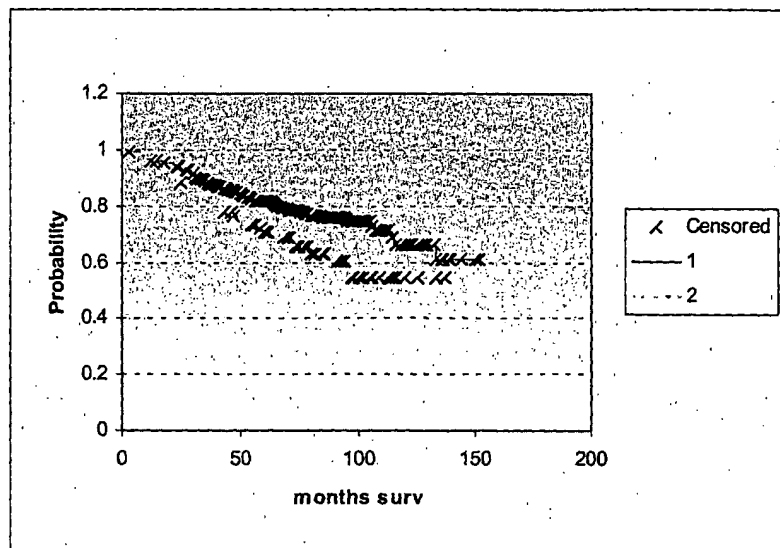
Figure 5B
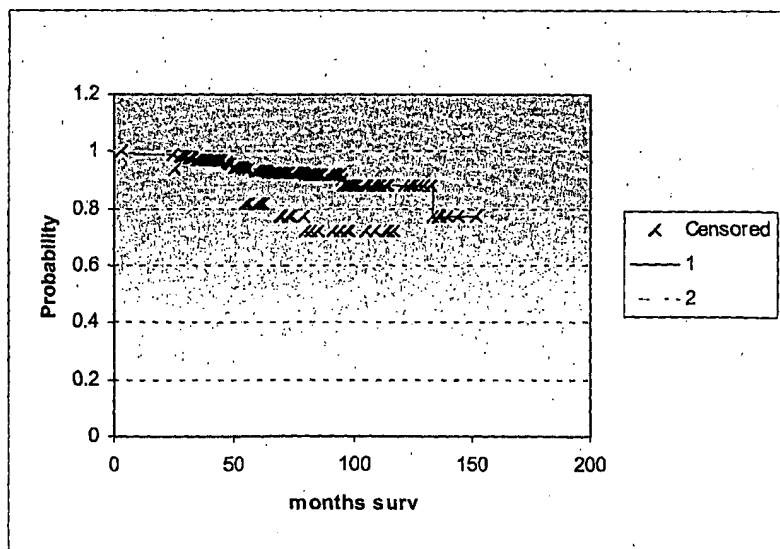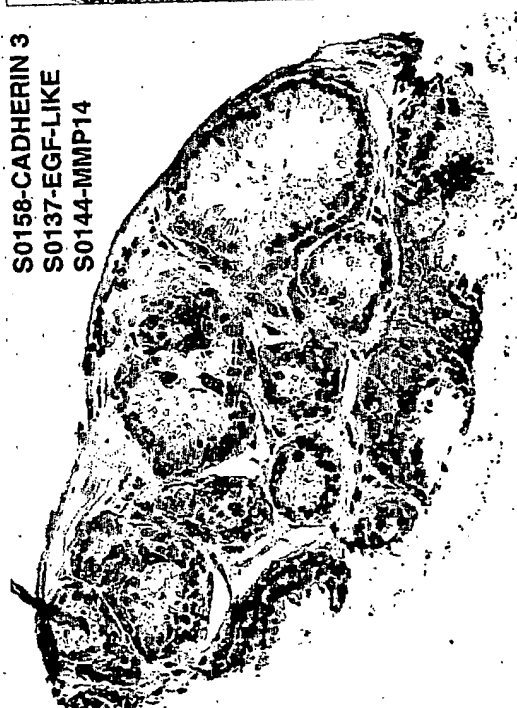
FIGURE 6

A. CK5/6

B. S0137

C. S0158

FIGURE 7

Table 3

Common Reference Cell Line List

Name	Description	ATCC# or Reference
MCF7	breast adenocarcinoma derived cell line	ATCC #HTB-22
Hs578T	breast carcinosarcoma derived cell line	ATCC #HTB-126
NTERA2	teratoma derived cell line	ATCC #CRL-1973
Colo205	colon tumor derived cell line	ATCC #CCL-222
OVCAR-3	ovarian tumor derived cell line	ATCC #HTB-161
UACC-62	melanoma derived cell line	Stinson et al. Anticancer Res. Jul-Aug;12(4):1035-53 1992
MOLT-4	T-cell leukemia derived cell line	ATCC #CRL-1582
RPMI-8226	multiple myeloma derived cell line	ATCC #CCL-155
NB4+ATRA	APL-like cell line	Lanotte et al. Blood. Mar 1;77(5):1080-6, 1991
SW872	liposarcoma derived cell line	ATCC #HTB-92
HepG2	liver tumor derived cell line	ATCC #HB-8065

Table 4

TUMOR + TISSUE SAMPLES

Array ID	Sample ID/old name	Patient ID	New Name	Comments: before and after pair (Y or N), etc.
svcc98.2	BC107B-BE	norway 7	NORWAY 7-BE	yes
svcc63.2	BC107A-AF	norway 7	NORWAY 7-AF	
svcc78.2	BC110B-BE	norway 10	NORWAY 10-BE	yes
svcc77.2	BC110A-AF	norway 10	NORWAY 10-AF	
svcc122.2	BC111A-BE	norway 11	NORWAY 11	no, no after
svcc68.2	BC111B-BE	norway 19	NORWAY 19	no, no after
svcc53.2	BC112B-BE	norway 12	NORWAY 12-BE	yes
svcc97.2	BC112A-AF	norway 12	NORWAY 12-AF	
svcc81.2	BC114A-BE	norway 14	NORWAY 14-BE	yes
svcc52.2	BC114B-AF	norway 14	NORWAY 14-AF	
svcc106.2	BC115B-BE	norway 15	NORWAY 15-BE	yes
svcc64.2	BC115A-AF	norway 15	NORWAY 15-AF	
svcc108.2	BC116A-BE	norway 16	NORWAY 16	no, no after
svcc88.2	BC117A-BE	norway 17	NORWAY 17	no, no after
svcc134.2	BC118B-BE	norway 18	NORWAY 18-BE	yes
svcc112.2	BC118A-AF	norway 18	NORWAY 18-AF	
svcc89.2	BC123B-BE	norway 26	NORWAY 26-BE	yes
svcc91.2	BC123A-AF	norway 26	NORWAY 26-AF	
svcc111.2	BC124A-BE	norway 27	NORWAY 27-BE	yes
svcc109.2	BC124B-AF	norway 27	NORWAY 27-AF	
svcc1077.2	BC1257	new york 1	NEW YORK 1	no
svcc132.2	BC1369	new york 2	NEW YORK 2	no
svcc61.2	BC14	stanford 14	STANFORD 14	no
svcc137.2	BC16	stanford 16	STANFORD 16	no
svcc119.2	BC17	stanford 17	STANFORD 17	no
svcc96.2	BC2	stanford 2	STANFORD 2-P	primary tumor
svcc113.2	BC2-LN2	stanford 2	STANFORD 2-LN	lymph node metastasis
svcc93.2	BC206A-BE	norway 39	NORWAY 39-BE	yes
svcc135.2	BC206B-AF	norway 39	NORWAY 39-AF	
svcc107.2	BC208A-BE	norway 41	NORWAY 41-BE	yes
svcc125.2	BC208B-AF	norway 41	NORWAY 41-AF	
svcc76.2	BC213B-BE	norway 47	NORWAY 47-BE	yes
svcc79.2	BC213A-AF	norway 47	NORWAY 41-AF	
svcc92.2	BC214B-BE	norway 48	NORWAY 48-BE	yes
svcc103.2	BC214A-AF	norway 48	NORWAY 48-AF	
svcc99.2	BC23	stanford 23	STANFORD 23	no
svcc100.2	BC24	stanford 24	STANFORD 24	no.

Table 4

svcc131.2	BC305A-BE	norway 53	NORWAY 53-BE	yes	
svcc58.2	BC305B-AF	norway 53	NORWAY 53-AF		
svcc87.2	BC308B-BE	norway 56	NORWAY 56	no, no after	
svcc51.2	BC309A-BE	norway 57	NORWAY 57	no, no after	
svcc118.2	BC35-0	stanford 35	STANFORD 35	no	
svcc117.2	BC37-FA	stanford 37	STANFORD 37-FA	no	
svcc115.2	BC38	stanford 38	STANFORD 38-P	Lymph node met of tumor/LNmet pair 2	
svcc116.2	BC38-LN38	stanford 38	STANFORD 38-LN	is a LN met with NO corresponding primary tumor sample	
svcc83.2	BC402B-BE	norway 61	NORWAY 61-BE	yes	
svcc66.2	BC403B-AF	norway 61	NORWAY 61-AF		
svcc123.2	BC406A-BE	norway 65	NORWAY 65	no, no after	
svcc104.2	BC708B-BE	norway 100	NORWAY 100-BE	yes	
svcc86.2	BC708A-AF	norway 100	NORWAY 100-AF		
svcc84.2	BC709B-BE	norway 101	NORWAY 101-BE	yes	
svcc85.2	BC709A-AF	norway 101	NORWAY 101-AF		
svcc101.2	BC710A-BE	norway 102	NORWAY 102-BE	yes	
svcc82.2	BC710B-AF	norway 102	NORWAY 102-AF		
svcc120.2	BC711B-BE	norway 104	NORWAY 104-BE	yes	
svcc65.2	BC711A-AF	norway 104	NORWAY 104-AF		
svcc130.2	BC790	new york 3	NEW YORK 3	no	
svcc105.2	BC805A-BE	norway 109	NORWAY 109-BE	yes	
svcc121.2	BC805B-AF	norway 109	NORWAY 109-AF		
svcc55.2	BC807A-BE	norway 111	NORWAY 111	no, no after	
svcc124.2	BC808A-BE	norway 112	NORWAY 112-BE	yes	
svcc126.2	BC808A-AF	norway 112	NORWAY 112-AF		
svcc70.2	Normal Breast 1	clontech 1	NORMAL 1	Normal Breast 1 (6 pooled whole normal breasts specimens)	
svcc127.2	Normal Breast2	clontech 2	NORMAL 2	Normal Breast 2 (2 pooled whole nomral breast specimens)	
svcc18.2	NorwNorBst1	norway NB	NORMAL 3	NorwNorBst1 (sample from a single individual)	
CELL LINE SAMPLES					
svcc128.2	BT-474	Cell line	BT-474	cell line; luminal epithelial, ERBB2 positive	
svcc69.2	BT-549	Cell line	BT-549	cell line; breast derived	
svcc500.2	HMEC+INFa	Cell line	HMEC+IFNα	cell line; HMEC-C isolate, basal epithelial cell line plus IFN alpha	
svcc94.2	HMEC-C	Cell line	HMEC-C	cell line; HMEC-C isolate, basal epithelial cell line untreated	
svcc47.2	HMEC-C_Confl2	Cell line	HMEC-C CON	cell line; HMEC-C isolate, basal epithelial cell line after 2 days at 100% confluence	
svcc41.2	HMVEC	Cell line	HMVEC	cell line; dermal microvacsular endothelial cells	
svcc110.2	Hs578T	Cell line	Hs578T	cell line; breast carcinosarcoma derived	
svcc42.2	HUVEC	Cell line	HUVEC	cell line; human umbilical vein derived endothelial cell line	
svcc1299.2	MCF7-NCI	Cell line	MCF7	cell line; luminal epithelial, Estrogen receptor positive	

Table 4

svcc73.2	MDA-MB-321	Cell line	MDA-MB-231	cell line; breast derived
svcc72.2	MOLT4	Cell line	MOLT4	cell line; t-cell leukemia derived
svcc67.2	NB4+ATRA	Cell line	NB4+ATRA	cell line; neutrophil-like after Retinoic Acid induced differentiation (72 hours)
svcc54.2	RPMI-8226	Cell line	RPMI-8226	cell line; b-cell like (derived from a multiple myeloma)
svcc15.2	SK-BR-3	Cell line	SK-BR-3	cell line; luminal epithelial, ERBB2 positive;
svcc74.2	SW872	Cell line	SW872	cell line;liposacroma derived cell line
svcc71.2	T47D	Cell line	T47D	cell line; luminal epithelial, Estrogen receptor positive
svcc38.2	184A1-LATE	Cell line	184A1	cell line; basal epithelial, immortal derivative of 184Aa
svcc17.2	184Aa	Cell line	184Aa	cell line; basal epithelial, a second HMEC isolate unrelated to HMEC-C
svcc40.2	184B5	Cell line	184B5	cell line; basal epithelial, immortal derivative of 184Aa

Legend for Table 5

1= tumor name as it appears in the figures
2= clinical estrogen receptor status (determined by dextran binding assay or immunohistochemistry)
3= average R/G ratio of two independent sequence verified *ESR1* clones (the correlation between clinical ER status and the microarray data is best if one calls a R/G ratio of 2.25 or greater "positive" for estrogen receptor status)
4= *Erb-B2* clinical status as determined using immunohistochemistry
5= average R/G ratio of four independent sequence verified *Erb-B2* clones (the correlation between clinical ERBB2 status and the microarray data is best if one calls a microarray ratio of 3.15 or greater "positive")
6= tumor grade
7= differentiation status
8= patient survival status: NED=no evidence of disease, AWD=alive with disease, DOD=dead of disease, DOC=dead of other cause
9= survival time in months
10= age at diagnosis
11=doxorubicin response: PR = reduction in tumor of 50% or more, PD = increase in tumor size over the course of the doxorubicin therapy, NT = not tested (described in T. Aas et al., Nature Medicine Vol. 2, p811-814 (1996))
12= p53 mutational status summary
13= p53 gene codon affected by mutation, if present
14= p53 gene nucleotide change identified
15= effect on p53 amino acid sequence, if applicable
16= additional findings and notes

Table 5

	TUMOR ID	NEW YORK 3	STANFORD 14	NORWAY 41	STANFORD 23	NEW YORK 2	NORWAY 109	NORWAY 53
2	ESR Clinical	negative	negative	positive	negative	negative	negative	positive
3	ESR Array	0.42	1.25	1.1	0.83	1	0.44	0.93
4	ERBB2 Clinical	not tested	not tested	negative	negative	not tested	negative	positive
5	ERBB2 Array	3.4	6.1	2.97	1.48	1.7	1.35	21.5
6	Tumor Grade	3	2	3	3	3	3	3
7	Differentiation	DUCTAL	DUCTAL	DUCTAL	DUCTAL	DUCTAL	DUCTAL	ductal
8	Survival Status	DOD	AWD	DOD	NED	DOD	NED	DOD
9	Survival Time	6	28	9	14	12	26	34
10	Age at Diagnosis	80	57	49	34	54	48	32
11	Doxorubicin Response	NT	NT	PR	NT	NT	PR	PR
12	p53 Status	missense	missense	missense	frameshift	not tested	nonsense	frameshift
13	p53 Codon	178	248	273	294		213	239-242
14	p53 Mutation	CAC->CCC	CGG-CAG	CGT->CAT	G deletion		CGA->TGA	11bp del
15	p53 A.A. Seq	his->pro	arg->gln	arg->his	frameshift		arg->stopp	frameshift
16	Special Notes					had a high p53 immunostaining value		

Table 5

	TUMOR ID	STANFORD 2	NORWAY 57	NORWAY 47	NORWAY 101	STANFORD 37-FA	NORWAY 61	NORWAY 65
2	ESR Clinical	negative	negative	positive	positive	not tested	positive	negative
3	ESR Array	1	0.88	2.28	0.47	2.25	2.27	8.6
4	ERBB2 Clinical	positive	positive	not tested	positive	not tested	positive	negative
5	ERBB2 Array	22.6	15.5	9.5	23.3	4.44	12.1	1.52
6	Tumor Grade	3	3	not tested	3		2	3
7	Differentiation	ductal	ductal	DCIS	ductal	fibroadenoma	lobular	ductal
8	Survival Status	DOD	DOD	NED	AWD	NED	NED	DOD
9	Survival Time	6	10	66	20	14	57	23
10	Age at Diagnosis	44	46	51	73	32	58	66
11	Doxorubicin Response	NT	PD	PR	PR	NT	PR	PD
12	p53 Status	missense	missense	WT	nonsense	not tested	WT	WT
13	p53 Codon	273	248		136			
14	p53 Mutation	CGT->TGT	CGG->CAG		CAA->TAA			
15	p53 A.A. Seq	arg->cys	arg->gln		gln->stopp			
16	Special Notes					benign lesion		

Table 5

TUMOR ID	NORWAY 112	NORWAY 14	STANFORD 17	NORWAY 48	NORWAY 15	NORWAY 7	NORWAY 26
ESR Clinical	positive	positive	positive	negative	positive	positive	positive
ESR Array	3.35	0.71	9.1	0.81	5.48	6	9.1
ERBB2 Clinical	negative	negative	not tested	negative	negative	negative	positive
ERBB2 Array	1.75	8.15	4.6	2.7	1.57	1.9	10.8
Tumor Grade	3	2	2	3	3	2	2
Differentiation	DUCTAL	ductal	ductal	ductal	ductal	ductal	ductal
Survival Status	NED	DOD	NED	DOD	NED	AWD	DOD
Survival Time	22	12	35	7	79	89	43
Age at Diagnosis	37	82	53	54	47	66	72
Doxorubicin Response	PD	PR	NT	PD	PR	PR	PD
p53 Status	WT	WT	WT	WT	missense	missense	frameshift
p53 Codon					163	273	217-221
p53 Mutation					TAC->TGC	CGT->CAT	14bp del
p53 A.A. Seq					tyr->cys	arg->his	frameshift
Special Notes					p16 mutant (145 Ile->val)		

Table 5

		NORWAY 17	NORWAY 39	NORWAY 100	NORWAY 12	NORWAY 104	NORWAY 11	NORWAY 19
1	TUMOR ID							
2	ESR Clinical	positive	positive	positive	positive	positive	positive	positive
3	ESR Array	32.9	12	19	31.88	10.8	8.65	7.9
4	ERBB2 Clinical	negative	negative	negative	positive	positive	positive	negative
5	ERBB2 Array	2.5	1.46	1.45	3.9	3.15	3.3	1.43
6	Tumor Grade	2	2	3	3	3	3	3
7	Differentiation	ductal	ductal	ductal	ductal	ductal	ductal	ductal
8	Survival Status	NED	NED	DOD	DOD	NED	DOD	DOD
9	Survival Time	80	67	17	8	31	15	20
10	Age at Diagnosis	76	85	47	75	44	67	74
11	Doxorubicin Response	PR	PR	PR	PR	PD	PD	PD
12	p53 Status	WT	missense	nonsense	WT	WT	nonsense	missense
13	p53 Codon		237	165			204	249
14	p53 Mutation		ATG->ATT	CAG->TAG			GAG->TAG	AGG->GGG
15	p53 A.A. Seq		met->ile	gln->stopp			glu->stopp	arg->gly
16	Special Notes							

Table 5

	NORWAY 10	NORWAY 102	NEW YORK 1	STANFORD 35	STANFORD 38	STANFORD 16	NORWAY 111
1 TUMOR ID							
2 ESR Clinical	positive	positive	not tested	positive	positive	positive	positive
3 ESR Array	4.6	12.3	16	10.93	14.5	21.6	18.9
4 ERBB2 Clinical	negative	negative	not tested	positive	positive	not tested	negative
5 ERBB2 Array	2.2	2.2	2.4	2.47	5.76	1.68	0.87
6 Tumor Grade	2	3	2	3	2	3	3
7 Differentiation	lobular	ductal	ductal	ductal	ductal	ductal	ductal
8 Survival Status	DOD	NED	AWD	?	?	DOD	NED
9 Survival Time	30	29	188	?	10	14	30
10 Age at Diagnosis	58	65	46	52	45	77	55
11 Doxorubicin Response	PR	PR	NT	NT	NT	NT	PR
12 p53 Status	WT	WT	not tested	missense	WT	missense	WT
13 p53 Codon				173		273	
14 p53 Mutation				GTG->ATG		CGT->TGT	
15 p53 A.A. Seq				val->met		arg->cys	
16 Special Notes			tumor sample tested was from a metastasis to ovary				

Table 5

#	TUMOR ID	STANFORD 24	NORWAY 27	NORWAY 18	NORWAY 16	NORWAY 56
1						
2	ESR Clinical	positive	positive	positive	positive	positive
3	ESR Array	16.99	29	27.81	18.9	33
4	ERBB2 Clinical	negative	negative	negative	negative	negative
5	ERBB2 Array	1.88	2.8	2.32	3.96	1.49
6	Tumor Grade	2	1	2	3	3
7	Differentiation	ductal	ductal	ductal	ductal	ductal
8	Survival Status	NED	AWD	DOC	NED	NED
9	Survival Time	13	73	33	78	61
10	Age at Diagnosis	69	77	66	74	64
11	Doxorubicin Response	NT	PR	PR	PR	PR
12	p53 Status	WT	WT	WT	WT	WT
13	p53 Codon					
14	p53 Mutation					
15	p53 A.A. Seq					
16	Special Notes					

Table 6

GID	UID	NAME
AID		
EWEIGHT		
1 GENE369X	GF201:96(97D9):384(13H18)	AMYLO-1,6-GLUCOSIDASE, 4-ALPHA-GLUCANOTRANSFERASE (GLYCOGEN DEBRANCHING ENZYME, GLYCOGEN STORAGE DISEASE TYPE III) AA668425
2 GENE437X	PEROU:96(4C5):384(19F9)	GDNF FAMILY RECEPTOR ALPHA 1 AA512935
3 GENE15X	GF200:96(12C7):384(3F13)	GLUTATHIONE S-TRANSFERASE THETA 2 AA490777
4 GENE174X	GF200:96(7H5):384(2P10)	HUMAN CLONE 23907 MRNA SEQUENCE R06567
5 GENE74X	GF200:96(19B3):384(5D6)	A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 15 (METARGIDIN) AA292676
6 GENE449X	PEROU:96(6C4):384(20E8)	B-FACTOR, PROPERDIN H80257
7 GENE367X	GF201:96(97C2):384(13F4)	B-FACTOR, PROPERDIN AA401441
8 GENE57X	GF200:96(17D7):384(5G13)	MUCIN 1, TRANSMEMBRANE AA488073
9 GENE425X	PEROU:96(1G8):384(19M15)	156053 R72491
10 GENE385X	GF202:96(109D11):384(15G21)	SELENIUM BINDING PROTEIN 1 T65736
11 GENE356X	GF201:96(96E2):384(13I4)	ZA {REGION BETWEEN EXONS 35 AND 36 OF THE COMPLEMENT COMPONENT C4 GE} [HUMAN, FETAL ADRENAL GLAND, MRNA, 830 NT] AA664406
12 GENE131X	GF200:96(29D11):384(8G21)	ESTS, HIGHLY SIMILAR TO TRANSCRIPTION ELONGATION FACTOR TFIIS.H [H.SAPIENS] R09980
13 GENE162X	GF200:96(6D1):384(2G2)	KIAA0307 GENE PRODUCT AA019774
14 GENE252X	GF201:96(68E7):384(24I14)	H2A HISTONE FAMILY, MEMBER L N50797
15 GENE284X	GF201:96(85D6):384(10H12)	H2B HISTONE FAMILY, MEMBER Q AA010223
16 GENE172X	GF200:96(7D9):384(2H18)	H2B HISTONE FAMILY, MEMBER Q AA456695
17 GENE368X	GF201:96(97C6):384(13F12)	B-CELL CLL/LYMPHOMA 2 W63749
18 GENE403X	GF202:96(114A6):384(16A12)	ESTS, WEAKLY SIMILAR TO MEMBRANE GLYCOPROTEIN [M.MUSCULUS] AA159578
19 GENE383X	GF201:96(99H6):384(14O11)	51700 H22854
20 GENE474X	PEROU:96(8C5):384(20F9)	NEBULETTE N77806
21 GENE138X	GF200:96(31C3):384(8F6)	HUMAN DNA SEQUENCE FROM CLONE 167A19 ON CHROMOSOME 1P32.1-33. CONTAINS THREE GENES FOR NOVEL PROTEINS, THE DIO1 GENE FOR TYPE I IODOTHYRONINE DEIODINASE (EC 3.8.1.4, TXDI1, ITDI1) AND AN HNRNP A3 (HETEROGENOUS NUCLEAR RIBONUCLEOPR N74025
22 GENE293X	GF201:96(87B9):384(11C17)	PROLACTIN RECEPTOR R63647
23 GENE482X	PEROU:96(9B3):384(18D6)	202658 H53479
24 GENE471X	PEROU:96(8B3):384(20D5)	202658 H53479
25 GENE391X	GF202:96(111A12):384(15B24)	609283 AA167189
26 GENE316X	GF201:96(89G11):384(11N22)	MYOSIN VI AA625890
27 GENE132X	GF200:96(29E4):384(8I7)	470216 AA028987
28 GENE444X	PEROU:96(6B10):384(20C20)	N-ACETYLTRANSFERASE 1 (ARYLAMINE N-ACETYLTRANSFERASE) R91803
29 GENE217X	GF201:96(57B11):384(21D22)	HOMO SAPIENS MRNA; CDNA DKFZP434A091 (FROM CLONE DKFZP434A091) AA431988
30 GENE232X	GF201:96(64C7):384(23E14)	358936 W92233
31 GENE140X	GF200:96(32E12):384(8J23)	SEVEN IN ABSENTIA (DROSOPHILA) HOMOLOG 2 AA029041
32 GENE122X	GF200:96(26H10):384(7O20)	HEPSIN (TRANSMEMBRANE PROTEASE, SERINE 1) H62162

Table 6

33	GENE228X	GF201:96(61A3):384(22B6)	417081 W87826
34	GENE475X	PEROU:96(8D12):384(20H23)	470105 AA029949
35	GENE304X	GF201:96(88E10):384(11I20)	HUMAN SECRETORY PROTEIN (P1.B) MRNA, COMPLETE CDS N74131
36	GENE465X	PEROU:96(7F6):384(20L12)	HEPATOCYTE NUCLEAR FACTOR 3, ALPHA T74639
37	GENE271X	GF201:96(82C9):384(9F17)	X-BOX BINDING PROTEIN 1 W90128
38	GENE439X	PEROU:96(4D8):384(19H15)	ESTROGEN RECEPTOR 1 AA291702
39	GENE351X	GF201:96(96A7):384(13A14)	ESTROGEN RECEPTOR 1 AA291749
40	GENE17X	GF201:96(12E12):384(3I23)	GATA-BINDING PROTEIN 3 H72474
41	GENE479X	PEROU:96(9A4):384(18B8)	GATA-BINDING PROTEIN 3 R31441
42	GENE441X	PEROU:96(6A11):384(20A22)	GATA-BINDING PROTEIN 3 R31442
43	GENE483X	PEROU:96(9B5):384(18D10)	ANNEXIN XXXI N76688
44	GENE178X	GF201:96(8C12):384(2F23)	HUMAN BREAST CANCER, ESTROGEN REGULATED LIV-1 PROTEIN (LIV-1) MRNA, PARTIAL CDS H29407
45	GENE250X	GF201:96(67E2):384(24I3)	346321 W74079
46	GENE374X	GF201:96(98C7):384(13F13)	HUMAN CHROMOSOME 16 BAC CLONE CIT987SK-254P9 H23265
47	GENE196X	GF201:96(101C12):384(14F24)	71863 T52564
48	GENE267X	GF201:96(81E4):384(9J8)	271989 N31935
49	GENE3X	GF200:96(10C3):384(3E6)	ESTS, HIGHLY SIMILAR TO INOSITOL POLYPHOSPHATE 4-PHOSPHATASE TYPE II-ALPHA [H.SAPIENS] R86721
50	GENE481X	PEROU:96(9B2):384(18D4)	179211 H50224
51	GENE470X	PEROU:96(8B2):384(20D3)	179211 H50224
52	GENE222X	GF201:96(58D2):384(21H3)	MURINE LEUKEMIA VIRAL (BMI-1) ONCOGENE HOMOLOG T87515
53	GENE56X	GF200:96(17D5):384(5G9)	MURINE LEUKEMIA VIRAL (BMI-1) ONCOGENE HOMOLOG AA478036
54	GENE14X	GF200:96(12A2):384(3B3)	LUTHERAN BLOOD GROUP (AUBERGER B ANTIGEN INCLUDED) H24954
55	GENE372X	GF201:96(97G8):384(13N16)	HOMO SAPIENS (PWD) GENE MRNA, 3' END N26536
56	GENE238X	GF201:96(65D7):384(23H14)	782547 AA431796
57	GENE40X	GF200:96(14G9):384(4M18)	ACYL-COENZYME A DEHYDROGENASE, SHORT/BRANCHED CHAIN H96140
58	GENE277X	GF201:96(83C1):384(10E1)	CARNITINE PALMITOYLTRANSFERASE II N70848
59	GENE381X	GF201:96(99D10):384(14G19)	ALDO-KETO REDUCTASE FAMILY 7, MEMBER A2 (AFLATOXIN ALDEHYDE REDUCTASE) T62865
60	GENE31X	GF200:96(13D9):384(4G17)	CYTOCHROME P450, SUBFAMILY IIA (PHENOBARBITAL-INDUCIBLE), POLYPEPTIDE 7 T73031
61	GENE81X	GF200:96(1F2):384(1K3)	ANGIOTENSIN RECEPTOR 1 H66116
62	GENE319X	GF201:96(90E9):384(11I17)	LYMPHOID NUCLEAR PROTEIN RELATED TO AF4 H99588
63	GENE163X	GF200:96(6D3):384(2G6)	HUMAN MRNA FOR KIAA0303 GENE, PARTIAL CDS AA418846
64	GENE26X	GF200:96(12H10):384(3P19)	EPOXIDE HYDROLASE 2, CYTOPLASMIC R73525
65	GENE325X	GF201:96(91H2):384(12O3)	DUAL SPECIFICITY PHOSPHATASE 4 AA444049
66	GENE165X	GF200:96(6D8):384(2G16)	EGF-LIKE-DOMAIN, MULTIPLE 2 H39187
67	GENE105X	GF200:96(25C5):384(7E9)	CYCLIN D1 (PRAD1: PARATHYROID ADENOMATOSIS 1) AA487700
68	GENE142X	GF200:96(32G8):384(8N15)	ALPHA-1-ANTICHYMOTRYPSIN T80924
69	GENE431X	PEROU:96(2G10):384(19M20)	TREFOIL FACTOR 1 (BREAST CANCER, ESTROGEN-INDUCIBLE SEQUENCE EXPRESSED IN) R83818
70	GENE186X	GF200:96(9G1):384(3M1)	ESTS, MODERATELY SIMILAR TO CADHERIN 12 [H.SAPIENS] W02256

Table 6

71	GENE89X	GF200:96(22E10):384(6I20)	ESTS, MODERATELY SIMILAR TO CADHERIN 12 [H.SAPIENS] AA418564
72	GENE345X	GF201:96(95D3):384(13G5)	SMA3 AA028921
73	GENE22X	GF200:96(12G1):384(3N1)	FLAVIN CONTAINING MONOOXYGENASE 5 H52001
74	GENE323X	GF201:96(91C10):384(12E19)	HOMO SAPIENS BASIC TRANSCRIPTION FACTOR 2 P44 (BTF2P44) GENE, PARTIAL CDS, NEURONAL APOPTOSIS INHIBITORY PROTEIN (NAIP) AND SURVIVAL MOTOR NEURON PROTEIN (SMN) GENES, COMPLETE CDS W72437
75	GENE259X	GF201:96(79G2):384(9M3)	204740 H57306
76	GENE136X	GF200:96(2H4):384(1O8)	PLASMINOGEN ACTIVATOR, TISSUE AA453728
77	GENE123X	GF200:96(26H12):384(7O24)	H.SAPIENS MRNA FOR RAT HREV107-LIKE PROTEIN AA476543
78	GENE415X	PEROU:96(10B11):384(18D21)	ESTS WEAKLY SIMILAR TO HEAT SHOCK 27 KD PROTEIN [H.SAPIENS] AA010110
79	GENE128X	GF200:96(28E10):384(7I19)	ESTS, WEAKLY SIMILAR TO HSP 27 [H.SAPIENS] H57494
80	GENE240X	GF201:96(66D10):384(23H19)	267681 N25553
81	GENE155X	GF200:96(4G3):384(1N5)	547247 AA085318
82	GENE346X	GF201:96(95F4):384(13K7)	GLUTATHIONE S-TRANSFERASE THETA 1 H99813
83	GENE54X	GF200:96(16H3):384(4P5)	PARVALBUMIN AA010609
84	GENE191X	GF201:96(100C2):384(14E4)	50582 H17038
85	GENE347X	GF201:96(95G1):384(13M1)	GLUTAMATE DECARBOXYLASE 1 (BRAIN, 67KD) AA018457
86	GENE292X	GF201:96(87B4):384(11C7)	PROTEIN KINASE, CAMP-DEPENDENT, CATALYTIC, BETA AA018980
87	GENE291X	GF201:96(87A12):384(11A23)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, M H26426
88	GENE290X	GF201:96(87A11):384(11A21)	RAP1, GTPASE ACTIVATING PROTEIN 1 AA682897
89	GENE324X	GF201:96(91E8):384(12I15)	TRANSFORMING GROWTH FACTOR BETA-STIMULATED PROTEIN TSC-22 AA421687
90	GENE88X	GF200:96(22C1):384(6E2)	TISSUE SPECIFIC TRANSPLANTATION ANTIGEN P35B AA421687
91	GENE10X	GF200:96(11F5):384(3L10)	CHLORIDE CHANNEL, NUCLEOTIDE-SENSITIVE, 1A T52435
92	GENE337X	GF201:96(94A5):384(12B9)	KIAA0429 GENE PRODUCT AA676805
93	GENE242X	GF201:96(66D6):384(23H11)	504372 AA142842
94	GENE213X	GF201:96(56A5):384(21A10)	RETINOIC ACID RECEPTOR RESPONDER (TAZAROTENE INDUCED) 3 W47350
95	GENE45X	GF200:96(15C9):384(4F18)	TRANSPORTER 1, ABC (ATP BINDING CASSETTE) AA676637
96	GENE49X	GF200:96(15H8):384(4P16)	ESTS, HIGHLY SIMILAR TO SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA [H.SAPIENS] AA486367
97	GENE494X	PEROU:96(9G3):384(18N6)	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA AA079495
98	GENE493X	PEROU:96(9G2):384(18N4)	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA AA076085
99	GENE318X	GF201:96(90E5):384(11J9)	BONE MARROW STROMAL CELL ANTIGEN 2 AA485371
100	GENE376X	GF201:96(98F10):384(13L19)	INTERFERON-INDUCED PROTEIN 41, 30KD R54613
101	GENE71X	GF200:96(18H7):384(5O14)	INTERFERON-INDUCED PROTEIN 41, 30KD T62627
102	GENE305X	GF201:96(88E11):384(11I22)	INTERFERON-INDUCED PROTEIN 17 AA419251
103	GENE148X	GF200:96(4A8):384(1B15)	HUMAN MRNA FOR 56-KDA PROTEIN INDUCED BY INTERFERON AA489743
104	GENE61X	GF200:96(17H9):384(5O17)	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA448478
105	GENE492X	PEROU:96(9G1):384(18N2)	INTERFERON ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA075725
106	GENE116X	GF200:96(26C8):384(7E16)	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA432030

Table 6

107	GENE309X	GF201:96(88F1):384(11K2)	INTERFERON-STIMULATED PROTEIN, 15 KDA AA406020
108	GENE55X	GF200:96(17C9):384(5E17)	MYXOVIRUS (INFLUENZA) RESISTANCE 1, HOMOLOG OF MURINE (INTERFERON-INDUCIBLE PROTEIN P78) AA456886
109	GENE310X	GF201:96(88F3):384(11K6)	INTERFERON, ALPHA-INDUCIBLE PROTEIN 27 AA157813
110	GENE100X	GF200:96(24D3):384(6H5)	GLUTAMIC-OXALOACETIC TRANSAMINASE 2, MITOCHONDRIAL (ASPARTATE AMINOTRANSFERASE 2) AA487739
111	GENE406X	GF202:96(114E5):384(16I10)	509462 AA056377
112	GENE489X	PEROU:96(9D8):384(18H16)	416386 W86859
113	GENE11X	GF200:96(11G1):384(3N2)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] H97778
114	GENE205X	GF201:96(102D2):384(14H3)	85804 T72068
115	GENE432X	PEROU:96(2H1):384(19O2)	KIAA0182 AI023801
116	GENE442X	PEROU:96(6A8):384(20A16)	HOMO SAPIENS MRNA; CDNA DKFZP586C201 (FROM CLONE DKFZP586C201) R12563
117	GENE413X	GF202:96(116D8):384(16H15)	HOMO SAPIENS MRNA FOR HYPOTHETICAL PROTEIN AA487488
118	GENE477X	PEROU:96(8E4):384(20I7)	CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA036986
119	GENE419X	PEROU:96(10D1):384(18H1)	CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA036987
120	GENE107X	GF200:96(25E7):384(7I13)	CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA598508
121	GENE417X	PEROU:96(10C10):384(18F19)	PLACENTAL BIKUNIN (KUNITZ-TYPE SERINE PROTEASE INHIBITOR) AA031287
122	GENE261X	GF201:96(80F11):384(9K22)	HUMAN DNA SEQUENCE FROM CLONE 431H6 ON CHROMOSOME 16. CONTAINS A NOVEL GENE WITH SOME HOMOLOGY TO MOUSE HN1 (HEMATOLOGICAL AND NEUROLOGICAL EXPRESSED SEQUENCE 1) DOWNSTREAM OF A PUTATIVE CPG ISLAND. CONTAINS ESTS AND GSSS AA045658
123	GENE433X	PEROU:96(3B1):384(19D2)	KERATIN 18 AA070385
124	GENE59X	GF200:96(17G6):384(5M11)	KERATIN 8 AA598517
125	GENE414X	GF202:96(160G7):384(17N13)	44292 H06273
126	GENE90X	GF200:96(22E5):384(6I10)	TUMOR PROTEIN D52 AA459318
127	GENE210X	GF201:96(55F6):384(21K11)	PROTEIN KINASE, AMP-ACTIVATED, BETA 2 NON-CATALYTIC SUBUNIT N78582
128	GENE219X	GF201:96(57D11):384(21H22)	HOMO SAPIENS 14-3-3 PROTEIN MRNA, COMPLETE CDS AA609598
129	GENE0X	GF200:96(10A1):384(3A2)	124781 R01118
130	GENE227X	GF201:96(59D2):384(22G3)	365536 AA009596
131	GENE394X	GF202:96(111G2):384(15N4)	HOMO SAPIENS MRNA; CDNA DKFZP564H0223 (FROM CLONE DKFZP564H0223) AA160498
132	GENE226X	GF201:96(59C9):384(22E17)	CALMODULIN 1 (PHOSPHORYLASE KINASE, DELTA) R76554
133	GENE352X	GF201:96(96B1):384(13C2)	E2F TRANSCRIPTION FACTOR 5, P130-BINDING AA455521
134	GENE495X	PEROU:96(9G5):384(18N10)	530722 AA069820
135	GENE159X	GF200:96(5F11):384(2K21)	ATPASE, H+ TRANSPORTING, LYSOSOMAL (VACUOLAR PROTON PUMP) 21KD AA480826
136	GENE235X	GF201:96(64H11):384(23O22)	491778 AA115275
137	GENE4X	GF200:96(10D5):384(3G10)	LYSOPHOSPHOLIPASE 1 H00817
138	GENE457X	PEROU:96(6F3):384(20K6)	ESTS, WEAKLY SIMILAR TO KIAA0108 [H.SAPIENS] AA033947
139	GENE399X	GF202:96(112E11):384(15I21)	ESTS, WEAKLY SIMILAR TO KIAA0108 [H.SAPIENS] AA600214
140	GENE173X	GF200:96(7E12):384(2I24)	GAMMA-GLUTAMYL HYDROLASE (CONJUGASE, FOLYLPOLYGAMMAGLUTAMYL HYDROLASE) AA455800
141	GENE375X	GF201:96(98D9):384(13H17)	HOMO SAPIENS CLONE 23856 UNKNOWN MRNA, PARTIAL CDS AA487428

Table 6

142	GENE158X	GF200:96(5D4):384(2G7)	NUCLEOLAR PROTEIN P40 R45255
143	GENE92X	GF200:96(22H6):384(6O12)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, Y BOX-BINDING PROTEIN I; DNA-BINDING PROTEIN B AA599175
144	GENE143X	GF200:96(3C3):384(1F6)	PEPTIDYLPROLYL ISOMERASE F (CYCLOPHILIN F) H05580
145	GENE397X	GF202:96(112C10):384(15F19)	ESTS, WEAKLY SIMILAR TO R07G3.8 [C.ELEGANS] AA173423
146	GENE427X	PEROU:96(2A10):384(19A20)	TRANSFERRIN RECEPTOR (P90, CD71) N27985
147	GENE299X	GF201:96(88A12):384(11A24)	ESTS, HIGHLY SIMILAR TO MITOTIC KINESIN-LIKE PROTEIN-1 [H.SAPIENS] AA454098
148	GENE42X	GF200:96(15B4):384(4D8)	V-MYB AVIAN MYELOBLASTOSIS VIRAL ONCOGENE HOMOLOG-LIKE 2 AA456878
149	GENE272X	GF201:96(82D11):384(9H21)	430186 AA010188
150	GENE47X	GF200:96(15E12):384(4J24)	THYMOSIN, BETA 10 AA486085
151	GENE390X	GF202:96(110D6):384(15G12)	ECTODERMAL-NEURAL CORTEX (WITH BTB-LIKE DOMAIN) H72122
152	GENE389X	GF202:96(110D4):384(15G8)	HOMO SAPIENS MRNA; CDNA DKFZP434F152 (FROM CLONE DKFZP434F152) AA186605
153	GENE335X	GF201:96(93G12):384(12N24)	HOMO SAPIENS MRNA FOR LSM1 PROTEIN AA628430
154	GENE194X	GF201:96(101A7):384(14B14)	74223 T48412
155	GENE189X	GF201:96(100A10):384(14A20)	80292 T64433
156	GENE12X	GF200:96(11G7):384(3N14)	TRANSCRIPTION FACTOR AP-2 BETA (ACTIVATING ENHANCER-BINDING PROTEIN 2 BETA) AA018906
157	GENE286X	GF201:96(86B7):384(10D13)	URACIL-DNA GLYCOSYLASE 2 AA425900
158	GENE251X	GF201:96(68D5):384(24G10)	415229 W91879
159	GENE233X	GF201:96(64D4):384(23G8)	HOMO SAPIENS MRNA; CDNA DKFZP58612118 (FROM CLONE DKFZP58612118) R98407
160	GENE485X	PEROU:96(9C1):384(18F2)	297604 N69835
161	GENE473X	PEROU:96(8C4):384(20F7)	297604 N69835
162	GENE152X	GF200:96(4E5):384(1J9)	POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 1 (TWIK-1) N62620
163	GENE264X	GF201:96(80H6):384(9O12)	124447 R01094
164	GENE135X	GF200:96(2B10):384(1C20)	S100 CALCIUM-BINDING PROTEIN P R32952
165	GENE197X	GF201:96(101D6):384(14H12)	68818 T53431
166	GENE314X	GF201:96(89C12):384(11F24)	OCCLUDIN H94471
167	GENE60X	GF200:96(17H1):384(5O1)	JUNCTION PLAKOGLOBIN R06417
168	GENE422X	PEROU:96(10E9):384(18I17)	HOMO SAPIENS BREAST CANCER PUTATIVE TRANSCRIPTION FACTOR (ZABC1) MRNA, COMPLETE CDS AA460802
169	GENE421X	PEROU:96(10E8):384(18I15)	HOMO SAPIENS BREAST CANCER PUTATIVE TRANSCRIPTION FACTOR (ZABC1) MRNA, COMPLETE CDS AA782528
170	GENE9X	GF200:96(11D4):384(3H8)	LAMININ, ALPHA 5 AA459519
171	GENE77X	GF200:96(19F4):384(5L8)	773233 AA425259
172	GENE411X	GF202:96(116B10):384(16D19)	ESTS, WEAKLY SIMILAR TO KIAA0631 PROTEIN [H.SAPIENS] AA497001
173	GENE153X	GF200:96(4F3):384(1L5)	TRANSCRIPTION FACTOR AP-2 GAMMA (ACTIVATING ENHANCER-BINDING PROTEIN 2 GAMMA) AA399334
174	GENE246X	GF201:96(66H1):384(23P1)	KIAA0626 GENE PRODUCT N62737
175	GENE270X	GF201:96(82B4):384(9D7)	HUMAN DNA SEQUENCE FROM CLONE 71L16 ON CHROMOSOME XP11. CONTAINS A PROBABLE ZINC FINGER PROTEIN (PSEUDO)GENE, AN UNKNOWN PUTATIVE GENE, A PSEUDOGENE WITH HIGH SIMILARITY TO PART OF ANTIGEN KI-67, A PUTATIVE CHONDROITIN 6-SULFOTRAN W47116

Table 6

#	Gene	Clone	Description
176	GENE387X	GF202:96(110A5):384(15A10)	HOMO SAPIENS CLONE 23876 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN MRNA, PARTAL CDS H23124
177	GENE234X	GF201:96(64D5):384(23G10)	488431 AA047441
178	GENE334X	GF201:96(93E11):384(12122)	79935 T61475
179	GENE21X	GF200:96(12F4):384(3L7)	FUMARYLACETOACETATE H44956
180	GENE160X	GF200:96(5H10):384(2O19)	TRANSDUCER OF ERBB-2 AA490213
181	GENE146X	GF200:96(3D6):384(1H12)	DIAPHORASE (NADH/NADPH) (CYTOCHROME B-5 REDUCTASE) AA455538
182	GENE294X	GF201:96(87E9):384(11117)	DNA SEGMENT, SINGLE COPY PROBE LNS-CAI/LNS-CAII (DELETED IN POLYPOSIS H99681
183	GENE30X	GF200:96(13D4):384(4G7)	CYTOCHROME B-5 R92281
184	GENE491X	PEROU:96(9F3):384(18L6)	299664 N75017
185	GENE265X	GF201:96(81D9):384(9H18)	HOMO SAPIENS MRNA; CDNA DKFZP564J142 (FROM CLONE DKFZP564J142) N75017
186	GENE247X	GF201:96(66H8):384(23P15)	504678 AA142942
187	GENE326X	GF201:96(91H4):384(12O7)	KYNURENINASE; L-KYNURENINE HYDROLASE H87471
188	GENE41X	GF200:96(14H3):384(4O6)	ACTIVATED LEUCOCYTE CELL ADHESION MOLECULE R13558
189	GENE103X	GF200:96(24G9):384(6N17)	ELECTRON-TRANSFER-FLAVOPROTEIN, ALPHA POLYPEPTIDE (GLUTARIC ACIDURIA II) T58002
190	GENE119X	GF200:96(26F1):384(7K2)	130843 R22306
191	GENE379X	GF201:96(99B8):384(14C15)	PARAOXONASE 3 T57069
192	GENE121X	GF200:96(26G9):384(7M18)	PARAOXONASE 3 R95740
193	GENE348X	GF201:96(95G5):384(13M9)	GAP JUNCTION PROTEIN, BETA 1, 32KD (CONNEXIN 32, CHARCOT-MARIE-TOOTH NEUROPATHY, X-LINKED) N62394
194	GENE366X	GF201:96(97B6):384(13D12)	BONE MORPHOGENETIC PROTEIN 4 AA463225
195	GENE206X	GF201:96(55A8):384(21A15)	ACYL-COENZYME A OXIDASE 2, BRANCHED CHAIN T71782
196	GENE141X	GF200:96(32G3):384(8N5)	ESTS, HIGHLY SIMILAR TO AQUAPORIN 3 [H.SAPIENS] R91904
197	GENE322X	GF201:96(91A4):384(12A7)	470279 AA028905
198	GENE79X	GF200:96(1A9):384(1A17)	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY, MEMBER 5A W49672
199	GENE38X	GF200:96(14G12):384(4M24)	298155 N70794
200	GENE338X	GF201:96(94E8):384(12I15)	HUMAN HOX2.2 GENE FOR A HOMEOBOX PROTEIN AA610066
201	GENE68X	GF200:96(18G2):384(5M4)	HUMAN PROTEINASE ACTIVATED RECEPTOR-2 MRNA, 3'UTR AA454652
202	GENE461X	PEROU:96(7B4):384(20D8)	176461 H43515
203	GENE463X	PEROU:96(7B6):384(20D12)	364302 AA022462
204	GENE73X	GF200:96(19B1):384(5D2)	CREATINE KINASE, MITOCHONDRIAL 1 (UBIQUITOUS) AA019482
205	GENE358X	GF201:96(96F4):384(13K8)	CHROMOGRANIN B (SECRETOGRANIN 1) W37769
206	GENE95X	GF200:96(23H7):384(6P14)	M-PHASE PHOSPHOPROTEIN 6 AA478524
207	GENE203X	GF201:96(102B12):384(14D23)	83297 T68333
208	GENE154X	GF200:96(4G1):384(1N1)	3-OXOACID COA TRANSFERASE R40897
209	GENE207X	GF201:96(55D8):384(21G15)	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE AA136040
210	GENE229X	GF201:96(62H2):384(22P3)	302025 N89753
211	GENE28X	GF200:96(13C8):384(4E15)	ESTS, WEAKLY SIMILAR TO MEL-13A PROTEIN [M.MUSCULUS] AA464421
212	GENE260X	GF201:96(79G4):384(9M7)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.SAPIENS] AA454610

Table 6

213	GENE241X	GF201:96(66D12):384(23H23)	418240 W90241
214	GENE289X	GF201:96(86H1):384(10P1)	S100 CALCIUM-BINDING PROTEIN A8 (CALGRANULIN A) AA086471
215	GENE288X	GF201:96(86G1):384(10N1)	ESTS, HIGHLY SIMILAR TO STAT4 [M.MUSCULUS] R91570
216	GENE223X	GF201:96(58F9):384(21I.17)	UNTITLED R16098
217	GENE296X	GF201:96(87H11):384(11O21)	MATRIX METALLOPROTEINASE 15 (MEMBRANE-INSERTED) AA443300
218	GENE486X	PEROU:96(9C11):384(18F22)	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR AA025141
219	GENE428X	PEROU:96(2F1):384(19K2)	ERBB2 AA481939
220	GENE420X	PEROU:96(10E11):384(18J21)	ERBB2-POLYA X03363
221	GENE43X	GF200:96(15B6):384(4D12)	V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG) AA443351
222	GENE455X	PEROU:96(6E5):384(20I10)	V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG) AA025141
223	GENE312X	GF201:96(88H2):384(11I04)	GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 H53703
224	GENE97X	GF200:96(24B4):384(6D7)	STEROIDOGENIC ACUTE REGULATORY PROTEIN RELATED AA504710
225	GENE468X	PEROU:96(8A1):384(20B1)	68400 T57034
226	GENE440X	PEROU:96(6A1):384(20A2)	68400 T57034
227	GENE466X	PEROU:96(7F8):384(20L16)	SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY E, MEMBER 1 W63613
228	GENE98X	GF200:96(24B5):384(6D9)	TNF RECEPTOR-ASSOCIATED FACTOR 4 AA598826
229	GENE282X	GF201:96(84D8):384(10G16)	347348 W81186
230	GENE113X	GF200:96(26C12):384(7E24)	FLOTILLIN 2 R73545
231	GENE78X	GF200:96(19H6):384(5P12)	TGFB1-INDUCED ANTI-APOPTOTIC FACTOR 1 AA446222
232	GENE166X	GF200:96(6H10):384(2O20)	KIAA0130 GENE PRODUCT N76581
233	GENE150X	GF200:96(4B7):384(1D13)	ESTS, HIGHLY SIMILAR TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR [H.SAPIENS] H79047
234	GENE490X	PEROU:96(9E8):384(18J16)	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) AA054451
235	GENE171X	GF200:96(7D2):384(2H4)	HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) MRNA H08560
236	GENE306X	GF201:96(88E3):384(11I6)	HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) MRNA T52830
237	GENE1X	GF200:96(10A12):384(3A24)	PHOSPHOSERINE PHOSPHATASE-LIKE W05628
238	GENE137X	GF200:96(30G3):384(8M6)	122982 R00332
239	GENE109X	GF200:96(25G2):384(7M3)	CYTOCHROME C OXIDASE SUBUNIT VIC AA456931
240	GENE199X	GF201:96(101H5):384(14P10)	78921 T60482
241	GENE32X	GF200:96(13F4):384(4K7)	134783 R31701
242	GENE23X	GF200:96(12G2):384(3N3)	FIBRONECTIN 1 R62612
243	GENE221X	GF201:96(58A11):384(21B21)	H.SAPIENS MRNA FOR INHIBIN BETA(A) SUBUNIT N27159
244	GENE69X	GF200:96(7C3):384(2F6)	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE (CAM KINASE) II GAMMA T96083
245	GENE402X	GF202:96(114A5):384(16A10)	839904 AA490059
246	GENE330X	GF201:96(92E7):384(12I14)	MEMBRANE FATTY ACID (LIPID) DESATURASE W49667
247	GENE370X	GF201:96(97E4):384(13J8)	RIBOSOMAL PROTEIN L26 AA633569

Table 6

248	GENE216X	GF201:96(56E2):384(2I14)	HUMAN CHROMOSOME 16 BAC CLONE CIT987SK-A-362G6 N75498
249	GENE145X	GF200:96(3C7):384(1F14)	NON-SPECIFIC CROSS REACTING ANTIGEN AA054073
250	GENE396X	GF202:96(112A1):384(15B1)	261194 H98215
251	GENE278X	GF201:96(83E6):384(10I11)	503602 AA131299
252	GENE382X	GF201:96(99G5):384(14M9)	50114 H16743
253	GENE377X	GF201:96(99A4):384(14A7)	ESTS, HIGHLY SIMILAR TO CYTOPLASMIC DYNEIN LIGHT CHAIN 1 [H.SAPIENS] AA401429
254	GENE188X	GF200:96(9H12):384(3O23)	STEAROYL-COA DESATURASE (DELTA-9-DESATURASE) R00707
255	GENE168X	GF200:96(7A6):384(2B12)	LYSOSOMAL-ASSOCIATED MULTISPANNING MEMBRANE PROTEIN-5 AA410265
256	GENE6X	GF200:96(10G8):384(3M16)	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5 (16 KD) W55964
257	GENE269X	GF201:96(82B11):384(9D21)	345056 W72798
258	GENE273X	GF201:96(82F1):384(9L1)	487831 AA045083
259	GENE35X	GF200:96(14B7):384(4C14)	CATHEPSIN K (PYCNODYSOSTOSIS) R01515
260	GENE244X	GF201:96(66F1):384(23L1)	ESTS, WEAKLY SIMILAR TO MACROPHAGE LECTIN 2 [H.SAPIENS] N53421
261	GENE354X	GF201:96(96C1):384(13E2)	DERMATOPONTIN R48303
262	GENE429X	PEROU:96(2F2):384(19K4)	TISSUE INHIBITOR OF METALLOPROTEINASE 3 (SORSBY FUNDUS DYSTROPHY, PSEUDOINFLAMMATORY) AA445923
263	GENE435X	PEROU:96(3B9):384(19D18)	INTEGRIN, ALPHA 2 (CD49B, ALPHA 2 SUBUNIT OF VLA-2 RECEPTOR) AA069096
264	GENE149X	GF200:96(4B4):384(1D7)	INTEGRIN, ALPHA 2 (CD49B, ALPHA 2 SUBUNIT OF VLA-2 RECEPTOR) AA463610
265	GENE313X	GF201:96(89A1):384(11B2)	SER-THR PROTEIN KINASE RELATED TO THE MYOTONIC DYSTROPHY PROTEIN KINASE N35241
266	GENE129X	GF200:96(28E3):384(7I5)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 5262644) [H.SAPIENS] N91426
267	GENE384X	GF202:96(109C9):384(15E17)	MICROTUBULE-ASSOCIATED PROTEIN 1B AA219045
268	GENE266X	GF201:96(81E12):384(9I24)	259996 N32611
269	GENE215X	GF201:96(56C11):384(21E22)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.SAPIENS] N21103
270	GENE276X	GF201:96(83A5):384(10A9)	141726 R69584
271	GENE410X	GF202:96(115D7):384(16H14)	842848 AA486281
272	GENE212X	GF201:96(55G4):384(21M7)	C3H-TYPE ZINC FINGER PROTEIN; SIMILAR TO D. MELANOGASTER MUSCLEBLIND B PROTEIN W16832
273	GENE144X	GF200:96(3C6):384(1F12)	NUCLEAR FACTOR I/X (CCAAT-BINDING TRANSCRIPTION FACTOR) AA406269
274	GENE182X	GF200:96(9A3):384(3A5)	ESTS, HIGHLY SIMILAR TO LAR-INTERACTING PROTEIN 1A [H.SAPIENS] N52679
275	GENE94X	GF200:96(23F7):384(6L14)	FAS (TNFRSF6)-ASSOCIATED VIA DEATH DOMAIN AA430751
276	GENE263X	GF201:96(80H4):384(9O8)	ESTS, WEAKLY SIMILAR TO STRABISMUS [D.MELANOGASTER] T95333
277	GENE275X	GF201:96(82H5):384(9P9)	HOMO SAPIENS CLONE 23704 MRNA SEQUENCE N70212
278	GENE111X	GF200:96(26B7):384(7C14)	RAB6, MEMBER RAS ONCOGENE FAMILY H20138
279	GENE164X	GF200:96(6D7):384(2G14)	HUMAN MRNA FOR KIAA0280 GENE, PARTIAL CDS AA428746
280	GENE245X	GF201:96(66F4):384(23L7)	501731 AA127861
281	GENE183X	GF200:96(9A4):384(3A7)	V-MYC AVIAN MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG 1, LUNG CARCINOMA DERIVED R62862
282	GENE130X	GF200:96(29B7):384(8C13)	66864 T64994
283	GENE85X	GF200:96(21G10):384(6M19)	PATERNALLY EXPRESSED GENE 3 AA459941
284	GENE139X	GF200:96(31D12):384(8H24)	ESTS, WEAKLY SIMILAR TO PLACENTAL RIBONUCLEASE INHIBITOR [H.SAPIENS] N53214
285	GENE478X	PEROU:96(8H2):384(20P3)	N-MYC AA101678

Table 6

286	GENE408X	GF202:96(114H8):384(16O16)	KDEL (LYS-ASP-GLU-LEU) ENDOPLASMIC RETICULUM PROTEIN RETENTION RECEPTOR 3 AA181085
287	GENE190X	GF201:96(100B1):384(14C2)	51344 H21040
288	GENE13X	GF200:96(11H12):384(3P24)	MENINGIOMA (DISRUPTED IN BALANCED TRANSLOCATION) 1 R59212
289	GENE295X	GF201:96(87H1):384(11O1)	MONOAMINE OXIDASE B AA682423
290	GENE170X	GF200:96(7D12):384(2H24)	NEUREGULIN 1 R72075
291	GENE7X	GF200:96(10H9):384(3O18)	HEXABRACHION (TENASCIN C, CYTOTACTIN) T77595
292	GENE484X	PEROU:96(9B8):384(18D16)	TRANSFORMING GROWTH FACTOR, BETA 2 N48082
293	GENE33X	GF200:96(13H3):384(4O5)	CARBONIC ANHYDRASE II H23187
294	GENE361X	GF201:96(96G10):384(13M20)	CARNITINE ACETYLTRANSFERASE AA621218
295	GENE450X	PEROU:96(6C7):384(20E14)	RAS HOMOLOG GENE FAMILY, MEMBER B H89046
296	GENE82X	GF200:96(1F7):384(1K13)	RAS HOMOLOG GENE FAMILY, MEMBER B AA495846
297	GENE185X	GF200:96(9E4):384(3I7)	B-CELL TRANSLOCATION GENE 2 (PHEOCHROMACYTOMA CELL-3) H69582
298	GENE239X	GF201:96(65F2):384(23L4)	HOMO SAPIENS MRNA; CDNA DKFZP586B2420 (FROM CLONE DKFZP586B2420) W58343
299	GENE395X	GF202:96(111H12):384(15P24)	ESTS, HIGHLY SIMILAR TO SCK [H.SAPIENS] H10072
300	GENE24X	GF200:96(12G3):384(3N5)	FIBROMODULIN AA486471
301	GENE50X	GF200:96(16B4):384(4D7)	RIBONUCLEASE L (2',5'-OLIGOISOADENYLATE SYNTHETASE-DEPENDENT) T60223
302	GENE167X	GF200:96(7A12):384(2B24)	ACTIN-BINDING LIM PROTEIN AA406601
303	GENE124X	GF200:96(27B1):384(7D2)	FLAVIN CONTAINING MONOOXYGENASE 3 H71847
304	GENE177X	GF200:96(8C11):384(2F21)	179276 H50323
305	GENE224X	GF201:96(58G10):384(21N19)	SERUM-INDUCIBLE KINASE AA460152
306	GENE364X	GF201:96(97B1):384(13D2)	WASP FAMILY VERPROLIN-HOMOLOGOUS PROTEIN 3 AA629542
307	GENE407X	GF202:96(114G1):384(16M2)	HOMO SAPIENS DNA SEQUENCE FROM COSMID ICK0721Q ON CHROMOSOME 6. CONTAINS A 60S RIBOSOMAL PROTEIN L35A LIKE PSEUDOGENE, A GENE CODING FOR A 60S RIBOSOMAL PROTEIN L12 LIKE PROTEIN IN AN INTRON OF THE HSET GENE CODING FOR A KINESIN AA457543
308	GENE192X	GF201:96(100H6):384(14O12)	77911 T61269
309	GENE248X	GF201:96(67C6):384(24E11)	300038 N78909
310	GENE405X	GF202:96(114C7):384(16E14)	78736 T61888
311	GENE220X	GF201:96(57D6):384(21H12)	ENDOTHELIN RECEPTOR TYPE B N29914
312	GENE258X	GF201:96(79E10):384(9J19)	782730 AA447978
313	GENE424X	PEROU:96(1C10):384(19E19)	APOLIPOPROTEIN D AA457084
314	GENE36X	GF200:96(14D12):384(4G24)	APOLIPOPROTEIN D H15842
315	GENE315X	GF201:96(89F3):384(11L6)	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), SHORT BASIC DOMAIN, SECRETED, (SEMAPHORIN) 3C AA042990
316	GENE200X	GF201:96(102A3):384(14B5)	ESTS, WEAKLY SIMILAR TO F56A11.5 [C.ELEGANS] T61938
317	GENE300X	GF201:96(88B12):384(11C24)	LAMININ, ALPHA 3 (NICEIN (150KD), KALININ (165KD), BM600 (150KD), EPILEGRIN) AA001432
318	GENE204X	GF201:96(102D12):384(14H23)	46694 H10192
319	GENE297X	GF201:96(87H2):384(11O3)	MONOAMINE OXIDASE A AA011096
320	GENE371X	GF201:96(97E5):384(13J10)	ALDEHYDE DEHYDROGENASE 1, SOLUBLE AA664101
321	GENE418X	PEROU:96(10C7):384(18F13)	428431 AA004415

Table 6

322	GENE281X	GF201:96(84B4):384(10C8)	INTEGRAL MEMBRANE PROTEIN 2C N53447
323	GENE446X	PEROU:96(6B5):384(20C10)	HUMAN IG J CHAIN GENE H24896
324	GENE480X	PEROU:96(9A9):384(18B18)	IMMUNOGLOBULIN J CHAIN H24896
325	GENE63X	GF200:96(18A10):384(5A20)	HUMAN IG J CHAIN GENE T70057
326	GENE436X	PEROU:96(3E4):384(19J8)	CD36 ANTIGEN (COLLAGEN TYPE I RECEPTOR, THROMBOSPONDIN RECEPTOR) R09416
327	GENE34X	GF200:96(14B4):384(4C8)	CD36 ANTIGEN (COLLAGEN TYPE I RECEPTOR, THROMBOSPONDIN RECEPTOR) N39161
328	GENE398X	GF202:96(112C8):384(15F15)	KIAA0569 GENE PRODUCT N45100
329	GENE285X	GF201:96(85H7):384(10P14)	V-MAF MUSCULOAPONEUROTIC FIBROSARCOMA (AVIAN) ONCOGENE HOMOLOG AA043501
330	GENE157X	GF200:96(5C8):384(2E15)	PEROXISOME PROLIFERATIVE ACTIVATED RECEPTOR, GAMMA AA088517
331	GENE363X	GF201:96(96H9):384(13O18)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 2 N93505
332	GENE8X	GF200:96(11D12):384(3H24)	SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 14 R96668
333	GENE62X	GF200:96(18A1):384(5A2)	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 6 AA478724
334	GENE120X	GF200:96(26F3):384(7K6)	PHOSPHATIDIC ACID PHOSPHATASE TYPE 2B T72119
335	GENE83X	GF200:96(21C4):384(6E7)	PHOSPHATIDIC ACID PHOSPHATASE TYPE 2B T71976
336	GENE362X	GF201:96(96G3):384(13M6)	CAVEOLIN 1, CAVEOLAE PROTEIN, 22KD AA055835
337	GENE44X	GF200:96(15C10):384(4F20)	TRANSFORMING GROWTH FACTOR, BETA RECEPTOR II (70-80KD) AA487034
338	GENE64X	GF200:96(18A3):384(5A6)	HUMAN KRUEPPEL-RELATED ZINC FINGER PROTEIN (H-PLK) MRNA, COMPLETE CDS N54596
339	GENE184X	GF200:96(9A5):384(3A9)	HUMAN KRUEPPEL-RELATED ZINC FINGER PROTEIN (H-PLK) MRNA, COMPLETE CDS N54596
340	GENE307X	GF201:96(88E4):384(11J8)	INSULIN-LIKE GROWTH FACTOR 2 (SOMATOMEDIN A) N74623
341	GENE231X	GF201:96(63E2):384(23J3)	212489 H68404
342	GENE350X	GF201:96(95G9):384(13M17)	PHOSPHORYLASE, GLYCOGEN; MUSCLE (MCARDLE SYNDROME, GLYCOGEN STORAGE DISEASE TYPE V) AA496032
343	GENE298X	GF201:96(87H7):384(11O13)	MICROFIBRILLAR-ASSOCIATED PROTEIN 4 AA496022
344	GENE401X	GF202:96(113H3):384(16O5)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA487895
345	GENE443X	PEROU:96(6B1):384(20C2)	CYCLIN-DEPENDENT KINASE INHIBITOR 1C (P57, KIP2) R81336
346	GENE373X	GF201:96(97H6):384(13P12)	AQUAPORIN 1 (CHANNEL-FORMING INTEGRAL PROTEIN, 28KD) H24316
347	GENE193X	GF201:96(100H7):384(14O14)	78946 T61792
348	GENE70X	GF200:96(18H1):384(5O2)	484535 AA036974
349	GENE39X	GF200:96(14G2):384(4M4)	ALCOHOL DEHYDROGENASE 2 (CLASS I), BETA POLYPEPTIDE N93428
350	GENE66X	GF200:96(18E1):384(5I2)	FOUR AND A HALF LIM DOMAINS 1 AA456394
351	GENE93X	GF200:96(23A7):384(6B14)	GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1 (SOLUBLE) AA192547
352	GENE202X	GF201:96(102A5):384(14B9)	85660 T62068
353	GENE303X	GF201:96(88D12):384(11G24)	INTEGRIN, ALPHA 7 AA055979
354	GENE112X	GF200:96(26C1):384(7E2)	RETINOL-BINDING PROTEIN 4, INTERSTITIAL T72220
355	GENE301X	GF201:96(88B9):384(11C18)	LIPOPROTEIN LIPASE AA633835
356	GENE388X	GF202:96(110B10):384(15C20)	GLUTATHIONE PEROXIDASE 3 (PLASMA) AA664180
357	GENE332X	GF201:96(92H12):384(12O24)	AQUAPORIN 7 H27752
358	GENE460X	PEROU:96(7A10):384(20B20)	FATTY ACID BINDING PROTEIN 4, ADIPOCYTE AI652163
359	GENE456X	PEROU:96(6E7):384(20I14)	FATTY ACID BINDING PROTEIN 4, ADIPOCYTE AA046090

Table 6

360	GENE133X	GF200:96(29G2):384(8M3)	47043 H10721
361	GENE386X	GF200:96(109G3):384(15M5)	HOMO SAPIENS CLONE 23698 MRNA SEQUENCE AA680300
362	GENE404X	GF202:96(114B5):384(16C10)	ESTS, MODERATELY SIMILAR TO FAT-SPECIFIC PROTEIN FSP27 [M.MUSCULUS] AA088749
363	GENE201X	GF201:96(102A4):384(14B7)	HOMO SAPIENS BRAIN MY047 PROTEIN MRNA, COMPLETE CDS T62031
364	GENE181X	GF200:96(8H9):384(2P17)	MESENCHYME HOMEO BOX 1 AA426311
365	GENE458X	PEROU:96(6G3):384(20M6)	HHCPA78 HOMOLOG AA044633
366	GENE151X	GF200:96(4E1):384(1J1)	ENDOTHELIAL KRUPPEL-LIKE ZINC FINGER PROTEIN H45711
367	GENE355X	GF201:96(96D8):384(13G16)	CYCLIN-DEPENDENT KINASE 5, REGULATORY SUBUNIT 1 (P35) AA442853
368	GENE87X	GF200:96(22B11):384(6C22)	FBJ MURINE OSTEOSARCOMA VIRAL ONCOGENE HOMOLOG B T62179
369	GENE198X	GF201:96(101F5):384(14L10)	79412 T57691
370	GENE341X	GF201:96(94G6):384(12N11)	DUAL SPECIFICITY PHOSPHATASE 6 AA630374
371	GENE343X	GF201:96(94H6):384(12P11)	LAMININ, GAMMA 2 (NICEIN (100KD), KALININ (105KD), BM600 (100KD), HERLITZ JUNCTIONAL EPIDERMOLYSIS BULLOSA)) AA677534
372	GENE342X	GF201:96(94H5):384(12P9)	MATRIX METALLOPROTEINASE 14 (MEMBRANE-INSERTED) N33214
373	GENE327X	GF201:96(92B12):384(12C24)	COLLAGEN, TYPE XVII, ALPHA 1 H87536
374	GENE161X	GF200:96(5H7):384(2O13)	CALPONIN 1, BASIC, SMOOTH MUSCLE AA399519
375	GENE462X	PEROU:96(7B5):384(20D10)	PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1) AA001449
376	GENE52X	GF200:96(16F12):384(4L23)	PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1) AA001449
377	GENE454X	PEROU:96(6E4):384(20I8)	1912786 AI304356
378	GENE19X	GF200:96(12E9):384(3I17)	GELSOLIN (AMYLOIDOSIS, FINNISH TYPE) H72027
379	GENE176X	GF200:96(8C10):384(2F19)	BULLOUS PEMPHIGOID ANTIGEN 1 (230/240KD) H44784
380	GENE329X	GF201:96(92B7):384(12C14)	SMALL INDUCIBLE CYTOKINE SUBFAMILY D (CYS-X3-CYS), MEMBER 1 (FRACTALKINE, NEUROTACTIN) R66139
381	GENE488X	PEROU:96(9D1):384(18H2)	KERATIN 17 aa026642
382	GENE476X	PEROU:96(8D6):384(20H11)	KERATIN 17 AA026642
383	GENE487X	PEROU:96(9C6):384(18F12)	KERATIN 5 (EPIDERMOLYSIS BULLOSA SIMPLEX DOWLING-MEARA/KOBNER/WEBER-COCKAYNE TYPES) W72110
384	GENE472X	PEROU:96(8C11):384(20F21)	ESTS, HIGHLY SIMILAR TO KERATIN K5, 58K TYPE II, EPIDERMAL W72110
385	GENE336X	GF201:96(93G2):384(12N4)	ESTS, HIGHLY SIMILAR TO PROBABLE ATAXIA-TELANGIECTASIA GROUP D PROTEIN [H.SAPIENS] AA055486
386	GENE106X	GF200:96(25C8):384(7E15)	CRYSTALLIN, ALPHA B AA504943
387	GENE175X	GF200:96(8B12):384(2D23)	CAVEOLIN 2 T89391
388	GENE37X	GF200:96(14E11):384(4I22)	ANNEXIN I (LIPOCORTIN I) H63077
389	GENE353X	GF201:96(96B2):384(13C4)	DYSTROPHIN (MUSCULAR DYSTROPHY, DUCHENNE AND BECKER TYPES), INCLUDES DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 AA461118
390	GENE76X	GF200:96(19D7):384(5H14)	DIHYDROPYRIMIDINASE-LIKE 2 AA487674
391	GENE256X	GF201:96(79B4):384(9C7)	272038 N31948
392	GENE29X	GF200:96(13D12):384(4G23)	CYSTEINE DIOXYGENASE, TYPE I AA497111

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393	GENE412X	GF202:96(116B11):384(16D21)	HUMAN LIVER CARBOXYLESTERASE MRNA, 3' END T68878
394	GENE127X	GF200:96(27H11):384(7P22)	ESTS, WEAKLY SIMILAR TO W01A11.2 GENE PRODUCT [C.ELEGANS] H25606
395	GENE5X	GF200:96(10E2):384(3I4)	KIAA0914 GENE PRODUCT N51424
396	GENE464X	PEROU:96(7E6):384(20J12)	MITOGEN INDUCIBLE 2 H29253
397	GENE268X	GF201:96(81H8):384(9P16)	307645 N93582
398	GENE236X	GF201:96(65A12):384(23B24)	HOMO SAPIENS MRNA FOR KIAA0786 PROTEIN, PARTIAL CDS W74533
399	GENE110X	GF200:96(26A2):384(7A4)	VON WILLEBRAND FACTOR AA487787
400	GENE46X	GF200:96(15E10):384(4J20)	TISSUE FACTOR PATHWAY INHIBITOR (LIPOPROTEIN-ASSOCIATED COAGULATION INHIBITOR) T47454
401	GENE339X	GF201:96(94F10):384(12L19)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4704754) [H.SAPIENS] AA426053
402	GENE58X	GF200:96(17F4):384(5K7)	FATTY-ACID-COENZYME A LIGASE, LONG-CHAIN 1 T73556
403	GENE195X	GF201:96(101B6):384(14D12)	HOMO SAPIENS MRNA; CDNA DKFZP586A0522 (FROM CLONE DKFZP586A0522) T50041
404	GENE308X	GF201:96(88E5):384(11I10)	INSULIN RECEPTOR SUBSTRATE 1 AA460841
405	GENE48X	GF200:96(15F5):384(4L10)	SYNDECAN 2 (HEPARAN SULFATE PROTEOGLYCAN 1, CELL SURFACE-ASSOCIATED, FIBROGLYCAN) H64346
406	GENE430X	PEROU:96(2F4):384(19K8)	FIBROBLAST GROWTH FACTOR RECEPTOR 1 AA281189
407	GENE125X	GF200:96(27B3):384(7D6)	ALKALINE PHOSPHATASE, LIVER/BONE/KIDNEY T94626
408	GENE27X	GF200:96(13B9):384(4C17)	ALDO-KETO REDUCTASE FAMILY 1, MEMBER C1 (DIHYDRODIOL DEHYDROGENASE 1; 20-ALPHA (3-ALPHA)-HYDROXYSTEROID DEHYDROGENASE) R93124
409	GENE447X	PEROU:96(6C11):384(20E22)	6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BIPHOSPHATASE 3 N93901
410	GENE18X	GF200:96(12E4):384(3I7)	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1 AA495936
411	GENE279X	GF201:96(83H11):384(10O21)	811020 AA485369
412	GENE214X	GF201:96(56A7):384(21A14)	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA STIMULATING ACTIVITY POLYPEPTIDE 1 AA035620
413	GENE101X	GF200:96(24E11):384(6J21)	814526 AA459588
414	GENE209X	GF201:96(55F4):384(21K7)	DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT-INTERACTING PROTEIN 2 N79761
415	GENE365X	GF201:96(97B5):384(13D10)	BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) W73473
416	GENE243X	GF201:96(66E1):384(23I1)	BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) AA029597
417	GENE274X	GF201:96(82G11):384(9N21)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA459296
418	GENE393X	GF202:96(111D4):384(15H8)	757383 AA437140
419	GENE69X	GF200:96(18G9):384(5M18)	PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA AA598817
420	GENE179X	GF200:96(8D1):384(2H1)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] H59915
421	GENE438X	PEROU:96(4D3):384(19H5)	CYTOCHROME P450, SUBFAMILY I (DIOXIN-INDUCIBLE), POLYPEPTIDE 1 (GLAUCOMA 3, PRIMARY INFANTILE) AA029776
422	GENE104X	GF200:96(25C2):384(7E3)	CYTOCHROME P450, SUBFAMILY I (DIOXIN-INDUCIBLE), POLYPEPTIDE 1 (GLAUCOMA 3, PRIMARY INFANTILE) AA448157
423	GENE53X	GF200:96(16G12):384(4N23)	PHOSPHODIESTERASE 4B, CAMP-SPECIFIC (DUNCE (DROSOPHILA)-HOMOLOG PHOSPHODIESTERASE E4) AA453293
424	GENE67X	GF200:96(18G10):384(5M20)	PRE-B-CELL COLONY-ENHANCING FACTOR AA281932
425	GENE360X	GF201:96(96F8):384(13K16)	CERULOPLASMIN (FERROXIDASE) H86554

Table 6

426	GENE344X	GF201:96(95A7):384(13A13)	148225 H13688
427	GENE72X	GF200:96(18H9):384(5O18)	NUCLEAR FACTOR I/B W87611
428	GENE426X	PEROU:96(1H4):384(19O7)	EPIDERMAL GROWTH FACTOR RECEPTOR (AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL (V-ERB-B) ONCOGENE HOMOLOG) AA234783
429	GENE349X	GF201:96(95G6):384(13M11)	GRO1 ONCOGENE (MELANOMA GROWTH STIMULATING ACTIVITY, ALPHA) W42723
430	GENE86X	GF200:96(21G12):384(6M23)	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT, POLYPEPTIDE 1 (P85 ALPHA) R54050
431	GENE328X	GF201:96(92B2):384(12C4)	HUMAN DNA-BINDING PROTEIN ABP/ZF MRNA, COMPLETE CDS W88571
432	GENE416X	PEROU:96(10C1):384(18F1)	ANTILEUKOPROTEINASE AA026192
433	GENE331X	GF201:96(92H10):384(12O20)	FATTY ACID BINDING PROTEIN 7, BRAIN W72051
434	GENE359X	GF201:96(96F6):384(13K12)	CHITINASE 3-LIKE 2 AA668821
435	GENE467X	PEROU:96(7F9):384(20L18)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1 AA088439
436	GENE451X	PEROU:96(6D1):384(20G2)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1 N47476
437	GENE91X	GF200:96(22G5):384(6M10)	HOMO SAPIENS MRNA FOR CALPAIN-LIKE PROTEASE CANPX AA457330
438	GENE75X	GF200:96(19B4):384(5D8)	KERATIN 7 AA489569
439	GENE320X	GF201:96(90F1):384(11L1)	LADININ 1 T97710
440	GENE108X	GF200:96(25G1):384(7M1)	CADHERIN 3, P-CADHERIN (PLACENTAL) AA425556
441	GENE156X	GF200:96(5B4):384(2C7)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, K R79082
442	GENE134X	GF200:96(2A12):384(1A24)	SRY (SEX-DETERMINING REGION Y)-BOX 9 (CAMPOMELIC DYSPLASIA, AUTOSOMAL SEX-REVERSAL) AA400739
443	GENE147X	GF200:96(4A3):384(1B5)	KERATIN 13 W23757
444	GENE257X	GF201:96(79D8):384(9G15)	KERATIN 13 W60057
445	GENE469X	PEROU:96(8A7):384(20B13)	2255577 AI679149
446	GENE434X	PEROU:96(3B12):384(19D24)	INTEGRIN, BETA 4 AA076514
447	GENE287X	GF201:96(86C6):384(10F11)	TROPONIN 1, SKELETAL, FAST AA181334
448	GENE65X	GF200:96(18A6):384(5A12)	INHIBITOR OF DNA BINDING 4, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN AA464856
449	GENE459X	PEROU:96(6G5):384(20M10)	510165 AA053251
450	GENE255X	GF201:96(69E2):384(24J4)	321902 W37448
451	GENE218X	GF201:96(57C10):384(21F20)	PUTATIVE PROSTATE CANCER TUMOR SUPPRESSOR H13424
452	GENE423X	PEROU:96(1A3):384(19A5)	MDGI/FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART W04872
453	GENE20X	GF200:96(12F11):384(3L21)	FOLATE RECEPTOR 1 (ADULT) R24635
454	GENE357X	GF201:96(96F11):384(13K22)	CELLULAR RETINOIC ACID-BINDING PROTEIN 1 AA421218
455	GENE211X	GF201:96(55F8):384(21K15)	CELLULAR RETINOIC ACID-BINDING PROTEIN 1 AA454702
456	GENE321X	GF201:96(90H10):384(11P19)	DERMATAN SULPHATE PROTEOGLYCAN 3 AA131238
457	GENE237X	GF201:96(65A8):384(23B16)	357396 W93847
458	GENE2X	GF200:96(10B8):384(3C16)	SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 18, PULMONARY AND ACTIVATION-REGULATED AA495985
459	GENE117X	GF200:96(26C9):384(7E18)	CD79A ANTIGEN (IMMUNOGLOBULIN-ASSOCIATED ALPHA) T87012
460	GENE114X	GF200:96(26C3):384(7E6)	NEUTROPHIL CYTOSOLIC FACTOR 1 (47KD, CHRONIC GRANULOMATOUS DISEASE, AUTOSOMAL 1) AA489666

Table 6

	Gene	Clone	Description
461	GENE445X	PEROU:96(6B12):384(20C24)	IMMUNOGLOBULIN LAMBDA LIGHT CHAIN R50297
462	GENE311X	GF201:96(88F6):384(11K12)	IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 2 W73790
463	GENE452X	PEROU:96(6D6):384(20G12)	HUMAN REARRANGED IMMUNOGLOBULIN LAMBDA LIGHT CHAIN MRNA N64851
464	GENE118X	GF200:96(26D3):384(7G6)	HUMAN REARRANGED IMMUNOGLOBULIN LAMBDA LIGHT CHAIN MRNA T67053
465	GENE84X	GF200:96(21D8):384(6G15)	BUTYROPHILIN, SUBFAMILY 3, MEMBER A3 AA478585
466	GENE302X	GF201:96(88C3):384(11E6)	LACTOTRANSFERRIN AA677706
467	GENE253X	GF201:96(69A2):384(24B4)	322223 W38022
468	GENE51X	GF201:96(16D9):384(4H17)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, F AA598513
469	GENE208X	GF201:96(55E12):384(21I23)	HUMAN DNA SEQUENCE FROM CLONE 466N1 ON CHROMOSOME 22Q12-13 CONTAINS H1F0(H1 HISTONE FAMILY, MEMBER 0) GENE, 2-AMINO-3-KETOBUTYRATE -COA LIGASE(NUCLEAR GENE ENCODING MITOCHONDRIAL PROTEIN), GALR3 (GALANIN RECEPTOR) GENE, ESTS, N93695
470	GENE187X	GF200:96(9G2):384(3M3)	METALLOTHIONEIN 1G H53340
471	GENE115X	GF200:96(26C4):384(7E8)	METALLOTHIONEIN 1L N80129
472	GENE317X	GF201:96(89G6):384(11N12)	S100 CALCIUM-BINDING PROTEIN A1 AA425934
473	GENE249X	GF201:96(67D6):384(24G11)	810459 AA457138
474	GENE400X	GF202:96(112G10):384(15N19)	ESTS, WEAKLY SIMILAR TO POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A [H.SAPIENS] AA130596
475	GENE96X	GF200:96(24B11):384(6D21)	EPIDIDYMIS-SPECIFIC, WHEY-ACIDIC PROTEIN TYPE, FOUR-DISULFIDE CORE AA451904
476	GENE225X	GF201:96(59A12):384(22A23)	364555 AA022601
477	GENE283X	GF201:96(85B6):384(10D12)	359597 AA010818
478	GENE126X	GF200:96(27C4):384(7F8)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4502327) [H.SAPIENS] R65792
479	GENE262X	GF201:96(80F3):384(9K6)	321488 W32509
480	GENE80X	GF200:96(1B7):384(1C13)	V-MYC AVIAN MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG AA464600
481	GENE380X	GF201:96(99C12):384(14E23)	ELECTRON-TRANSFER-FLAVOPROTEIN, BETA POLYPEPTIDE T62040
482	GENE333X	GF201:96(92H8):384(12O16)	GLUTATHIONE S-TRANSFERASE A4 AA152347
483	GENE230X	GF201:96(63C4):384(23E7)	415064 W93120
484	GENE378X	GF201:96(99A7):384(14A13)	IGG FC BINDING PROTEIN R52030
485	GENE254X	GF201:96(69D7):384(24H14)	323260 W42736
486	GENE392X	GF202:96(111B9):384(15D18)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4502327) [H.SAPIENS] T72850
487	GENE448X	PEROU:96(6C2):384(20E4)	220376 H86813
488	GENE180X	GF200:96(8E2):384(2I3)	MANNOSIDASE, ALPHA 6A8 H45455
489	GENE453X	PEROU:96(6E1):384(20I2)	GLUTATHIONE S-TRANSFERASE M1 W02680
490	GENE99X	GF200:96(24C12):384(6F23)	GLUTATHIONE S-TRANSFERASE M4 AA486669
491	GENE16X	GF200:96(12C8):384(3F15)	GLUTATHIONE S-TRANSFERASE M1 AA290737
492	GENE409X	GF202:96(115A2):384(16B4)	HLA-B ASSOCIATED TRANSCRIPT-3 H67876
493	GENE280X	GF201:96(84A4):384(10A8)	272262 N35592
494	GENE102X	GF200:96(24F4):384(6L7)	FIBROBLAST GROWTH FACTOR RECEPTOR 2 (BACTERIA-EXPRESSED KINASE, KERATINOCYTE GROWTH FACTOR RECEPTOR, CRANIOFACIAL DYSOSTOSIS 1, CROUZON SYNDROME, PFEIFFER SYNDROME, JACKSON-WEISS SYNDROME) AA443093

Table 6

495	GENE25X	GF200:96(12G5):384(3N9)	FIBROBLAST GROWTH FACTOR RECEPTOR 2 (BACTERIA-EXPRESSED KINASE, KERATINOCYTE GROWTH FACTOR RECEPTOR, CRANIOFACIAL DYSOSTOSIS 1, CROUZON SYNDROME, PFEIFFER SYNDROME, JACKSON-WEISS SYNDROME) AA456160
496	GENE340X	GF201:96(94F6):384(12L11)	H.SAPIENS MRNA FOR TRE ONCOGENE (CLONE 210) AA437374

Table 7: Epithelial-enriched gene set

197474 H52098	
786609 AA478481	
FIBROBLAST ACTIVATION PROTEIN, ALPHA AA405569	
LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR AA056022	
LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR AA056022	
CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN AA722599	
PLASMINOGEN ACTIVATOR, UROKINASE RECEPTOR AA147962	
FIBRONECTIN 1 R62612	
FIBRONECTIN 1 R62612	
HUMAN ISOLATE JUSO MUC18 GLYCOPROTEIN MRNA (3' VARIANT), COMPLETE CDS AA497002	
H.SAPIENS MRNA FOR INHIBIN BETA(A) SUBUNIT N27159	
HUMAN MRNA FOR FIBRONECTIN (FN PRECURSOR) N26285	
ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] H77494	
244703 N52533	
HOMO SAPIENS MRNA FOR NIDOGEN-2 AA479199	
LIM DOMAIN ONLY 7 H22826	
TACHYKININ, PRECURSOR 1 (SUBSTANCE K, SUBSTANCE P, NEUROKININ 1, NEUROKININ 2, NEUROMEDIN L, NEUROKININ ALPHA, NEUROPEPTIDE K,NEUROPEPTIDE GAMMA) AA446659	
INTERLEUKIN 1, BETA W47101	
INTERLEUKIN 1, BETA AA150507	
RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (RHO FAMILY, SMALL GTP BINDING PROTEIN RAC1) AA626787	
PROTEIN TYROSINE PHOSPHATASE J AA644448	
ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.SAPIENS] N21103	
FAT TUMOR SUPPRESSOR (DROSOPHILA) HOMOLOG A159194	
271952 N35301	
179276 H50323	
INOSITOL POLYPHOSPHATE-5-PHOSPHATASE, 145KD AA521067	

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CHOLINERGIC RECEPTOR, NICOTINIC, EPSILON POLYPEPTIDE R02058
ALDO-KETO REDUCTASE FAMILY 1, MEMBER C1 (DIHYDRODIOL DEHYDROGENASE 1; 20-ALPHA (3-ALPHA)- HYDROXYSTEROID DEHYDROGENASE) R93124
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 6 AA293571
CYSTATIN A (STEFIN A) W72207
347436 W81192
ANTILEUKOPROTEINASE AA026192
JAGGED1 (ALAGILLE SYNDROME) R70685
PRION PROTEIN (P27-30) (CREUTZFELD-JAKOB DISEASE, GERSTMANN-STRAUSLER-SCHEINKER SYNDROME, FATAL FAMILIAL INSOMNIA) AA455969
ESTS, WEAKLY SIMILAR TO KIAA0639 PROTEIN [H.SAPIENS] AA284277
843045 AA488420
ALDEHYDE DEHYDROGENASE 6 AA455235
CADHERIN 3, P-CADHERIN (PLACENTAL) AA425556
MDGI/FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART W04872
TROPONIN I, SKELETAL, FAST AA181334
MATRIX METALLOPROTEINASE 14 (MEMBRANE-INSERTED) N33214
LAMININ, GAMMA 2 (NICEIN (100KD), KALININ (105KD), BM600 (100KD), HERLITZ JUNCTIONAL EPIDERMOLYSIS BULLOSA)) AA677534
ANNEXIN VIII AA252968
ESTS, HIGHLY SIMILAR TO PROBABLE ATAXIA-TELANGIECTASIA GROUP D PROTEIN [H.SAPIENS] A A055486
KERATIN 17 AA026642
KERATIN 17 aa026642
ESTS, HIGHLY SIMILAR TO KERATIN K5, 58K TYPE II, EPIDERMAL [H.SAPIENS] AA160507
KERATIN 5 (EPIDERMOLYSIS BULLOSA SIMPLEX DOWLING-MEARA/KOBNER/WEBER-COCKAYNE TYPES) W72110
ESTS, HIGHLY SIMILAR TO KERATIN K5, 58K TYPE II, EPIDERMAL W72110
BULLOUS PEMPHIGOID ANTIGEN 1 (230/240KD) H44784
S100 CALCIUM-BINDING PROTEIN A2 AA458884
INTEGRIN, BETA 4 AA485668
INTEGRIN, BETA 4 AA076514

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2255577 AI679149
LAMININ, ALPHA 3 (NICEIN (150KD), KALININ (165KD), BM600 (150KD), EPILEGRIN) AA001432
COLLAGEN, TYPE XVII, ALPHA 1 H87536
BASONUCLIN R26526
504940 AA150619
HUMAN DNA SEQUENCE FROM CLONE 973M2 ON CHROMOSOME 1Q24.3-31.1 CONTAINS PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE 2 (PROSTAGLANDIN G/H SYNTHASE AND CYCLOOXYGENASE) GENE, ESTS, STS, GSSS AA644211
810904 AA459285
MYOSIN IC AA029956
EPHRIN-B1 AA428778
MATRIX METALLOPROTEINASE 7 (MATRILYSIN, UTERINE) AA031513
294682 W01603
INTEGRIN, ALPHA 3 (ANTIGEN CD49C, ALPHA 3 SUBUNIT OF VLA-3 RECEPTOR) AA293040
INTEGRIN, ALPHA 3 (ANTIGEN CD49C, ALPHA 3 SUBUNIT OF VLA-3 RECEPTOR) AA424695
SERUM AMYLOID A1 H25546
GM2 GANGLIOSIDE ACTIVATOR PROTEIN AA453978
ESTS, WEAKLY SIMILAR TO TRANSPOSON LRE2 REVERSE TRANSCRIPTASE HOMOLOG [H.SAPIENS] W48580
CARBONIC ANHYDRASE II H23187
LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 2 AA424629
SECRETED FRIZZLED-RELATED PROTEIN 1 T68892
LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 7 (GALECTIN 7) W72436
PLASMINOGEN ACTIVATOR, UROKINASE AA284668
ENDOTHELIN RECEPTOR TYPE A AA452627
ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 5231137) [H.SAPIENS] W30988
N-MYC DOWNSTREAM REGULATED AA489261
EPIDERMAL GROWTH FACTOR RECEPTOR (AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL (V-ERB-B) ONCOGENE HOMOLOG) AA234783
359285 AA016234
INTERLEUKIN 4 RECEPTOR AA292025
DIACYLGLYCEROL KINASE, ALPHA (80KD) AA456900

770670 AA476272
FOLATE RECEPTOR 1 (ADULT) R24635
HUMAN MRNA FOR KIAA0300 GENE, PARTIAL CDS AA405458
HUMAN GABA-A RECEPTOR EPSILON SUBUNIT (GABRE) RNA, ALTERNATIVE TRANSCRIPT H63934
SMALL INDUCIBLE CYTOKINE SUBFAMILY D (CYS-X3-CYS), MEMBER 1 (FRACTALKINE, NEUROTACTIN) R66139
HUMAN DNA SEQUENCE FROM PAC 196E23 ON CHROMOSOME XQ26.1-27.2. CONTAINS THE TAT-SF1 (HIV-1 TRANSCRIPTIONAL ELONGATION FACTOR TAT COFACTOR TAT-SF1) GENE, THE BRS3 (BOMBESIN RECEPTOR SUBTYPE-3 (UTERINE BOMBESIN RECEPTOR, BRS-3) GEN AA700322
HUMAN DNA-BINDING PROTEIN ABP/ZF MRNA, COMPLETE CDS W88571
PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, TYPE I, BETA R39069
51406 H18950
503051 AA149250
FATTY ACID BINDING PROTEIN 7, BRAIN N46862
FATTY ACID BINDING PROTEIN 7, BRAIN W72051
MACROPHAGE RECEPTOR WITH COLLAGENOUS STRUCTURE AA485867
HOMO SAPIENS MRNA FOR CALPAIN-LIKE PROTEASE CANPX AA457330
298662 N74313
FORKHEAD (DROSOPHILA)-LIKE 7 N22552
ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA459296
MEGAKARYOCYTE POTENTIATING FACTOR AA488406
PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA AA598817
EYES ABSENT (DROSOPHILA) HOMOLOG 2 AA402207
SYNAPTOGYRIN 1 AA007632
PHOSPHOLIPASE C, BETA 4 H22563
TRANSCRIPTION FACTOR AP-2 GAMMA (ACTIVATING ENHANCER-BINDING PROTEIN 2 GAMMA) AA399334
KERATIN 4 AA629189
BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) AA029597
BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) W73473
KIAA0626 GENE PRODUCT N62737
HUMAN MRNA FOR KIAA0338 GENE, PARTIAL CDS R71689

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CERULOPLASMIN (FERROXIDASE) H86554
ESTS, MODERATELY SIMILAR TO (DEFLINE NOT AVAILABLE 4159884) [H.SAPIENS] AA001222
DESMOCOLLIN 2 AA074677
321902 W37448
KERATIN 13 W60057
KERATIN 13 W23757
134011 R31262
49630 H29256
VITAMIN D (1,25- DIHYDROXYVITAMIN D3) RECEPTOR AA485226
SYNDECAN 1 AA074511
SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), SHORT BASIC DOMAIN, SECRETED, (SEMAPHORIN) 3F AA454570
PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, F AA598513
BUTYRATE RESPONSE FACTOR 1 (EGF-RESPONSE FACTOR 1) AA424743
ANTHRACYCLINE RESISTANCE-ASSOCIATED AA495766
MEMBRANE COMPONENT, CHROMOSOME 1, SURFACE MARKER 1 (40KD GLYCOPROTEIN, IDENTIFIED BY MONOCLONAL ANTIBODY GA733) AA454810
KERATIN 7 AA489569
813520 AA455591
HOMO SAPIENS MRNA; CDNA DKFZP586B2022 (FROM CLONE DKFZP586B2022) T52325
HOMO SAPIENS AGRIN PRECURSOR MRNA, PARTIAL CDS AA458878
ESTS, WEAKLY SIMILAR TO KIAA0319 [H.SAPIENS] AA136133
ANTIQUITIN 1 AA101299
HEXOKINASE 1 AA485272
HEXOKINASE 1 AA485271
LADININ 1 T97710
H.SAPIENS MRNA FOR RECEPTOR TYROSINE KINASE EPH (PARTIAL) N90246
144834 R77251
CREATINE KINASE, MITOCHONDRIAL 1 (UBIQUITOUS) AA019482
364302 AA022462
176461 H43515

RECEPTOR PROTEIN-TYROSINE KINASE EDDR1 H41900	
HOMO SAPIENS MRNA FOR INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE ISOENZYME, PARTIAL CDS N46828	
PLEXIN 5 AA496565	
810873 AA459197	
504225 AA131934	
SNF2-RELATED CBP ACTIVATOR PROTEIN AA419088	
ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] H97778	
ESTS, WEAKLY SIMILAR TO KIAA0281 [H.SAPIENS] N54395	
85804 T72068	
JUNCTION PLAKOGLOBIN R06417	
CDP-DIACYLGLYCEROL SYNTHASE (PHOSPHATIDATE CYTIDYLYLTRANSFERASE) 1 R31562	
PROLINE-RICH GLA (G-CARBOXGLUTAMIC ACID) POLYPEPTIDE 2 AA430552	
HUMAN DNA SEQUENCE FROM PAC 127B20 ON CHROMOSOME 22Q11.2-QTER, CONTAINS GENE FOR GTPASE-ACTIVATING PROTEIN SIMILAR TO RHOGAP PROTEIN. RIBOSOMAL PROTEIN L6 PSEUDOGENE, ESTS AND CA REPEAT AA037410	
ESTS, WEAKLY SIMILAR TO LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR [H.SAPIENS] AA489246	
416386 W86859	
PLACENTAL BIKUNIN (KUNITZ-TYPE SERINE PROTEASE INHIBITOR) AA031287	
SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2 AA459039	
HUMAN PLACENTAL BIKUNIN MRNA COMPLETE CDS AA031287	
810728 AA457707	
HOMO SAPIENS MRNA; CDNA DKFZP586F1318 (FROM CLONE DKFZP586F1318) T77847	
147447 R81173	
365517 AA009593	
417081 W87826	
ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4929751) [H.SAPIENS] AA004846	
HOMO SAPIENS MRNA; CDNA DKFZP586J2118 (FROM CLONE DKFZP586J2118) R98407	
297604 N69835	
297604 N69835	
DNA SEGMENT, SINGLE COPY PROBE LNS-CAI/LNS-CAII (DELETED IN POLYPOSIS H99681	

ESTROGEN RECEPTOR 1 AA164586
275798 R93185
TUMOR PROTEIN D52 AA459318
HUMAN D9 SPLICE VARIANT B MRNA, COMPLETE CDS AA453832
MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA733-2 PRECURSOR AA055808
KIAA0351 GENE PRODUCT AA402863
RAB2, MEMBER RAS ONCOGENE FAMILY-LIKE AA401972
NEBULETTE N77806
ESTS, WEAKLY SIMILAR TO UNKNOWN [H.SAPIENS] R01499
486828 AA042878
486828 AA042878
XMP T84249
EPITHELIAL MEMBRANE PROTEIN 2 T88721
KERATIN 8 AA598517
44292 H06273
KERATIN 18 AA070385
KERATIN 18 AA664179
CLAUDIN 4 AA430665
HCPE-R MRNA FOR CPE-RECEPTOR AA506754
HCPE-R MRNA FOR CPE-RECEPTOR W74492
HOMO SAPIENS EPITHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1A (ESE-1) MRNA, COMPLETE CDS AA433851
EPITHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1B (ESE-1) MRNA COMPLETE CDS H27938
SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1 AA464250
TRANSFORMING GROWTH FACTOR, BETA 3 AA040617
TRANSFORMING GROWTH FACTOR BETA 3 AA040616
TRANSFORMING GROWTH FACTOR BETA 3 AA040616
LYSOSOMAL-ASSOCIATED MEMBRANE PROTEIN 1 H29077
ISLET CELL AUTOANTIGEN 1 (69KD) AA491302
ESTS, MODERATELY SIMILAR TO K02E10.2 [C.ELEGANS] T62552

82869	
T69270	
SELENIUM BINDING PROTEIN 1	
T65736	
HOMO SAPIENS MRNA FOR HYPOTHETICAL PROTEIN	
AA487488	
PROLACTIN RECEPTOR	
R63647	
321658	
W32933	
321658	
W32933	
202658	
H53479	
202658	
H53479	
ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS]	
AA464739	
197520	
H52110	
KIAA0182	
AA037466	
HUMAN MRNA FOR KIAA0182 GENE, PARTIAL CDS	
H05563	
SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), ISOFORM 3 REGULATORY FACTOR 1	
AA425299	
179211	
H50224	
179211	
H50224	
FRUCTOSE-BISPHOSPHATASE 1	
AA699427	
HUMAN ENDOGENOUS RETROVIRUS ENVELOPE REGION MRNA (PL1)	
AA701655	
X-BOX BINDING PROTEIN 1	
W90128	
HEPATOCYTE NUCLEAR FACTOR 3, ALPHA	
T74639	
GATA-BINDING PROTEIN 3	
H72474	
GATA-BINDING PROTEIN 3	
R31442	
GATA-BINDING PROTEIN 3	
R31441	
GATA-BINDING PROTEIN 3	
AA058828	
ESTROGEN RECEPTOR 1	
AA291702	
ESTROGEN RECEPTOR 1	
AA291749	
ANNEXIN XXXI	
N76688	
ANNEXIN XXXI	
N76688	
HOMO SAPIENS MRNA; CDNA DKFZP434A091 (FROM CLONE DKFZP434A091)	
AA431988	
CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER C	
N80617	

HOMO SAPIENS MRNA FOR NEUROBLASTOMA, COMPLETE CDS AA481950	
CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA036987	
CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA598508	
CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA036986	
HUMAN SECRETORY PROTEIN (P1.B) MRNA, COMPLETE CDS N74131	
MSH (DROSOPHILA) HOMEO BOX HOMOLOG 2 AA195636	
HUMAN CHROMOSOME 16 BAC CLONE CIT987SK-254P9 H23265	
204483 H58234	
HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) MRNA T52830	
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) AA054451	
HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) MRNA H08560	
HUMAN MRNA FOR KIAA0061 GENE, PARTIAL CDS N33237	
HUMAN MRNA FOR KIAA0143 GENE, PARTIAL CDS AA112057	
CYSTEINE-RICH PROTEIN 2 AA485427	
PDGF BETA T49539	
67654 T49539	
RAS HOMOLOG GENE FAMILY, MEMBER B H89046	
RAS HOMOLOG GENE FAMILY, MEMBER B AA495846	
140018 R63971	
140018 R63971	
81475 T63511	
CYTOCHROME P450, SUBFAMILY IIJ (ARACHIDONIC ACID EPOXYGENASE) POLYPEPTIDE 2 H09076	
P53-INDUCED PROTEIN H12189	
HOMO SAPIENS BREAST CANCER PUTATIVE TRANSCRIPTION FACTOR (ZABC1) MRNA, COMPLETE CDS AA460802	
HOMO SAPIENS BREAST CANCER PUTATIVE TRANSCRIPTION FACTOR (ZABC1) MRNA, COMPLETE CDS AA782528	
SULFOTRANSFERASE FAMILY 2B, MEMBER 1 R73584	
HEREDITARY HEMOCHROMOTOSIS R07647	
MUCIN 1, TRANSMEMBRANE AA488073	
156053 R72491	

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447786 AA702350	
415317 W92160	
IGG FC BINDING PROTEIN R52030	
EPIDIDYMIS-SPECIFIC, WHEY-ACIDIC PROTEIN TYPE, FOUR-DISULFIDE CORE AA451904	
SRC KINASE-ASSOCIATED PHOSPHOPROTEIN OF 55 KDA R01281	
CARBONIC ANHYDRASE XI N52089	
PHOSPHOFRUCTOKINASE, MUSCLE AA099169	
HUMAN HEART MRNA FOR HEAT SHOCK PROTEIN 90, PARTIAL CDS AA064973	
130843 R22306	
470105 AA029949	
H2B HISTONE FAMILY, MEMBER Q AA010223	
H2B HISTONE FAMILY, MEMBER Q AA456695	
H2A HISTONE FAMILY, MEMBER L N50797	
H1 HISTONE FAMILY, MEMBER 2 T66816	
322461 W15305	
289734 N62965	
DUAL SPECIFICITY PHOSPHATASE 4 AA444049	
CALCIUM CHANNEL, VOLTAGE-DEPENDENT, ALPHA 2/DELTA SUBUNIT 2 N53512	
ACYL-COENZYME A DEHYDROGENASE, SHORT/BRANCHED CHAIN H96140	
CYTOCHROME P450, SUBFAMILY IIB (PHENOBARBITAL-INDUCIBLE), POLYPEPTIDE 6 H41908	
PROTEASE INHIBITOR 12 (NEUROSERPIN) AA115876	
HUMAN DNA SEQUENCE FROM CLONE 167A19 ON CHROMOSOME 1P32.1-33. CONTAINS THREE GENES FOR NOVEL PROTEINS, THE DIO1 GENE FOR TYPE I IODOTHYRONINE DEIODINASE (EC 3.8.1.4, TXDI1, ITDI1) AND AN HNRNP A3 (HETEROGENOUS NUCLEAR RIBONUCLEOPR N74025	
AUTOCRINE MOTILITY FACTOR RECEPTOR AA479243	
CYTOCHROME P450, SUBFAMILY IIA (PHENOBARBITAL-INDUCIBLE), POLYPEPTIDE 7 T73031	
ANGIOTENSIN RECEPTOR 1 H66116	
ESTS, WEAKLY SIMILAR TO TUMOROUS IMAGINAL DISCS PROTEIN TID56 HOMOLOG [H.SAPIENS] T95268	
QUINOID DIHYDROPTERIDINE REDUCTASE R38198	
LYMPHOID NUCLEAR PROTEIN RELATED TO AF4 H99588	

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NUCLEOPORIN 88KD AA479888
307220 N95180
HOMO SAPIENS MRNA; CDNA DKFZP564P0662 (FROM CLONE DKFZP564P0662) R27680
HEPSIN (TRANSMEMBRANE PROTEASE, SERINE 1) H62162
ESTS, HIGHLY SIMILAR TO TRANSCRIPTION ELONGATION FACTOR TFIIS.H [H.SAPIENS] R09980
795744 AA460298
N-ACETYLTRANSFERASE 1 (ARYLAMINE N-ACETYLTRANSFERASE) R91803
N-ACETYLTRANSFERASE 1 (ARYLAMINE N-ACETYLTRANSFERASE) T67128
503581 AA131239
HUMAN BREAST CANCER, ESTROGEN REGULATED LIV-1 PROTEIN (LIV-1) MRNA, PARTIAL CDS H29407
N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAMIDASE) AA664155
EPOXIDE HYDROLASE 2, CYTOPLASMIC R73525
B-CELL CLL/LYMPHOMA 2 W63749
ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4929557) [H.SAPIENS] T74688
BASIC HELIX-LOOP-HELIX DOMAIN CONTAINING, CLASS B, 2 T62084
FORKHEAD (DROSOPHILA) HOMOLOG 1 (RHABDOMYOSARCOMA) AA448277
ACTIVATED P21CDC42HS KINASE AA427891
HUMAN MRNA FOR KIAA0303 GENE, PARTIAL CDS AA418846
487929 AA045481
ZINC FINGER PROTEIN HOMOLOGOUS TO ZFP103 IN MOUSE AA429297
CELL DIVISION CYCLE 4-LIKE AA041499
ESTS, WEAKLY SIMILAR TO P1.11659_5 N47593
ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4502327) [H.SAPIENS] T72850
ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] R70598
220376 H86813
HOMO SAPIENS MRNA; CDNA DKFZP434H071 (FROM CLONE DKFZP434H071) T41078
ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA669222
T3 RECEPTOR-ASSOCIATING COFACTOR-1 [HUMAN, FETAL LIVER, MRNA, 2930 NT] AA400234

416556	
W86987	
418240	
W90241	
KIAA0130 GENE PRODUCT	
N76581	
ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR	
AA025141	
STEROIDOGENIC ACUTE REGULATORY PROTEIN RELATED	
AA504710	
ERBB2-POLYA	
X03363	
V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG)	
AA025141	
V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG)	
AA443351	
ERBB2	
AA481939	
GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7	
H53703	
68400	
T57034	
68400	
T57034	
SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY E, MEMBER 1	
W63613	
ESTS, WEAKLY SIMILAR TO ENVELOPE PROTEIN [H.SAPIENS]	
W37778	
271076	
N29918	

Table 8: Luminal gene subset

B-CELL CLL/LYMPHOMA 2
W63749
ESTS, WEAKLY SIMILAR TO MEMBRANE GLYCOPROTEIN [M.MUSCULUS]
AA159578
51700
H22854
NEBULETTE
N77806
HUMAN DNA SEQUENCE FROM CLONE 167A19 ON CHROMOSOME 1P32.1-33. CONTAINS THREE GENES FOR NOVEL PROTEINS, THE DIO1 GENE FOR TYPE I IODOTHYRONINE DEIODINASE (EC 3.8.1.4, TXDI1, ITDI1) AND AN HNRNP A3 (HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN
N74025
PROLACTIN RECEPTOR
R63647
202658
H53479
202658
H53479
609283
AA167189
MYOSIN VI
AA625890
470216
AA028987
N-ACETYLTRANSFERASE 1 (ARYLAMINE N-ACETYLTRANSFERASE)
R91803
HOMO SAPIENS MRNA; CDNA DKFZP434A091 (FROM CLONE DKFZP434A091)
AA431988
358936
W92233
SEVEN IN ABSENTIA (DROSOPHILA) HOMOLOG 2
AA029041
HEPSIN (TRANSMEMBRANE PROTEASE, SERINE 1)
H62162
417081
W87826
470105
AA029949
HUMAN SECRETORY PROTEIN (P1.B) MRNA, COMPLETE CDS
N74131
HEPATOCYTE NUCLEAR FACTOR 3, ALPHA
T74639
X-BOX BINDING PROTEIN 1
W90128
ESTROGEN RECEPTOR 1
AA291702
ESTROGEN RECEPTOR 1
AA291749
GATA-BINDING PROTEIN 3
H72474
GATA-BINDING PROTEIN 3
R31441
GATA-BINDING PROTEIN 3
R31442

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ANNEXIN XXXI	
N76688	
HUMAN BREAST CANCER, ESTROGEN REGULATED LIV-1 PROTEIN (LIV-1) MRNA, PARTIAL CDS	
H29407	
346321	
W74079	
HUMAN CHROMOSOME 16 BAC CLONE CIT987SK-254P9	
H23265	
71863	
T52564	
271989	
N31935	
ESTS, HIGHLY SIMILAR TO INOSITOL POLYPHOSPHATE 4-PHOSPHATASE TYPE II-ALPHA [H.SAPIENS]	
R86721	
179211	
H50224	
179211	
H50224	
MURINE LEUKEMIA VIRAL (BMI-1) ONCOGENE HOMOLOG	
T87515	
MURINE LEUKEMIA VIRAL (BMI-1) ONCOGENE HOMOLOG	
AA478036	
LUTHERAN BLOOD GROUP (AUBERGER B ANTIGEN INCLUDED)	
H24954	
HOMO SAPIENS (PWD) GENE MRNA, 3' END	
N26536	
782547	
AA431796	
ACYL-COENZYME A DEHYDROGENASE, SHORT/BRANCHED CHAIN	
H96140	
CARNITINE PALMITOYLTRANSFERASE II	
N70848	
ALDO-KETO REDUCTASE FAMILY 7, MEMBER A2 (AFLATOXIN ALDEHYDE REDUCTASE)	
T62865	
CYTOCHROME P450, SUBFAMILY IIA (PHENOBARBITAL-INDUCIBLE), POLYPEPTIDE 7	
T73031	
ANGIOTENSIN RECEPTOR 1	
H66116	
LYMPHOID NUCLEAR PROTEIN RELATED TO AF4	
H99588	
HUMAN MRNA FOR KIAA0303 GENE, PARTIAL CDS	
AA418846	
EPOXIDE HYDROLASE 2, CYTOPLASMIC	
R73525	
DUAL SPECIFICITY PHOSPHATASE 4	
AA444049	

Table 9: Basal gene subset 1

DUAL SPECIFICITY PHOSPHATASE 6 AA630374
LAMININ, GAMMA 2 (NICEIN (100KD), KALININ (105KD), BM600 (100KD), HERLITZ JUNCTIONAL EPIDERMOLYSIS BULLOSA)) AA677534
MATRIX METALLOPROTEINASE 14 (MEMBRANE-INSERTED) N33214
COLLAGEN, TYPE XVII, ALPHA 1 H87536
CALPONIN 1, BASIC, SMOOTH MUSCLE AA399519
PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1) AA001449
PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1) AA001449
1912786 AI304356
GELSOLIN (AMYLOIDOSIS, FINNISH TYPE) H72027
BULLOUS PEMPHIGOID ANTIGEN 1 (230/240KD) H44784
SMALL INDUCIBLE CYTOKINE SUBFAMILY D (CYS-X3-CYS), MEMBER 1 (FRACTALKINE, NEUROTACTIN) R66139
KERATIN 17 aa026642
KERATIN 17 AA026642
KERATIN 5 (EPIDERMOLYSIS BULLOSA SIMPLEX DOWLING-MEARA/KOBNER/WEBER-COCKAYNE TYPES) W72110
ESTS, HIGHLY SIMILAR TO KERATIN K5, 58K TYPE II, EPIDERMAL W72110
ESTS, HIGHLY SIMILAR TO PROBABLE ATAXIA-TELANGIECTASIA GROUP D PROTEIN [H.SAPIENS] AA055486
CRYSTALLIN, ALPHA B AA504943
CAVEOLIN 2 T89391
ANNEXIN I (LIPOCORTIN I) H63077
DYSTROPHIN (MUSCULAR DYSTROPHY, DUCHENNE AND BECKER TYPES), INCLUDES DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 AA461118
DIHYDROPYRIMIDINASE-LIKE 2 AA487674

Table 9: Basal gene subset 2

EPIDERMAL GROWTH FACTOR RECEPTOR (AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL (V-ERB-B) ONCOGENE HOMOLOG) AA234783
GRO1 ONCOGENE (MELANOMA GROWTH STIMULATING ACTIVITY, ALPHA) W42723
PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT, POLYPEPTIDE 1 (P85 ALPHA) R54050
HUMAN DNA-BINDING PROTEIN ABP/ZF MRNA, COMPLETE CDS W88571
ANTILEUKOPROTEINASE AA026192
FATTY ACID BINDING PROTEIN 7, BRAIN W72051
CHITINASE 3-LIKE 2 AA668821
TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1 AA088439
TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1 N47476
HOMO SAPIENS MRNA FOR CALPAIN-LIKE PROTEASE CANPX AA457330
KERATIN 7 AA489569
LADININ 1 T97710
CADHERIN 3, P-CADHERIN (PLACENTAL) AA425556
PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, K R79082
SRY (SEX-DETERMINING REGION Y)-BOX 9 (CAMPOMELIC DYSPLASIA, AUTOSOMAL SEX-REVERSAL) AA400739
KERATIN 13 W23757
KERATIN 13 W60057
2255577 AI679149
INTEGRIN, BETA 4 AA076514
TROPONIN I, SKELETAL, FAST AA181334

Table 10: ErbB2 gene subset

ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR AA025141
ERBB2 AA481939
ERBB2-POLYA X03363
V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG) AA443351
V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG) AA025141
GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 H53703
STEROIDOGENIC ACUTE REGULATORY PROTEIN RELATED AA504710
68400 T57034
68400 T57034
SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY E, MEMBER 1 W63613
TNF RECEPTOR-ASSOCIATED FACTOR 4 AA598826
347348 W81186
FLOTILLIN 2 R73545
TGFB1-INDUCED ANTI-APOPTOTIC FACTOR 1 AA446222

Table 11: Endothelial Gene Subset

TISSUE FACTOR PATHWAY INHIBITOR (LIPOPROTEIN-ASSOCIATED COAGULATION INHIBITOR) T47454
ALDEHYDE DEHYDROGENASE 1, SOLUBLE AA664101
HOMO SAPIENS MRNA FOR KIAA0758 PROTEIN, PARTIAL CDS N95226
VON WILLEBRAND FACTOR AA487787
PLATELET/ENDOTHELIAL CELL ADHESION MOLECULE (CD31 ANTIGEN) R22412
MANIC FRINGE (DROSOPHILA) HOMOLOG H22922
INTERCELLULAR ADHESION MOLECULE 2 R21535
245147 N76361
REGULATOR OF G-PROTEIN SIGNALLING 5 AA668470
TEK TYROSINE KINASE, ENDOTHELIAL (VENOUS MALFORMATIONS, MULTIPLE CUTANEOUS AND MUCOSAL) H02848
LIM BINDING DOMAIN 2 H74106
KINASE SCAFFOLD PROTEIN GRAVIN AA478542
359722 AA011182
TYROSINE KINASE WITH IMMUNOGLOBULIN AND EPIDERMAL GROWTH FACTOR HOMOLOGY DOMAINS AA432062
CD34 ANTIGEN AA434483
HUMAN DNA SEQUENCE FROM CLONE 1033B10 ON CHROMOSOME 6P21.2-21.31. CONTAINS THE BING5 GENE, EXONS 11 TO 15 OF THE BING4 GENE, THE GENE FOR GALT3 (BETA3-GALACTOSYLTRANSFERASE), THE RPS18 (40S RIBOSOMAL PROTEIN S18) GENE, THE SACM2 N78611
69672 T53626
HOMO SAPIENS KDR/FLK-1 PROTEIN MRNA, COMPLETE CDS AA026831

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Table 12: Stromal/Fibroblast Gene Subset

MUSCULIN (ACTIVATED B-CELL FACTOR-1) AA470081
COLLAGEN, TYPE V, ALPHA 1 R75635
471748 AA035018
SMOOTH MUSCLE ACTIN, ALPHA2 AA040169
TRANSGELIN/SM22 AA010664
SMOOTH MUSCLE PROTEIN 22-ALPHA AA010664
LUMICAN AA035657
FIBULIN 1 AA614680
COLLAGEN, TYPE VI, ALPHA 3 R62603
HOMO SAPIENS OSF-2 MRNA FOR OSTEOBLAST SPECIFIC FACTOR 2 (OSF-2P1), COMPLETE CDS AA598653
COLLAGEN, TYPE III, ALPHA 1 (EHLERS-DANLOS SYNDROME TYPE IV, AUTOSOMAL DOMINANT) T98612
COLLAGEN, TYPE I, ALPHA 1 W90360
COLLAGEN, TYPE I, ALPHA 2 AA490172
COLLAGEN, TYPE III, ALPHA 1 (EHLERS-DANLOS SYNDROME TYPE IV, AUTOSOMAL DOMINANT) AA044829
COLLAGEN, TYPE III, ALPHA 1 (EHLERS-DANLOS SYNDROME TYPE IV, AUTOSOMAL DOMINANT) T98612
COLLAGEN, TYPE I, ALPHA 2 W93067
THY-1 CELL SURFACE ANTIGEN AA496283
HOMO SAPIENS, ALPHA-1 (VI) COLLAGEN AA046525
COLLAGEN, TYPE VI, ALPHA 1 AA047209
COLLAGEN, TYPE VI, ALPHA 1 AA047209
HUMAN ALPHA-2 COLLAGEN TYPE VI MRNA, 3' END AA633747
HUMAN METHIONINE SYNTHASE MRNA, COMPLETE CDS AA233650
265694 N25353

Table 13: B-cell gene subset

IMMUNOGLOBULIN GAMMA 3 (GM MARKER) AA663981
COLONY STIMULATING FACTOR 1 (MACROPHAGE) N92646
NEUTROPHIL CYTOSOLIC FACTOR 1 (47KD, CHRONIC GRANULOMATOUS DISEASE, AUTOSOMAL 1) AA489666
IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 2 W73790
IMMUNOGLOBULIN LAMBDA LIGHT CHAIN R50297
HUMAN REARRANGED IMMUNOGLOBULIN LAMBDA LIGHT CHAIN MRNA N64851
HUMAN REARRANGED IMMUNOGLOBULIN LAMBDA LIGHT CHAIN MRNA T67053
HUMAN IG J CHAIN GENE H24896
IMMUNOGLOBULIN J CHAIN H24896
HUMAN IG J CHAIN GENE T70057
MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ BETA 1 R73128
IMMUNOGLOBULIN MU H73590
EARLY DEVELOPMENT REGULATOR 2 (HOMOLOG OF POLYHOMEOTIC 2) AA598840
MAX-INTERACTING PROTEIN 1 AI087032

Table 14: Adipose-enriched/Normal breast gene subset

MESENCHYME HOMEO BOX 1
AA426311
INSULIN-LIKE GROWTH FACTOR 1 (SOMATOMEDIN C)
AA456321
CYCLIN-DEPENDENT KINASE INHIBITOR 1C (P57, KIP2)
R81336
78946
T61792
FATTY ACID BINDING PROTEIN 4, ADIPOCYTE
AA046090
FATTY ACID BINDING PROTEIN 4, ADIPOCYTE
AI652163
FATTY ACID BINDING PROTEIN 4, ADIPOCYTE
N92901
MDGI/FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART
AA128926
CD36 ANTIGEN (COLLAGEN TYPE I RECEPTOR, THROMBOSPONDIN RECEPTOR)
R09416
CD36 ANTIGEN (COLLAGEN TYPE I RECEPTOR, THROMBOSPONDIN RECEPTOR)
N39161
GLUTATHIONE PEROXIDASE 3 (PLASMA)
AA664180
FOUR AND A HALF LIM DOMAINS 1
AA456394
ALCOHOL DEHYDROGENASE 2 (CLASS I), BETA POLYPEPTIDE
N93428
AQUAPORIN 7
H27752
484535
AA036974
LIPOPROTEIN LIPASE
AA633835
GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1 (SOLUBLE)
AA192547
RETINOL-BINDING PROTEIN 4, INTERSTITIAL
T72220
INTEGRIN, ALPHA 7
AA055979
85660
T62068
PHOSPHOLEMMAN
H57136
AQUAPORIN 1 (CHANNEL-FORMING INTEGRAL PROTEIN, 28KD)
H24316
APOLIPOPROTEIN A-I
R97710
SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 14
R96668
PEROXISOME PROLIFERATIVE ACTIVATED RECEPTOR, GAMMA
AA088517
ENDOTHELIN RECEPTOR TYPE B
H28710

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Table 15: Macrophage gene subset

ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.SAPIENS] T94293
CHITINASE 1 T94272
53341 R15934
SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 18, PULMONARY AND ACTIVATION-REGULATED AA495985
FOLYLPOLYGLUTAMATE SYNTHASE R44864
LYSOZYME (RENAL AMYLOIDOSIS) N63943
LYSOZYME (RENAL AMYLOIDOSIS) N63943
TRANSCRIPTION FACTOR AP-2 ALPHA (ACTIVATING ENHANCER-BINDING PROTEIN 2 ALPHA) N63770
LIPASE A, LYSOSOMAL ACID, CHOLESTEROL ESTERASE (WOLMAN DISEASE) AA630104
CD68 ANTIGEN AA421296
ACID PHOSPHATASE 5, TARTRATE RESISTANT R08816
FC FRAGMENT OF IGE, HIGH AFFINITY I, RECEPTOR FOR; GAMMA POLYPEPTIDE R79170
CATHEPSIN Z AA488341

Table 16: T-cell gene subset

INTERLEUKIN 10 RECEPTOR, ALPHA AA437226
INTEGRIN, ALPHA L, CD11A R48796
742143 AA406027
T-CELL RECEPTOR, BETA CLUSTER N91921
80186 T64192
T-CELL RECEPTOR, DELTA (V,D,J,C) AA670107
ESTS, WEAKLY SIMILAR TO S-ACYL FATTY ACID SUNTHETASE THIO ESTER HYDROLASE, MEDIUM CHAIN [R.NORVEGICUS] AA470066
LYMPHOCYTE-SPECIFIC PROTEIN TYROSINE KINASE AA420981
CD3D ANTIGEN, DELTA POLYPEPTIDE (TIT3 COMPLEX) AA055946
CD3G ANTIGEN, GAMMA POLYPEPTIDE (TIT3 COMPLEX) T66800
TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2) AA465444

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
		1	1	1	1	1	1	1	1	1
1	1	0.2038	-0.5431	-0.045	0.04438	-0.1831	-0.4656	0.065	0.4644	-4.215
2	1	-0.03563	-0.8125	-2.014	-0.525		-2.595	0.3356	0.475	-0.4644
3	1	-0.1206	0.4425	0.6706	-0.65	0.2825	-1.04	0.3706	1.14	-1.829
4	1	0.02	1.693	-0.4388		-0.5369	-1.559		-0.01938	
5	1	-0.4288		-0.6375	-0.2581		-2.018	1.882	1.442	1.952
6	1	-0.1513		-0.33	-0.1206				1.209	0.36
7	1	-0.07125	-0.2781	-0.47	0.1194	-0.5581	-0.5506	1.5	1.389	1.09
8	1	-0.6612	0.3319	-0.3	-0.000625	-0.8081	-0.8606	0.95	0.4894	0.53
9	1	0.4538		-0.175	0.6044	-0.5831	-0.4056	0.075	-0.5456	-0.205
10	1	0.6588		0.47	-0.01062	-1.238	0.3194	0.13	0.5794	0.49
11	1	0.2644	0.8975	0.8356		0.6275	-0.245	0.3056		0.2456
12	1	-0.3812	0.2519	-2.91E-09		0.6619	-0.2206	0.22		0.59
13	1	0.01875	-0.4881	-0.43	1.409	-0.4481	0.4994	0.53	1.189	0.3
14	1	-1.059	1.184	-1.348	1.012	-1.936	-1.948	-0.6775	0.6119	2.122
15	1	-0.755	1.438	-0.6638	1.336		-2.544		0.8456	
16	1	-0.86	-0.4669	0.7812	0.5706	-0.5069	0.4706	-0.3788	0.6306	-0.2988
17	1	1.353	0.01594	0.7141	1.673	-0.5741		1.484	-0.7366	1.314
18	1	0.7628	0.01594	-0.02594	0.6934	-1.394	-0.9466	-0.2859	-0.01656	3.454
19	1	0.2587	1.952	-0.27	-1.211	-0.5681	-1.071		-1.801	-0.34
20	1	-0.3913	-0.9681	-0.64	-0.5806	-0.7181	-1.001	0.26	0.06937	0.33
21	1	-0.1306	2.583	-0.4894	-0.53	-0.8875				
22	1	0.05875	0.5119	-0.56	-0.5006	-0.5181	-0.1406	-0.68	-1.291	0
23	1	-1.161	-0.1981	0.3	-0.8506	-0.7181	0.6894	1.68	0.4694	1.53
24	1	-0.1513	-0.07813	-0.64	0.4194	0.5719	-2.131	1.17	0.6894	-0.23
25	1	-0.4663	-1.203	-1.065	0.5844	-0.4731	-3.336	1.115	-0.8144	-0.585
26	1	-1.08	0.3231	0.5912	0.9506	0.8831	0.2606		0.000625	0.3812
27	1	1.793	3.056	3.094	2.123	-0.2741	-1.217			-1.366
28	1	-0.7863	-0.7331	-0.465	-0.7456	1.537	-1.676	-1.435	2.154	0.145
29	1	0.1288	-0.8881	-0.83	-0.000625	-0.1981	-0.9706	-1.81	1.209	1.36
30	1	-0.1312	-0.7681	-2.91E-09	-0.5306	-0.3481	0.3894	1.84	1.009	1.4
31	1	-0.01656	0.01656	-0.1053	-0.2859		0.09406	2.425	0.7841	1.555
32	1	-0.4713	-0.5381	0.93	-1.231	0.2219	0.1994	3.46	-0.7306	2.74
33	1	-1.156	0.5769	2.095	-1.086					1.405
34	1	-0.4612		-0.2	-0.5206	-0.02812	0.3794			1.17
35	1	0.4687	0.3719	0.81	-0.02063	-1.168	-1.201	2.34	3.429	0.1
36	1	0.4828	-0.1441	0.2341	0.3134	0.03594		1.984	2.253	-0.07594

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
37	1	0.06875	-0.7681	-1.22		-2.208	-1.671	1.96	2.869	2.04
38	1	-0.8188	1.014	-1.278	-1.118		-1.178	3.412	3.262	-0.6075
39	1	-0.2612	0.7819	-0.96	-1.971	-1.458	-1.421	3.13	3.069	-1.05
40	1	-0.9263		-2.365	-1.896			1.445	2.244	1.265
41	1	-0.6712	-1.098	-1.34	-1.821	-1.398	-1.821	1.77	2.299	1.64
42	1	-0.1512	-1.198	-0.8	-1.321	-0.1381	-1.921	2.65	3.129	2.53
43	1	-0.3512	-0.6981	-0.14	-0.1306	-0.2481	-0.7706	1.94	2.789	-0.47
44	1	-0.07719	-0.06406	0.01406	-0.4666	-0.01406	0.1734	3.424	2.133	-0.05594
45	1	-0.2488	0.1244	-0.2775	2.252	0.8744	0.4819	2.002	0.3019	-0.7475
46	1	0.02438	0.2575	0.1456	-0.025	-0.2425	-0.865	1.016	0.425	1.076
47	1	-0.1206	-0.5675	-1.559	-1.21	-0.4475	0.86	2.731	2	1.921
48	1	-0.005625	0.3375	0.005625	-0.175		-1.075	1.026	3.195	-0.4144
49	1	-2.26E-09		1.941	-0.7894	-4.047	-1.719		4.131	0.4812
50	1	-0.9212			-1.281	-0.5781	-1.091	2.87	2.959	
51	1	1.87		1.551	0.1906	0.7531	-0.5094	3.611	3.561	1.911
52	1	-0.03125		-0.55	2.589			4.83	3.229	2.45
53	1	-1.332	1.423	0.4491	-1.752	0.03094	-1.122	3.719	4.498	1.969
54	1	0.1494		-1.159	-0.68		3.26	7.041	6.48	
55	1	-0.8588	0.5244	0.2125	-0.09813	0.4644	-0.5281	5.022	2.552	3.982
56	1	0.3212		0.2025	-0.6081	-0.2756			4.922	-0.1075
57	1	-0.7462	1.047	0.755	-0.8856	0.09688	0.2944		7.354	-0.975
58	1	1.921	1.754	1.132	-0.3881		-2.428	4.462	5.242	-0.2575
59	1	-0.8612		-0.19	-1.041	-0.05812	-2.071	7.66	8.849	2.34
60	1	-0.5622	-0.1891	-0.5009	-1.592	-0.02906	-1.072	3.969	4.698	
61	1	-1.036	0.7969	-0.345	-1.286	0.9669	-1.146		8.644	0.025
62	1	-0.3012		-2.91E-09		-0.2419	0.06937	5.39	-4.829	-0.91
63	1	-2.26E-09	0.1131	-0.6488	-2.129	0.1631	-1.399	5.261	5.331	-1.419
64	1	-2.26E-09	0.4531	-0.4988	-1.239		-2.021	5.661	4.221	0.1712
65	1	0.1588	1.572	-0.24	-0.1406	-1.068		6.78	5.629	-0.89
66	1	-0.1112	0.05188	-0.51	-0.7406	-0.4381		7.67	6.439	0.11
67	1	-1.161	0.7219	-0.23			-1.851	5.83	4.629	
68	1	0.1838	-0.2431	-0.055	0.02438	-0.1431	-0.3656	3.975	3.864	-0.045
69	1	0.2188	-0.1181	-2.91E-09	-0.000625	-0.1681	-0.01063	6.11	6.689	0.98
70	1	0.3787		0.57	2.079	0.8319	2.719	5.47	4.389	-0.35
71	1	-0.4612	-0.2181	-0.07	0.6594	1.532	0.7794	3.05	2.999	-0.4
72	1	-0.3013	1.792	0.19	-1.331			3.99	3.279	-4.02E-09
73	1	-0.8213	0.2619	-0.78	-1.781	-0.4781	-1.641	4.66	4.689	1.33

2

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
74	1	-0.4513	-0.8881	-1.22	-0.01063	-0.06813	-1.391	2.34	2.159	1.2
75	1	-2.26E-09	-0.06687	0.1312	-0.009375	0.3831	0.2306	3.861	3.621	-1.399
76	1	-0.1244	-0.8512	0.3569	0.2063	-0.8112	0.6262	3.907	3.696	
77	1	0.2688	-0.2381	0.16	0.2094	-0.6281	-0.2906	3.03	2.829	-0.47
78	1	-0.1312	0.7719	0.89	1.159	0.3719	-0.4906	1.07	1.599	-0.04
79	1	1.121	1.144	0.5125	3.042	1.974	-1.198	3.602	4.302	1.022
80	1	1.389	-0.2981	0.58	2.609	1.642	-0.9206	3.61	4.329	0.75
81	1	0.9078	0.7209	0.7591	1.778	-0.7991		1.659	3.218	-1.541
82	1	-0.1331	0	-0.4619	-1.063	-0.88	-1.723	4.528	5.727	-0.07188
83	1	0.1794	-0.2575	-0.4994	-0.85		-1.08	4.631	5.98	-0.2294
84	1	0.3188	0.7169	-0.1	-1.261		-0.2406		3.749	0
85	1	3.004			-1.166	-0.7931				-0.495
86	1	4.229	2.112	1.03	-1.541	0.2519	-1.181	-0.13	3.319	-0.13
87	1	2.049	1.492	1.27	0.8994		-2.691	1.43	3.249	0
88	1	-2.26E-09		-0.2988	-1.709		0.4706			-0.2088
89	1	-0.03063	1.032	0.8206	-1.12	-0.2775	-0.64	1.211	3	1.921
90	1	0.1478	0.09094	-0.09094	-0.9716	-1.929	-2.772	3.469	2.538	2.649
91	1	2.79	2.373	1.831	2.491	-0.5169	0.000625	3.081	3.271	0.9513
92	1	2.8	2.193	1.371	3.011	-0.4369	0.000625	3.891	3.681	1.051
93	1	1.673	1.626	1.544	2.273	-0.01406		3.124	3.203	-1.106
94	1	2.769	2.592	2.08	3.739	-1.688	-2.973		4.189	-1.09
95	1	0.6269	0	0.008125	2.167	-0.05	-3.211	3.098	2.257	2.598
96	1	1.029	-0.1881	-2.91E-09	0.7294	-3.168	-4.061	2.96	2.979	0.66
97	1	1.049	-0.3681	-2.91E-09	0.6294	-3.898	-2.787	3.05	3.319	1.04
98	1	1.503	0.07594	0.3941	0.6034	-0.8041	-1.022	2.154	2.733	-3.156
99	1	1.188	0.04094	-0.04094	0.5484	-0.3409	-2.751	1.999	2.708	-2.391
100	1	1.399	-0.1281	0.09	0.4294	-0.3881	-3.801	2.18	3.249	-2.48
101	1	1.759	0.2419	-0.05	0.6394	-0.3781	-2.682	2.41	3.069	-3.27
102	1	1.758	0.2609	1.669	2.248	-2.099		1.789	3.348	-1.731
103	1	0.4769	0		0.8675	-0.93		0.5781	2.237	-1.142
104	1	0.2937	-0.6131	-0.125	0.7444	-1.423	-1.266	2.205	2.664	-0.455
105	1	-0.2912	-0.1581	-2.91E-09	0.1494	0.2419	-2.081	1.92	2.119	-0.85
106	1	1.667	0	1.228	0.8275	-0.53	-2.273	3.128	3.297	1.728
107	1	-0.4313	-0.8581	0.05	0.4994	-0.03813	-0.6206	0.8	1.499	0.2
108	1	0.4312	-0.05562	-0.0375	0.2519	0.1844	-0.1881	1.592	2.392	1.062
109	1	1.294	0.4969	0.015	0.8944	-1.533	-1.376	4.185	2.514	0.045
110	1	2.269	1.242	0.95	1.679	-1.008	-1.331	7.29	4.239	-0.31

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
111	1	1.559	1.262		1.299	-0.1581	-1.201		3.379	-0.78
112	1	-0.2812	0.4319	0.73	-0.1306	0.3119	-0.5706	0.87	1.219	0
113	1	1.439	1.502	1.13				2.37	2.309	0
114	1	1.329	0.5119	0.5	-0.4406	-1.608	-1.451	2.63	3.059	0.88
115	1	1.117	0	-0.6819	-0.5425	-2.56	-1.923	4.738	5.377	2.438
116	1	1.269	0.1519	-0.51	-0.2606	-1.688	-1.381	4.57	5.029	2.54
117	1	1.367	0	-0.5519	-0.4225	-1.83	-1.873	4.018	5.357	2.728
118	1	-0.1706	-0.4275	0.5306	-0.03	0.6725	0.03	1.731	4.47	-2.349
119	1	-2.19		-0.5788	-2.639		0.000625		2.261	0.00125
120	1	-2.321	-0.3781	-2.26	-2.521		-2.681	2.03	2.209	0.91
121	1	-0.6731		-1.622	-3.023	-2.79E-10		3.658	3.037	-2.132
122	1	-1.146	0.4369	-1.155	-2.526				2.954	-0.015
123	1	0.4369	0	1.738	0.6775	1.96	-0.05562	2.468	3.127	-2.652
124	1	4.174	2.717	0.035	1.954	-1.063	-0.5106	6.655	6.744	5.055
125	1	2.089	1.742		-0.000625	-1.288			3.239	2.23
126	1	-0.4912	-1.558	-1.02	-0.5206	-2.438	-3.281	2.65	4.079	1.69
127	1	-0.1188	-0.09562	-0.4275	-0.7381	-0.5556	-1.598	2.422	3.922	1.432
128	1	-0.002187	-0.2291	-1.271	-0.2116	0.0009375	-1.422	0.8591		1.259
129	1	-0.535	-0.8581	-0.8738	-2.714			2.686	2.576	1.546
130	1	-1.081	-0.1841	-2.91E-09	-1.411	-2.668	-3.651	2.51	2.319	0.72
131	1	-0.5472	-0.7881					3.404	2.383	
132	1	0.1987	-0.09812	-0.89	-2.411	-0.2881	-1.791	3	4.579	4.59
133	1	-0.2812		-0.74		2.702	-0.1006	6.68	3.469	1.71
134	1	-0.4712	0.01813	-0.98	0.2094	0.8019	-1.071	2.4	2.019	-0.5
135	1	-0.575		-0.3838	-0.3844	1.378	-1.104	2.166	2.216	-0.8637
136	1	-1.131	0.5319	-0.29	0.2894		0.9794		2.449	-1.47
137	1	-0.1912		0.01	0.1194	-0.8281	0.4194		1.689	-1.3
138	1	-0.1113		0.98	-1.261	-1.158	-1.001	-0.29	-1.461	2.72
139	1	-0.1113	1.332			-0.6981	-1.071		-1.001	
140	1	-0.4512	-0.3181	-0.44	-1.041	0.05188	0.3794	-0.31	-0.2406	0.97
141	1	1.769	1.022	0.84	-0.7806	-0.1181	-0.2206		-1.441	-0.24
142	1	0.01875	1.112	0.33	-2.041			-1.37	-2.151	
143	1	0.2988	0.6519	0.29	-1.111	0.7019	0.5844	-1.26	-2.421	-0.7
144	1	0.3438	0.4669	0.025		-0.7231	0.8084			-0.025
145	1	2.018	0.7409	1.079	0.1284	-0.1291			-1.672	-1.711
146	1	1.599	0.6219	0.46	1.739	-0.6981	-0.3906		1.489	-1.22
147	1	4.549		4.36	-0.4706		3.729			

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
148	1	2.17	0.5031	0.9112	-0.2394	-0.6169	0.6906		0.000625	0.4112
149	1	1.789	0.9525	1.191	1.07	-1.927	-0.2	-0.6694	-0.12	1.301
150	1	2.929	1.812	2.34	3.119		1.749		-3.231	-3.52
151	1	1.509	-0.05812	2.04	2.389		1.099			-1.86
152	1	2.689	1.622	3.07	3.539	-2.518	2.129			-2.09
153	1	2.459	1.302	3.18	3.439	-1.798	1.999			-0.69
154	1	2.409								0.1
155	1	2.629	1.862	3	1.299	-4.248	-0.4506	0.82	1.559	-2.34
156	1	2.659	2.132	3.17	1.249	-4.658	-0.3606	0.75	1.569	-2.33
157	1	1.909	1.872	1.7		-0.8181	0.4894	1.24	0.8394	-2.05
158	1	3.159	3.792	2.671	0.88	-0.7475	0.69	1.081	-0.44	-0.5594
159	1	2.009	1.242	1.04	1.089	-1.178	-0.5406	0.67	0.4594	-0.74
160	1	4.439	2.452	1.94	0.4994	-2.758	-1.601	1.38	2.169	0.13
161	1	2.189	1.382	1.56	-1.411	-0.1081	0.3994		0.1194	-0.41
162	1	1.88	1.163	0.1912	1.261	-0.9069	-0.7494		-0.2394	-0.3188
163	1	0.4488	0.05188	0.56	0.7494	-0.06812	1.709	0	-0.8806	1.36
164	1	0.1678	0.1409	0.2191	0.5884		1.698		-1.362	1.009
165	1	-0.05125	0.8019	-0.11	-0.2806			-0.1409		0.46
166	1	0.06937		0.1606	-0.07	0.9625	0.57		0.41	0.5706
167	1	0.6087	-0.9981	0.85	0.5394	-0.2081			-0.6506	-0.06
168	1	-0.7212	0.3719	-0.12	-1.031	0.4619			-0.66	-0.66
169	1	0.02344				-0.02344	0.1741		-0.6259	
170	1	-0.085	-0.3219	0.3862		0.05594	0.08562		-2.014	0.2562
171	1	-0.1272	-0.2441	0.3841	0.2234		-0.2066	-1.166		
172	1	-0.3213		-0.72	0.2194	0.2219	-1.081	-0.36	-0.5506	0.78
173	1	-2.26E-09	-0.2669	0.5512	-0.5994		0.09062		-0.8894	0.5512
174	1	-0.3363	0.2369	0.015	-1.086	0.5969	0.03437			-1.325
175	1	-0.5412		0.27	-1.201	-0.6781	-0.7806		0.009375	0
176	1	0.2537		0.125	-0.7756		-1.016		-2.646	
177	1		1.402	-0.64	-0.7306	-1.648	-1.291		2.429	-0.1
178	1	0.6144	-0.3981	-0.9344	-0.875		-0.145			-0.4644
179	1	-0.2312	0.1419	-0.42	0.4294	-0.4681	0.4494	-0.12		-0.32
180	1	0.8688	0.8219	1.17	2.569	-1.228	-0.3106	-0.21	-0.4106	1.27
181	1	0.8187	2.118	1.36	2.629	-0.3119	-0.07063	0.2	-0.4106	1
182	1	0.155		-0.3538	-0.5544		-0.1544			-0.2144
183	1	0.04438		-1.364			-2.165			
184	1	0.03	-0.9869	0.2312	-1.169	-1.187	-0.02938		-1.379	1.001

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Table 2

| | GWEIGHT | HMEC-C | HMEC+INFA | HMEC-C_CONFL2 | 184AA | 184A1-LATE | 184B5 | HMVEC | HUVEC | MDA-MB-321 |
		ARRY2X	ARRY4X	ARRY3X	ARRY5X	ARRY1X	ARRY0X	ARRY7X	ARRY6X	ARRY11X
185	1	0.1888	-0.3981		-0.8406	-0.2781	-0.7006		-1.631	0.83
186	1	-0.06125	-0.3981	0.76	-0.9406	-0.1081	-0.8006	-0.85	-1.051	-0.37
187	1	0.66		-0.5988	-1.219	-1.557	-0.8194		-2.329	-0.2788
188	1	0.6378	-0.04906	-1.191		-1.729	-1.572	-1.041	-0.1816	-0.3009
189	1	0.1669	0	-0.7219	-2.663	-1.68	-1.523	-0.9919	-1.453	0.4281
190	1	0.6488	-0.7381	-0.66	-1.181	-1.198	-1.041	-2.09	-0.9706	0.23
191	1	0.2344		-0.2344	-0.695	1.568	-0.895		-1.485	
192	1	0.9788	2.322	0.79	-0.000625	2.912	0.7194	-1.59	-1.471	-0.91
193	1	-0.04875	-0.7156	-0.0475	0.6919	1.374	-0.5581	0.9325	-0.04813	0.3925
194	1	0.09	-0.5369	0.4712	-0.4694	-0.6369	-0.9494	-0.1788	0.000625	0.5813
195	1	-0.4612	-1.038	-2.91E-09	-1.371	-1.008				0.37
196	1	0.00875	-0.1581	-0.74	-1.261	0.8519	-1.321	-0.47	-1.731	-0.17
197	1	-0.61	0.6631	-0.8788	-1.019	1.063	0.000625	-0.9888	-0.2694	-0.6787
198	1	-0.6913	1.362	-1.78						-0.28
199	1	-0.3812	3.152	2.43	-0.03062	1.272	3.299		-0.7106	-0.58
200	1	-2.26E-09	0.7431	0.9812	0.3006	0.2631	1.401	-0.6688	-0.7394	-0.4288
201	1	-0.6031		1.328	-0.6625	-2.79E-10	1.747		-1.793	-1.632
202	1	-0.125	-0.8219	-0.05375	0.5956	-0.08188	1.786	0.4262	-0.07438	-0.1138
203	1	-0.24	-0.08687	-0.06875	0.4406	0.3931	1.461	-0.1788	0.000625	-0.4287
204	1	-1.232		-0.8809	-0.9216	-0.1591			-2.052	0.3391
205	1	-0.7663	-0.9331	-0.665	-0.1856	0.8769	1.974	0.705	1.874	1.075
206	1	-1.331	-1.938	-1.52	-0.09063	1.132	3.549	-0.22	1.929	1
207	1	0.05937		0.4406	1.26	1.743	4.33		-1.43	-0.05938
208	1	-0.1672	-0.5341	0.1241	-0.1466	-0.07406	3.133	0.2741	0.3934	1.074
209	1	1.089	0.9419	1.46	1.429	1.952	2.719	-0.14	-1.531	0
210	1	1.749	1.222	1.76	1.259	2.432	2.729	-0.34	-1.021	0
211	1	0.8088	0.3619	1.17	2.829	2.072	1.419	-1.56	-1.981	-1.8
212	1	-0.4613	-0.09812	-0.48	-0.4606	-1.248	0.6794		0.1194	0.72
213	1	-0.2312	0.06188	-0.42	-0.9406	-0.4781	-0.4206	0	2.649	-1
214	1	-0.33		-0.09875	-0.7694	1.393	0.000625			
215	1	0.8469	0.37	1.418	0.0975	-2.79E-10	-0.6725	-1.722	0.2275	3.038
216	1	-1.641	-1.277	0.5906	-2.04	-2.857	1.34E-09	-1.949	3.1	3.331
217	1	1.309		-0.53	1.399					3.14
218	1	-0.11	0.1931	0.7412	-0.6694	-0.1569	0.000625			-1.429
219	1	1.339		-0.24		-0.1481	-0.2206	-3.54E-10	1.389	
220	1	0.9969	0	0.5081	0.4575	-0.1	0.1875		-0.4625	-0.3019
221	1	0.7938	1.477	0.115	0.1744	-0.6531	0.1844		-1.166	-0.475

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Table 7

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
222	1	1.109	1.762	0		-2.898	-2.001		-1.551	
223	1	0.6788	-0.2681	0.99	0.4394	0.4319	-0.8706	1.2	1.349	-0.76
224	1	1.299	0.2819	0.68	0.8294	-0.6481	-0.1806	1.04	1.599	-0.83
225	1	-2.26E-09	-0.3769	0.09125	-0.5394	0.06313	0.3606		-1.029	0.9512
226	1	0.3188	0.8919	0.03	-0.03062	0.6919	1.279			
227	1	-1.376			0.07438	0.1369	-0.6856		1.124	
228	1	-1.732	0.1809	-1.821	-1.482	-1.999		-1.301	1.088	1.399
229	1	0.3669	0	-1.202	0.3375	-0.32	-2.003	0.09812	1.017	2.178
230	1	-0.7012	0.08188	-1.33	-0.7306	0.2719	0.1894	-6.89E-09	0.1794	-0.03
231	1	-0.3212	-1.368	-0.26	-0.3206	0.7519	0.1594	-0.08	0.1794	0.08
232	1	0.4888	-0.3181	0.02	0.4494	-0.1781	0.8794	0.95	0.4894	0
233	1	1.519								-0.84
234	1	0.2788	-0.1981	-2.91E-09	0.4694	-0.3481	0.3694	0.42	0.5994	0.96
235	1	0.2488	0.1819	0.43	-0.000625	-0.6781	0.6194	-5.59E-09	0.7294	1.09
236	1	-2.26E-09	-0.6869	0.2012	-0.1194	0.01313	-0.3094			0.5512
237	1	-2.26E-09	-0.1969	-0.4088		1.183	0.5006	1.441	1.161	0.2412
238	1	-2.26E-09	2.363	-0.8288	-0.02938	-0.3669	0.2506		-0.5594	-1.259
239	1	1.119		0.67	-1.031	0.1619	-0.8906			1.32
240	1	-0.4312	-1.038	-0.88	0.7594	0.3019	-1.321	0.66	0.4594	0.11
241	1	-0.4712	-1.138	-1.06	0.6994	0.7019	-1.251	0.87	0.5794	0
242	1	0.01687	-0.24	0.4681	1.347	-2.79E-10	-1.423	1.568	0.6175	0.8081
243	1	1.439	0.2619	0.02	0.01938	-1.178	-2.001	0.73	-0.2606	0
244	1	1.159	0.1719	0.84	0.5694	-0.2681	-1.051	0.87	0.6494	-1.95
245	1	1.044	0.7675	0.8556	1.715	1.588	-0.045	0.04562	1.185	-0.5644
246	1	-0.003125	0	-0.6819	0.3975	-0.34	-0.3725	1.088	1.247	0.5794
247	1	0.3787	-0.6081	0.27	0.09937	-0.02813	-0.2206	0.76	0.1594	0.89
248	1	-0.2612	1.712	0.7	-0.9206	-0.3681	1.829	2.79		-0.26
249	1	2.081	1.324	0.9425	1.482	-0.3256	-0.01813			1.692
250	1	0.1288	2.042	0.83	0.3494	-0.4381				-0.02
251	1	0.3788		0.09	0.4894	-0.6081	-0.6406		2.339	-0.55
252	1	0.2288	-0.7581	0.81	-0.000625	-0.5981	-1.051	1.86	4.029	-0.61
253	1	-0.9562	-2.433	-1.075	-0.4456	0.3869	-0.8756	2.085	0.9644	0.345
254	1	-1.546	-2.143	0.105	-0.3256	0.9969	1.304	0.915	0.4844	-1.415
255	1	-0.02062		-1.079	0.38		0.99		-0.07	0
256	1	0.8028	0.2359	0.2141		0.03594	-0.5966			-1.976
257	1	-2.26E-09		-0.8388	-0.6794		0.1406		5.511	0.4612
258	1	0.2991	-0.1578	0.2703	-0.5303		-0.7903		3.18	-0.3197

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
259	1	2.439	2.072	1.49	-0.2106	-0.8681	-0.4706	-0.46	6.569	-0.66
260	1	2.209	1.742		-0.09062	-0.6381	-0.1506	0	3.809	-0.25
261	1	0.32	2.173	1.351	0.7406		0.000625	-2.019	2.031	-0.9687
262	1	-2.26E-09	0.1031	0.4212	1.181	-1.437	0.4806		1.511	
263	1	1.037	0.05	0.6681	0.6775	-2.79E-10	0.0175	0.2081	-0.3725	0.7981
264	1	0.5088	0.2919	0.38	0.4894	-0.4481	0.4894			0
265	1	0.3694	-0.7975	-0.2894	0.64	0.4825	-0.05	-3.119	1.17	1.811
266	1	1.15	0.8831	1.541	1.061	-0.6369	2.101	-2.999	0.000625	-2.079
267	1	-0.2231	-1.8	0.7081	-0.1325	-2.79E-10	0.7475		-1.233	-0.4219
268	1	0.3488	0.2319	0.38	-0.7906	-0.4181		-0.76	-0.5506	-0.06
269	1	2.169	1.572	1.91	1.639	0.5119	-0.9206	-3.55	-3.431	-1.55
270	1	2.347	1.9	1.528	1.697	-2.79E-10	-0.9025	0.4081	-1.163	0.3381
271	1	3.869	3.382	3.45	0.4994	0.1119	-1.951		-2.461	-1.26
272	1	3.11	3.053	2.811	0.3806	0.01313	0.000625	-1.049	-1.349	-0.5887
273	1	2.309	1.522	3.21	0.04937	0.9519	2.249		-1.851	-0.49
274	1	2.095	0.6281	1.276	1.906	0.2581	1.386		-2.854	1.996
275	1	2.11	1.193	1.571	2.651	1.323	1.621	-0.3688	0.000625	-0.3187
276	1	1.729	1.442	1.81	2.129	0.8619	2.059	-1.65	-0.8506	0
277	1	0.01125	2.264	1.952	2.182	2.064	2.732	2.582	2.022	-0.7775
278	1	2.439	2.572	3.33	3.339	1.652	3.119	1.96	1.259	
279	1	1.084	1.427	2.295	0.9044	2.867	2.214	-0.335	-0.4656	-0.065
280	1	1.981	1.034	1.772	2.342	2.824	1.932	2.222	2.202	-0.2775
281	1	2.737	0	1.448	0.9575	1.14	3.737			-0.03188
282	1	0.4238	0.3369	0.575	2.254	2.827	2.954			-0.445
283	1	-0.1131	0	0.4581	2.417	2.51	2.147	2.278	1.964	-0.7519
284	1	1.79	1.863	2.051	1.371	1.293	0.2806	1.811	2.927	-0.2794
285	1	1.429	1.052	1.2	0.8194	-0.7919	0.2094	-0.39	-0.4206	-0.32
286	1	3.384	2.607	2.215	3.204	-1.023	-1.186	2.475	1.444	-0.585
287	1	3.598	2.581	2.659	3.378	-0.1091	-0.7516	2.509	1.338	0.1091
288	1	0.1106	0.3037	1.232	0.8112	1.544	2.201		-0.01875	0.5919
289	1	1.839	0.7819	0.39	0.9894		-0.07063		-1.041	
290	1	1.287	0	0.4481	1.467	-0.79	0.7575			
291	1	0.8828	0.2759	3.174	1.353	-1.434	2.183			1.174
292	1	0.1044		1.106	2.065	1.848			0.695	-1.054
293	1	1.004	0.2469	1.235	1.304	0.4069	1.354		-0.3956	-0.085
294	1	0.4988	0.4619	0.74	1.209	1.382	1.409	0	-0.07062	1.01
295	1	0.4488	-0.8681	0.33	-0.000625		0.7294	1.43	0.9594	-0.08

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	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
296	1	0.5469	-0.01	0.7081	-0.0825	-2.79E-10	0.9875	1.428	0.7675	1.108
297	1	1.469	0.6419	1.24	0.06938	0.4019	-0.2606			1.37
298	1	1.234	0.8675	1.366	0.725	-0.4625	0.275	1.506	1.025	1.186
299	1	1.854	2.427	1.075	0.2144	-0.6931	0.2344	3.775	1.384	0.345
300	1	0.5388	0.1419	0.22	1.409	-1.108	-0.2506		-1.501	-2.72
301	1	1.084	0.5869	0.455	1.644	0.4569	0.7344		-7.016	-0.455
302	1	-2.26E-09	0.8531	2.201	1.851	1.473	0.8806			
303	1	2.064	1.607	3.235	4.834			2.055	0.7644	1.775
304	1	0.8488	0.5019	0.95	0.5594	0.4119	-0.7306	0	-0.4106	0.92
305	1	0.7828	0.4059	0.8241	0.6134	0.03594	-0.7466	-0.03594	-0.4466	0.6741
306	1	1.269	0.6519	0.88	1.749	-0.5781	1.159	1.56	0.7394	0
307	1	0.7288	0.5519	0.31	1.479	0.2819	0.06938	-0.96	-2.531	0.71
308	1	1.419	0.3619	1.67	1.569	1.572	1.979	-0.67	-0.7906	0
309	1	0.98	0.5931	1.311	1.651	2.143	1.591	1.061	0.000625	1.311
310	1	0.07781	-0.009062	0.3891	2.048	2.361	2.218	0.009062	0.03844	0.4391
311	1	0.5988	0.001875	0.24	1.619	1.762	1.339	0.42	0.9194	0.39
312	1	0.1688	0.1619	0.25	0.8094	1.662	1.139	0.55	0.2794	0.47
313	1	0.5088	0.03188	0.34	1.759	1.642	1.399	1.77	0.5694	0.71
314	1	-2.26E-09	0.3131	0.06125	0.4306	1.593	1.031	0.1812	0.1606	0.3312
315	1	0.06	0.4831	0.2812	1.141	2.163	1.141	0.5012	0.000625	0.4512
316	1	1.614	0.7872	1.045	1.285	-0.3928	1.325	1.095	0.4647	-0.5947
317	1	0.7788	0.1719	-0.46	-0.000625	-1.748	-1.441	0.42	0.4194	2.53
318	1	0.6888	0.2819	-0.14	0.1394	-1.418		0.56	0.7394	2.2
319	1	0.85	0.7931	0.6512	0.4206	-1.917	0.000625	0.4612	0.9606	1.661
320	1	3.118	3.121	3.479	2.568	0.09094	-1.842	0.3191		2.079
321	1	1.049	0.4019	1.4	0.4394	-0.3881	0.1594	0.78	0.2894	0
322	1	0.6788	0.7819	0.89	2.679	0.9819	1.929	1.01	0.6894	-0.87
323	1	0.8088	0.8519	1.17	1.889	0.6619	1.589	0.49	0.4994	-1.19
324	1	0.8769	0	1.218	2.007	2.68	1.927	0.1281	0.4075	-0.6819
325	1	0.9369	0	1.468	2.007	1.48	1.747	0.02812	0.5575	-0.3519
326	1	1.214	0.6169	1.225	2.044	2.187	2.054		0.3744	0.025
327	1	4.019	2.392	3.67	2.909	1.162	1.369	1.28	0.8094	-0.02
328	1	3.629	2.333	3.361	1.61	0.5825	1.12	0.8206	0.32	-0.3394
329	1	4.159	2.412	3.57	2.779	0.9219	1.339	1.5	0.7894	0
330	1	4.109	2.762	3.66	2.939	1.082	1.349	1.29	0.7694	0
331	1	0.8028	0.2259	0.7041	0.3734		-0.9166		0.3534	1.374
332	1	2.364		-0.465	1.314	1.447				0.885

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
333	1	0.5188	-0.8281	-0.41	0.5694	0.06188	0.9694	1.08	0.6794	0.75
334	1	1.409	0.3119	1.47	0.1994	0.6919	0.9994	0.23	-0.7506	-0.09
335	1	1.653	0.7259	1.514	1.903	0.2559	1.763	1.734	0.6934	-1.826
336	1	0.9669	0.57	1.768	0.6975	-2.79E-10	1.697	1.688	1.257	-4.352
337	1	0.2588	0.3519	1.19	1.259	0.7219	0.5394			-1.87
338	1	0.6128	-0.4841	0.4841	1.663	0.5259	0.7234	1.644	1.163	-1.196
339	1	-0.2106	-0.5075	-0.2894	0.97	1.823	1.5	1.241	2.01	0.2106
340	1	0.7528	-0.5541	0.1041	0.3234	-0.1041	-0.1766	1.444	2.193	0.2641
341	1	0.73	0.2031	0.5512	1.481	0.7931	1.441	1.051	0.000625	1.141
342	1	1.049	-0.9081	-2.91E-09	1.059	1.222	1.019	1.81	1.349	0.61
343	1	0.5812	-0.07562	0.8625	0.8719	0.2744	1.042	0.5925	0.3619	0.3025
344	1	0.6712	-0.3956	0.7525	0.8419	0.02438	0.9719	0.8425	0.6319	0.3025
345	1	0.4469	0	0.8981	2.147	1.11	1.407	0.8781	-1.363	-7.302
346	1	0.6869	0	1.358	2.167	1.35	1.787	1.158	-1.063	
347	1	0.83	0.4331	0.9812	1.751	0.2431	1.011	1.161	0.000625	-4.399
348	1	1.438	0.5816	1.53	0.5391	0.1816	-0.1809	-1.79	2.989	-1.19
349	1	1.399	0.3725	1.201	0.37	0.1925	-0.07	1.301	2.66	-1.499
350	1	0.9994	0.7025	0.8506	1.17	-0.0175	-1.31E-09	0.8106	1.51	0.2906
351	1	0.9769	1.42	1.158	1.427	-2.79E-10	0.7175	2.378	2.047	1.778
352	1	0.09844	-0.5784	-0.7303	1.029	-0.09844	0.5291	0.5597	0.3891	-0.8703
353	1	0.16	0.8531	0.4712	1.201	-0.2169	0.000625	0.8412	-0.8394	0.6913
354	1	1.499	0.2519	1.34	1.869	4.162	4.419	0	-1.371	-2.88
355	1	1.659	0.8519	1.4	1.519	-0.4881	1.339	0	0.3194	-0.88
356	1	1.518	0.02094	0.2891	0.6584	0.1209	0.1184	-0.08094	0.4784	-0.8909
357	1	1.323	0.04594	0.2641	0.6034	-0.1841		0.1041	0.8834	-0.7759
358	1	0.01438	-0.7025	-0.3044	-0.015	-0.0375	1.075	2.166	-2.345	0.3756
359	1	-2.26E-09	-0.6969	-0.3688	0.1406	0.1431	1.011	1.891	1.891	0.1312
360	1	1.769	0.4425	0.8006	-0.47	-1.087	0.31	1.121	1.36	-0.5794
361	1	2.147	1.48	0.4481	1.587	-2.79E-10	-0.5725	0.7481	-0.5525	1.268
362	1	1.987	0	1.428	1.797	-0.79	-0.6825	1.138	0.6675	0.6781
363	1	0.2188	0.01188	0.66	1.619	0.4519	2.589	1.87	2.389	-1.27
364	1	0.1488		1.47	1.829	1.952	3.219	2.14	2.509	-2.02
365	1	1.109	1.072	2.05	1.119	0.1719	1.909	3.71	4.319	-0.66
366	1	0.9288	1.022	1.25	1.549	2.582	2.059	2.43	3.369	0
367	1	0.3769	0	1.758	1.487	1.3	2.167	-0.5319	-0.0525	0.03812
368	1	0.4488	-0.3881	-2.91E-09	0.5394	0.5719	0.1594	-0.3	0.2594	1.69
369	1	3.869	2.142	3.3	3.779	0.7319	2.239		2.009	-2.45

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
370	1	3.819	2.132	3	3.629	0.2219	1.579		1.599	
371	1	0.1269	-0.23	-0.04188	0.0175	-2.79E-10	0.0975	1.468	1.407	0.6681
372	1	-0.08625	-0.3431	0.075	1.424	1.637	0.3644	1.695	1.724	1.905
373	1	-0.5772	-0.2841	-0.9959	0.8534	0.04594	1.423	3.184	3.383	0.4541
374	1	2.264	1.967	1.885	3.004	0.8669	1.344	3.905	2.454	-0.035
375	1	2.179	1.422	1.68	0.9994	-0.2081	-0.2806	1.88	3.419	1
376	1	1.38	1.433	2.131	3.011		1.621		0.000625	0.3113
377	1	1.529	2.582	2.14	0.2094	-2.138	-0.9006	2.43	0.9394	2.4
378	1	2.389	1.932	1.78	2.069	-2.428	-3.171	0.54	1.149	1.44
379	1	2.699	2.432	1.94	0.5594	-1.608	-1.581		0.8794	0.64
380	1	2.109	1.262	1.28	1.889	-0.01812	-0.2606	3.04	2.439	0.16
381	1	0.7328	0.1059	-0.1059	1.153	-1.294	0.1634	1.494	1.863	0.2841
382	1	1.389	0.6019	1.4	1.239	1.622	1.099	0.67	0.09938	-0.9
383	1	0.8988	0.3419	0.32	1.009	0.7919	1.619	-0.85	-1.431	1.32
384	1	0.98	0.6631	1.151	1.891	0.04313	0.000625	1.591	1.451	-0.1287
385	1	1.28	1.183	1.591	1.971	-0.1069	0.000625	2.361	1.701	0.1413
386	1	2.101	1.204	1.942	3.262	2.214	1.882		3.652	-1.688
387	1	0.2012	1.884	1.832	1.482	0.9044	2.012	0.8425	0.02187	-2.698
388	1	0.5788	0.5619	1.35	1.679	1.522	0.5194		-3.161	-4.45
389	1	1.204	1.547	0.995	1.534	0.6269	0.8344	1.875	-0.2856	-2.375
390	1	1.177	0	0.2581	0.6975	-6.25E-17	0.0575		1.957	-0.4519
391	1	0.4688	-0.3481	0.64	0.8994	0.2519	0.4994	0.52	1.219	1.15
392	1	-0.4466	-0.3334	-0.3953	0.8341	0.6766	0.4941	-0.8053	0.3341	2.245
393	1	0.3569	-2.79E-10	-0.2719	1.047	-2.79E-10	-0.4825	1.788	0.6475	1.048
394	1	0.1588	-0.6681	-0.19	0.5194	-0.3481	-1.021	1.55	1.499	-0.04
395	1	0.3688	-0.7981	-0.43	0.1794	-0.4181	0.5194	0	0.06938	0.12
396	1	0.9169	0.49	0.1381	-0.0425	-2.79E-10	0.5175			0.8881
397	1	-2.26E-09	-0.4069	-0.03875	0.7706	1.803	0.6106	0.7512	0.8506	1.161
398	1	1.239	0.3719	0.86	1.039	0.6019	1.349		-0.5106	0.26
399	1	0.1088	-0.1281	0.18	0.5194	1.102	0.7094	-0.55	-1.271	0
400	1	1.829	1.672	1.62	2.359			-1.49	-1.481	
401	1	3.468	3.581	2.869	2.418	0.1209	2.668			
402	1	4.261	4.624	3.352	2.952	1.304	3.412		-3.488	-1.078
403	1	1.799	0.8919	2.2	1.779	1.772	1.919			0
404	1	1.941	1.154	2.222	1.902	1.444	2.402		-2.118	-3.388
405	1	1.699	2.732	3.04	0.8994		1.389	0.49	-0.6206	
406	1	2.689	1.362	1.91	3.569		1.599	-2.7	-3.721	0.23

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
407	1	2.719	1.032	0.85	1.499	0.6819	-0.1206	-0.74	-1.471	0.23
408	1	1.729	1.012	2.72	3.309	1.522	3.349	-0.62	-0.7906	-1.22
409	1	1.114	1.257	1.855	2.504	2.627	3.134	-0.545	0.9444	-0.695
410	1	1.079	1.062	1.73	1.129	0.2919	1.329		0.3694	-0.64
411	1	1.48	2.043	3.461	3.241	5.383	4.801	2.581	0.000625	-2.119
412	1	2.289	1.572	2.39	2.599	1.892	2.249	-0.21	-1.701	-2.38
413	1	2.175	1.598	2.956	3.186	2.798	3.366			-3.244
414	1	2.279	1.023	2.811	2.26	-0.3975	1.84		-0.01	-1.089
415	1	2.284		4.345	1.794	3.817	4.414			-2.695
416	1	2.749	3.152	3.33	2.439	1.032	2.009	2.77	-0.01062	-0.51
417	1	2.829	2.002	2.98	1.909	0.5719	1.479	-0.79	-0.7806	1.77
418	1	1.599	1.042	1.64	1.819	1.412	1.939		-0.8306	1.58
419	1	2.954	2.687	1.915	1.784	2.237	2.544	-2.125	-2.136	0.095
420	1	3.059	1.952	1.65	4.339	1.252	5.919	0.02	-0.3806	-0.98
421	1	2.7	2.183	2.501	3.461	2.293	2.671	1.041	0.000625	-0.1388
422	1	2.969	3.762	3.7	3.489	3.882	3.189		-0.4506	-1.11
423	1	3.249		3.45	4.019	3.322	4.849		-2.071	-1.43
424	1	4.349	3.932	4.33	4.669	1.982	2.079	0	0.1294	0.29
425	1	6.374	7.007	7.615	7.604	4.627	5.134	-0.175	0.2244	0.175
426	1	4.281	3.964	5.342	6.762	6.164	6.492			1.442
427	1	4.339	4.412	5.29	5.539	6.812	6.309		-1.781	-0.21
428	1	6.744	7.177	8.015		-7.437	8.244	-1.695	-3.746	-1.695
429	1	5.899	5.992	6.95			7.929			
430	1	5.38	5.683	6.561	6.291	6.433	7.181		-0.4494	-0.4188
431	1	3.6	4.283	3.831	3.911	4.163	4.851	-1.849	-1.489	
432	1	4.051	3.884	4.342	4.352	4.374	5.032	-1.678	-0.7481	-1.868
433	1	4.204	4.257	5.305	5.824	2.177	5.434	-2.225	-0.7556	-0.195
434	1	3.189	4.402	3.44	5.149	5.882	5.519	-1.17	-0.6906	1.47
435	1	4.299	4.252	4.87	5.449	3.172	4.499	0.29	-0.7306	-0.29
436	1	5.264	4.827	5.815	5.554	3.977	4.614	0.345	-0.7856	-0.595
437	1	4.684	4.307	4.565	5.594	3.997	4.804	-0.135	-0.9656	-1.015
438	1	6.069	5.962	6.68	6.499	3.382	4.639	-0.07	-0.3906	0.83
439	1	5.121	4.994	5.522	5.492	4.234	5.482	-0.3875	0.09187	-0.0375
440	1	3.201	2.444	2.862	3.702	3.264	3.572			
441	1	3.379	2.352		2.239	2.492	3.509		-0.3106	
442	1	3.171	4.404	3.972	1.882	-1.256	1.972	0.7025	0.1719	-1.048
443	1	3.134		3.235	2.744	-1.163	1.914			0.895

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Table 2

	GWEIGHT	HMEC-C	HMEC+INFA	HMEC-C_CONFL2	184AA	184A1-LATE	184B5	HMVEC	HUVEC	MDA-MB-321
		ARRY2X	ARRY4X	ARRY3X	ARRY5X	ARRY1X	ARRY0X	ARRY7X	ARRY6X	ARRY11X
444	1	1.599	1.272	1.83	2.249	0.8119	2.029	0.61	0.4394	-1.64
445	1	2.899	2.192	2.78	2.799	1.562	1.559	0.88	0.1694	-2.18
446	1	0.9887	1.372	3.19	3.979	3.702	5.479		-1.261	-0.36
447	1	2.931	2.184	2.382	2.352	2.164	2.122	-1.248	-0.4081	
448	1	3.469	3.272	3.76	3.789	1.302	1.659	0.47	-0.1106	2.1
449	1	2.749	2.732	3.2	2.919	0.9419	1.289	0.06	-0.3406	1.6
450	1	3.189	3.512	5.39	4.689	3.422		-1.28	-1.711	5.07
451	1	2.151	0.9544	1.332	2.232	2.644	4.042	-0.3775	-0.2981	-1.098
452	1	2.88		1.781	2.371	2.953	4.781	-0.2088	-0.2194	0.3513
453	1	3.939	3.222	5.81	4.539	4.322	4.989	0.28	-2.601	-1.14
454	1	2.544	1.827	3.425	1.494					
455	1	3.149	3.822	3.14	1.719	-0.2181	2.099			-0.86
456	1	2.334	2.608	4.116	1.505	1.428	-0.175	-1.404	-0.225	-2.464
457	1	3.359	3.422	3.46	2.379	-0.2581	-0.8306	0.7	-0.03062	2.22
458	1	4.005		3.716	3.976	0.7181	0.3556	0.1662	-1.134	
459	1	3.96	3.133	3.081	4.451	-0.1869	0.8106	0.2912	0.000625	-0.6788
460	1	2.759	2.082	3.19	2.299	2.382	2.929	0	-1.381	-0.24
461	1	2.379	1.562	2.17	2.629	1.392	2.199			-0.19
462	1	3.739	1.812	2.64	1.689	0.1419	-1.031		-4.591	0.93
463	1	1.699	1.432	2.06	1.859	0.1219	1.759	0.94	0.7394	-0.44
464	1	2.449	1.662	2.39	2.749	1.292	1.589	0	0.03938	-1.12
465	1	1.569	2.132	2.28	0.1294	-0.06812	2.129	0.67	-1.801	-0.6
466	1	1.509		1.49	1.309		2.689			
467	1	1.759	1.502	1.58	1.329	0.1419	0.6894	2.21	1.409	0.59
468	1	0.8269	0	-0.3619	1.377	0.1	0.4075		-2.093	0.7681
469	1	1.394	0.7375	0.9456	0.005		-0.005	-0.8444	-1.695	1.656
470	1	0.8444	0.8875	0.3856	0.335	-0.9025	0.215	-0.2144	-1.605	1.806
471	1	1.894	1.427	1.095	1.295	0.02719	-0.1153			3.745
472	1	2.339	2.602	2.03	2.049	-0.9481	-0.9806	0	-0.01062	2.32
473	1	1.551	1.504	1.392	1.272	-1.516	-1.798		-5.188	3.342
474	1	0.6438		-0.375	0.1344	-0.5031	-0.5656	-0.135	0.4144	3.685
475	1	0.03875	1.372	1.06					0.7894	
476	1	0.1788	0.2719	0.85	1.909	1.172	2.439	0	-0.5006	-0.21
477	1	2.407	1.8	1.928	3.297	-2.79E-10	0.4275	1.468		-2.232
478	1	1.741	1.394	1.432	1.402	-0.1256	-0.06813		0.6219	-3.238
479	1	1.959	1.262	1.87	0.6494	0.4719	-0.8306	0.33	1.149	
480	1	1.129	0.5619	0.03	1.099	0.7319	0.5994	-0.11	0.03938	2.15

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
481	1	0.6812	-0.02562	1.002	0.8819	1.034	1.452	-0.3375	-0.1681	0.1525
482	1	-2.26E-09	0.06313	0.3212	-0.5094	-1.217	-0.03938	1.271	0.6006	0.9212
483	1	0.5088	-0.6281	0.2	-0.09062	-1.688	0.9394	2.47	2.129	0.77
484	1	-0.3012	0.7919	-2.91E-09	0.9894	0.6719	1.209	-0.28	-0.1406	1.32
485	1	-1.08	0.1731	0.4812	-0.4594	-0.9469	0.6806	0.4312	0.000625	1.621
486	1	-2.26E-09	0.9831	0.3712	-0.8794	-0.2669	-0.7394	0.8912	1.171	2.131
487	1	0.3		1.291	0.9506	-0.04687	0.000625	2.201	0.5706	1.811
488	1	1.753	0.07594	0.7941	0.2634	-0.1341	-0.1966	2.114	2.323	-0.2159
489	1	2.027	0	0.6481	0.2275	-0.79	-0.2425	1.898	2.267	-0.1819
490	1	0.5688	0.4819	0.64	0.1994	-1.228	-1.291	0.34	1.299	-0.71
491	1	1.519	0.1019	0.03	-0.1306		-1.941	0.42	0.7094	2.04
492	1	1.899	-0.1081	0.69	-0.000625	-1.748	-0.9306			2.38
493	1	0.6588	-0.2581	0.44	0.8394	-1.388	-0.000625	0.58	0.6594	0.16
494	1	0.3088	0.3919	0.37	0.9494	0.8119	-0.3606	-0.85	0.2294	0.33
495	1	1.32	0.3031	0.4112	0.2706	0.4631		-0.03875	0.1006	2.201
496	1	0.14	-0.05687	0.5412	0.2006	0.7731	1.361		0.000625	2.001
497	1	0.57	0.3731	0.9012	0.3906	0.1831	1.401	-5.459	0.000625	2.591
498	1	0.9288	-0.03812	1.08	1.379	0.4119	0.5994	0.01	-0.2706	1.41
499	1	-0.1022	1.141	1.129	0.7784	0.0009375	0.6584	-1.841	-1.382	0.2791
500	1	0.9012	0.9944	1.822	0.2619	-0.1556	1.202	-1.318	-2.148	0.5125
501	1	0.8788	1.012	2.28	-0.000625		1.139	0.28	-0.6406	0.95
502	1	1.007	0	0.5181	0.2075	-3.72	0.3675	-0.2519	1.167	-3.512
503	1	1.509	0.2325	0.8306	0.57	-3.017	0.17	-0.3194	1.21	-0.1694
504	1	0.2887	-0.5781	0.1	0.08937	-1.528	-0.8306	0.43	0.4694	-0.09
505	1	0.5228	0.005938	-0.01594	-0.005563	-0.9641	-0.04656	0.6941	0.4834	
506	1	-0.06		0.1712	0.5506	-0.8769	0.08062		0.000625	-1.999
507	1	0.03875	-0.5481	0.42	-0.000625	0.2019	-0.9206	1.48	2.149	-1.8
508	1	-0.3112	0.2419	0.92	-1.111	-2.628		-0.08		
509	1	0.05875	-0.1881	0.11	-0.3306	-1.028	0.6594	1.23	1.489	-3.29
510	1	0.9969	0	0.1881	-0.6625		0.9375	0.5581	2.167	-1.502
511	1	0.1578	0.06094	-0.4009	-0.06156	-1.129				
512	1	0.3369	0.05	1.058	1.057	-2.79E-10	2.117	-0.9719	0.6575	
513	1	0.9938	0.9969	1.955	1.744	-0.5231	2.844	0.025	1.424	-1.025
514	1	0.2988	0.1219	0.5	-0.4806	1.952	0.6394	0.46	-0.2506	-0.67
515	1	-0.05875	-0.7656	0.5025	0.9719	2.334	2.202	2.142	0.9519	-0.5575
516	1	0.09687	0	0.01812	0.8575	0.52	0.9475	-0.9619	-1.263	-1.012
517	1	0.3387		0.32	-0.7206	0.4819	0.3794		-0.4906	-0.61

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
518	1	1.845	1.118	2.096	1.116	-0.5619	0.1456	-0.2738	0.6556	-4.044
519	1	0.6887	-0.1381	1.38	2.429	0.9819	-0.7906	-0.04	-0.6406	0.27
520	1	1.305	-0.7819	1.026	1.246	2.758	0.7856	-1.124	-0.7744	-0.2737
521	1	0.1212	-0.2756	-0.2975	1.182	0.07438	-0.5081	-0.9475	-1.658	-0.0475
522	1	0.7078	0.02094	0.09906	0.2184		-0.7216	-0.02094	0.1184	-0.5109
523	1	0.4412	0.5344	0.7925	0.4519	1.624	1.952	-1.168	-0.2281	-2.898
524	1	-0.8612	0.2119	0.12	-0.2106		0.3194		-0.3506	0.68
525	1	-0.3112	0.04188		0.5494		0.1294			-0.11
526	1	-0.06313	0	-0.2619	0.0975	4.86E-17	0.6275	0.1481	-0.1225	0.7681
527	1	-0.2412		0.36	-0.04062		0.1294	-0.95	0.4494	
528	1	-2.26E-09	0.1431	0.4512	0.9806	-1.197	4.151	2.811	0.7106	2.101
529	1	2.787	1.41	0.8081	2.147	-2.79E-10	-1.093	1.088	1.207	1.768
530	1	0.2688	0.7319	0.72	-1.151	-0.9781	-1.011	0.56	-0.8106	2.39
531	1	0.9087	0.4719	0.62	1.159		1.189		-1.661	0.22
532	1	0.8088	0.6019	0.78	-0.04062	0.2719	0.2594	-0.47	-1.001	1.61
533	1	-0.1444	-0.3213	0.2669	0.6462	0.5987	1.106	-0.4931	-3.524	-0.4431
534	1	-0.8062	-0.6431	-0.065	-0.2456	0.1469	0.1444		-1.686	0.135
535	1	0.1787	0.9419	0.5	-0.1406					-0.57
536	1	-0.07313	0.11	0.2281	-1.133	-2.79E-10	0.7175	-1.552	-1.123	-0.6419
537	1	-0.2312	1.072	0.1	-0.04062	-0.02812	0.1694	1.04	-0.6706	-0.79
538	1	-0.6213	-0.4081	-0.43	-2.371	1.112	2.029	-1.91		-0.76
539	1	0.8138	1.357	1.025		-0.5131				0.745
540	1	1.639	1.202	1.96	-0.000625		-1.161		-2.061	
541	1	1.361	0.5444	0.3325	-0.3281	-2.346	-1.438	0.1025	0.08187	-0.4775
542	1	0.9688	0.04188	0.64	-1.361	-1.468	-0.9706			-0.95
543	1	1.623		0.6047	1.684	0.06656	-0.06594			0.6247
544	1	1.399	0.1119	0.07	2.339			-0.8	-0.5606	-1.17
545	1	1.42	-0.1969	0.1812	0.9406	0.07313	0.000625	-1.949	-0.7494	-1.489
546	1	1.099	-0.1881	0.25	0.9294	0.7219	-1.321	0.63	0.3494	-0.39
547	1	-1.341	-0.5381	-1.15	1.029	0.5319	1.429	-1.41		-0.18
548	1	0.2288	-0.4581	0.96	1.179	1.222	1.119		-0.6806	0
549	1	-2.26E-09	0.5031	-0.3088	-0.6894	0.1331	-1.179		-1.959	-0.5988
550	1	-0.4812	0.2019	-2.91E-09	1.219	-0.6481	-1.041	-3.05	-0.1906	
551	1	0.1294	-0.1675	0.6606	-0.65	2.073	-0.06		-2.4	-0.3394
552	1	-2.26E-09	-0.4469	0.6112	-0.4594	0.4419	0.1606		-1.689	-0.5288
553	1	-0.5312	-0.6981	-0.62	-0.8106	-0.8275	-0.8406	-2.89	-0.3506	0.55
554	1	-0.3506			-1.12		-1.67			

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
555	1	1.67	0.3231	0.9312	0.9806	-0.2769	0.000625		-1.909	1.251
556	1	-0.4231			-0.0525	-2.79E-10	-0.9325			0.2081
557	1	1.493	1.336	1.424	1.623	0.1259	-3.247		-4.297	1.434
558	1	0.6588	2.402	-0.43	-0.000625	0.8819	-1.811		-3.161	-2.28
559	1	0.05875	-0.07812	-0.31	0.5094	0.6219	-0.1906	-0.47	-0.7906	-0.13
560	1	-0.2012	0.6319	0.02	-0.4606	0.8419	-0.2706	1.06	-0.4606	-0.9
561	1	-1.166	1.377	-0.795		0.8069			-1.666	-0.865
562	1	-0.4012	0.3319	1.79	-1.161	0.3219	-1.731	-0.72	-1.951	1.15
563	1	-2.26E-09	1.563	-0.4588	-0.7394	-1.637	-0.8894		-1.989	-0.6488
564	1	-0.06125		-0.15			-0.9506	-1		0
565	1	-0.3256	2.968	1.066	-1.095	0.8875	0.265		-2.465	-0.2644
566	1	-0.4013		-0.15	-1.891		-0.9506		-1.681	-0.1
567	1	-0.07063	1.893	-0.8394	0.07	0.8825	-1.38	-0.6894	-1.31	-0.2094
568	1	1.078	1.091	0.4891	0.9184	-0.1291	0.1384		-2.012	-1.511
569	1	0.3888	2.002	-1.14	-1.561	-0.4381	-0.9406		-2.091	-0.62
570	1	-1.231	0.2319	0.05	-0.6006	0.4419	-0.2406			0.2
571	1	-0.2456	0.0575	0.3856	-1.355	0.8475	-0.045	-0.7444	-1.445	-0.2244
572	1	0.355	0.2581	-0.07375	-1.544	0.2581	-0.5844		-2.244	0.04625
573	1	-0.1813			-1.211	0.3519	-1.491			1.12
574	1	-0.4812		-2.91E-09		0.8319	-0.1606			
575	1	-0.5062		0.935	-1.536	0.4469	-1.716	0.135	-2.066	-0.445
576	1	0.2388	0.1419	-0.16		-0.7019	-0.4606	-0.51		-0.19
577	1	-2.26E-09	0.6131	0.5412	-0.3994	0.3031	-0.4794	-2.109	-0.9894	0.8412
578	1	-2.26E-09	0.8331	-0.5088	-2.029	0.2731	-0.3094	-1.939	-1.819	2.911
579	1	-2.26E-09	0.6731	0.07125	-1.129	0.9531	-0.3594	-1.119	-1.069	-0.6588
580	1	-0.1612	0.4119	0.46	-0.8506	0.6419	3.759	-0.48	-0.6406	6.86E-09
581	1	0.1138	1.387	-0.455	-0.7156	-0.1531	-0.2556	-0.625		-0.045
582	1	0.4338	1.547	-0.455	-1.396		-1.256			
583	1	0.04687	-0.38	-0.6219	-1.563	-2.79E-10	-0.8425	-2.472	-2.353	-0.1519
584	1	0.3288	-0.05812	-0.56	-1.501	0.2819	-0.3606			-0.41
585	1	-0.2713	0.4919	0.14	-0.6306	0.6819	3.429	-0.98	-1.361	-1.16
586	1	0.08687	-0.3	-0.4219	-0.4525	-2.79E-10	-0.0525	-0.2319	-0.3925	0.3281
587	1	-0.1166	0.1166	0.4247	1.724	0.9666	-0.7259			-1.625
588	1	0.1937	1.277	-0.305	-1.416	-0.5331		-0.745	-0.7456	0.715
589	1	0.5938	1.327	0.025	-0.6556	-0.6731	-1.096	-2.145	-0.4456	-0.825
590	1	0.03781	0.03094	0.4691	0.07844		0.3284		-0.2116	-0.1209
591	1	1.744	0.2769	0.035	0.8544	0.4269	-1.616	-3.985		-2.185

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
592	1	0.045	0.3681	-0.1338	1.296	-0.1119	-0.04438		0.1156	-1.964
593	1	-0.1056	0.9975	0.8056	-1.235	0.2675			-2.415	0.7556
594	1	-0.1156	0.2175	0.6856	0.745	-0.7025	3.105		-1.685	-1.094
595	1	0.3237	1.417	-0.285	-1.026	-0.7231		1.585	-0.2356	
596	1	1.659	0.1319	1.08	-0.4806	-3.958	-0.6306		-1.411	0.67
597	1	0.8588	-0.1081	0.54	0.1594	-0.4181	-0.3906	0.02	-1.321	0.14
598	1	-0.43	-0.8669	-0.5188	0.07062	-1.187	-0.6894	-0.3688	-0.8394	0.5912
599	1	-0.2312	0.1419	1.46	-2.141	-0.7381	-1.581	-0.83	-1.511	0.17
600	1	0.3788	-1.208	2.29	-1.071	-0.3481	-0.9306	-0.24	-0.8606	0.24
601	1	1.009	0.4825	1.251	0.55	0.3825	-0.17	0.7806	-1.98	-1.359
602	1	-0.9063	0.3669	1.185	-1.686			1.145		-0.175
603	1	0.21	-1.277	-0.1988	-1.559	-0.5769	-0.9994			-1.049
604	1	-0.8209	0.01219	-1.53	-2.13	1.512	-0.7903	1.55	-0.2003	-0.6697
605	1	0.1288	0.5019	-0.61	-1.141	-0.7881	-0.7206	0	0.2194	-0.15
606	1	0.3138	1.427	-0.845	-0.9356	-0.8031	-1.646		-1.576	-0.115
607	1	0.3128	0.7059	-0.3459	-0.9866	-0.03406	0.1234		-1.117	-0.7759
608	1	1.51	1.023	0.1012	-0.5194	-0.5369	0.000625	-1.169	-0.8294	0.6413
609	1	0.8888	-1.078	-1	-1.941	-1.958				
610	1	2.115		-1.874	-0.8144	-0.2519				
611	1	1.004	0.6369	-0.505	-1.026	-1.043	-0.8856	-1.935	-1.816	-0.355
612	1	0.5712	-0.01562	-0.5175	-1.458	-1.476		-1.368	-1.248	
613	1	0.3712	0.9844	-0.9375						-0.3675
614	1	0.1888	0.7019	-0.22	-0.5806		-0.02063	-3.942	-0.9506	-0.07
615	1	0.7469	0	0.6081	1.517		1.317			-1.362
616	1	-0.8222	-1.269	-0.9809	-0.4016	0.03094			0.4784	0.4291
617	1	0.2678	0.08094	-0.1409	0.8684	-0.4791	0.7294	-1.081	-0.4706	0.3791
618	1	-0.1812	-0.3481	0.31	0.3794	0.5519	0.7994	-0.08		-0.05
619	1	0.6488	-0.5281	1.09	1.529	-1.378		0.18	1.479	1.221
620	1	-0.6806	-1.347	-0.9094	0.76	1.993	0.58	-0.11	-0.07	0.13
621	1	0.8288	0.1719	0.88	0.9594	-0.1481	0.7294	-1.13	-0.06063	0.7
622	1	1.319		2.14	0.4094	0.1719	-0.3406		-0.5506	0.26
623	1	0.2188	0.05188	-0.09	0.3794	-0.3281	0.3294	1.281	-0.4506	0.3912
624	1	-0.56	-0.9369	0.9712	-1.119	-1.137			1.401	0.1006
625	1	-0.1106		-0.3494	-0.05		-0.74	1.77	0.05	
626	1	-1.531		0.21	-1.871		0.6494			
627	1	-0.08063	-1.557	0.3706	0.15	-0.9975		-0.5394	0.24	
628	1	-0.4712	-0.4481	0.13	-0.4306	0.4319	-0.4706	0.26	0.5594	6.86E-09

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
629	1			-0.2	0.5794	0.5619	0.3094		0.07937	0
630	1	-0.1812	1.202	-0.38	0.3194	0.1519	-1.121	-1.87	0.6694	-1.29
631	1	0.8988	-0.07812	-2.91E-09	0.5294	-0.09812	0.2494	0.33	1.899	-2.36
632	1	-0.5962	-0.08312	0.615	-0.5056		0.7344			0.165
633	1	0.3338	0.8069	-0.005	-0.6856	0.2869	-0.3856		0.2044	
634	1	-0.1412	0.6119	0.69	-0.3406	0.07188		1.51	-0.03063	0
635	1	-0.4762		1.315	-0.5856		-1.986			-0.215
636	1	-0.3	1.013	0.08125	-0.9994		0.000625		0.4306	0.4813
637	1	-0.4412	1.012	-0.27	-0.03062	0.9119	0.1594	1.11	-1.321	
638	1	-1.081		-0.12	0.6494	-0.02812	0.6494			
639	1	-0.2706	0.6625	1.491	-0.42		0.04		-1.21	-1.109
640	1	-2.26E-09		2.241	-0.2094	1.113	-0.2694	0.6012	-0.8494	-0.1012
641	1	0.4788	0.6919	1.07	-0.000625		1.299	-0.73	0.03937	-1.59
642	1	-0.1413	0.2719	1.82	0.5294				0.1894	-0.07
643	1	-0.05125			0.6794				-0.3206	0.79
644	1	0.6244		-0.5144	-1.215	-0.3425			-0.215	
645	1	-0.2812	-0.1381	-0.04	-0.5106	0.2619	-0.02063	-0.59	-0.06063	0.5
646	1	-2.26E-09	1.113	-0.4788	-0.3394		0.5206	0.4712	-1.409	-0.6288
647	1	-1.101	0.1919	-0.14	-1.491			-1.27	-2.091	-0.24
648	1	-0.4812		0.08	-0.6006	0.7219	-0.06062	0.5	-1.061	-0.15
649	1	-0.525	0.04813	-0.00375	-0.1244	0.3281		-0.4638	-0.09438	0.5162
650	1	-1.326	0.1869	-0.075		0.4169			0.065	0.065
651	1	0.2588	0.1719	0.33	0.009375	0.02188	-0.07062	0.38	0.04938	-0.68
652	1	-2.26E-09	0.6031	1.621	-0.4094	-0.3069	-1.619	2.441	-0.4794	-1.039
653	1	0.2688	0.4519	-2.91E-09	-0.6406	-0.1181	-0.1206	-0.58	-0.2406	0.17
654	1	-0.1162	1.337	-0.105	0.3944	-0.4031			-0.6556	0.125
655	1	-0.00875	-0.2256	-0.3475	-0.2881	0.02438	-0.09813	-0.1975	-1.128	0.1325
656	1	0.6088	1.422	0.92	1.419	1.402	2.289	1.251	-0.2906	-0.91
657	1	-0.57	-0.7369	-0.6588	-0.3494	1.513	0.3606	1.25	1.191	1.671
658	1	-0.04125	0.2819	-0.5	-0.7106	1.082	0.1694		0.9894	0.13
659	1	-1.041		-1.52	0.8494	1.592	1.349		0.7994	
660	1	-2.26E-09	-1.427	0.03125	2.691	2.813	2.261	3.651	1.141	-0.3388
661	1	-0.2288	-1.136	0.4725	3.392	5.394	4.352	6.742	2.772	-2.118
662	1	-0.2012	-0.5581	-1.15	0.1494			1.96	-0.03062	
663	1	0.2188	-0.7681	-0.15	0.4894	0.9219	0.5994	3.53	0.1494	
664	1	-1.371	-0.9181	1.58	-0.2906	1.102	1.509			1.09
665	1	-0.5012	0.7719	-0.79	1.489	-1.278	-1.391	0.74	-0.3706	2.49

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
666	1	-0.2631	0	-0.4019	-0.1025		-0.2756		-0.9456	0.6981
667	1	0.1837	-0.4931	-0.075	0.7644	0.2469	-0.009375			
668	1	-2.26E-09	-0.8669	-0.08875	0.2006	0.5631		-0.995		0.2112
669	1	-0.8562	0.3469	-1.085					0.1144	0
670	1	-0.6212	0.5919	-1.81	-1.971					
671	1	-0.1006	1.003	-0.3394		0.4425	-0.49		-0.88	
672	1	0.3069		-1.042	-1.723	-2.79E-10	-1.583		-0.7725	0.1081
673	1	-0.1622	0.05094	0.1591	-0.8316	0.6709	-0.9216	-0.5009	-0.5716	0.3491
674	1	0.6138	0.6669		0.1744	1.707			-1.056	
675	1	0.6788	0.6619	0.2	-0.000625		-0.3706			0.05
676	1	-0.9731	0	1.288	-1.423	-0.3	-1.383	-0.1519	4.877	-0.4819
677	1	-0.09125	-0.2581	-0.44	-0.3006	0.2619	0.3294	-0.1	2.239	-0.1
678	1	0.1588	-0.1081	1.68						-0.02
679	1	-0.5931	0	-0.5419	-0.0925	2.44				3.218
680	1	-0.4256	-0.7525	-0.2344	-0.305	1.138	0.235			0.4456
681	1	-0.3313	0.2719	0.09	0.1794	-0.1281	2.069	0.68	1.159	-0.76
682	1	-1.621	-0.7881	0.13	-0.5606	0.7919	0.9894	-0.29	-1.061	0.03
683	1	0.5588	0.9819	1.13	-0.2606	-2.158	-1.201	0	0.1194	-0.95
684	1	-0.5762	0.3069	0.335	0.7144	-1.003	-1.226	-1.355	-1.196	-0.095
685	1	0.1288	0.1219	-2.91E-09	0.5794	-1.068	0.5194	-0.42	0.01937	-0.39
686	1	-0.01562	-0.5525	0.09562	0.575	-1.152	0.715	-1.534	-3.475	
687	1	0.09844	-0.09844	0.1997	0.9791	-0.5684	0.5891	-0.5903	-1.751	
688	1	-0.07125	-0.9281	-0.38	0.07938	0.02188	0.6294	0.07	-0.05062	-0.02
689	1	0.7388	0.7019	1.37	1.059	0.2019	1.339	-0.69	-1.311	-0.62
690	1	0.1869	0.62	1.088	0.7475	-2.79E-10	0.7275	-1.492	-1.653	-1.032
691	1		-1.198	0.63	-0.3106				-1.011	0
692	1	-2.26E-09	1.663	-0.5688	-0.2694	-0.07687	-1.949		-2.019	1.481
693	1		0.9519	-2.91E-09	1.869					
694	1	0.5587	0.07187	-0.26	-0.09063	-0.06813	0.3194	-3.7	-1.991	1.74
695	1	0.8037	0.3369	0.355	0.6044		0.3144	-1.875	-1.166	0.305
696	1	-0.1362	0.5769	1.245	0.2844	-0.3531	-0.5356		-1.356	0.025
697	1	0.7569	0	1.258	0.9675		-0.9425	-1.332	-2.353	-1.332
698	1	-0.5812	0.3519	-0.2	-0.5306	0.6419	0.3494	-0.25		-0.32
699	1	-0.5012	0.1419	-2.91E-09	-0.9406	-0.8281	-0.9306		-0.9106	0.09
700	1	-0.1912	0.9619	-0.01		0.07188	-0.7406			-1.03
701	1	-2.26E-09	-0.3869	-0.1588	-0.2094	-1.267	-0.6394	-0.1188	0.3106	0.09125
702	1	0.7787	0.6819	0.35	-2.091	-1.108	-0.9506			0.12

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
703	1	1.238	1.221	0.2991	-0.9616	-0.2991	-1.562	-0.4909	-1.072	0.8491
704	1	0.1987	1.662	-0.47		0.04187			0.2894	-0.61
705	1	-0.09125	1.462	-2.91E-09	0.6594				-0.8006	
706	1	0.2788		0.77	1.209	1.062	-0.3606	-0.47		
707	1	0.2044		-0.4044	0.595	0.8675		-4.774		-1.074
708	1	1.529		0.85	-0.6706	-0.1081	-1.531			0
709	1	-0.4412	0.8619	-0.35	-1.471	0.1019	-1.061		-1.261	1.67
710	1	-2.26E-09	1.363	-0.1688	-0.4494	0.2731			-0.5594	
711	1	0.5944	0.3275	-1.294	-0.655	-1.672			-0.025	0.3156
712	1	0.4112	0.6244	-0.4375	-1.118	0.5244	-0.5581		-0.4881	-0.4375
713	1	0.1587	-1.598	-0.24	0.01937	-0.3781	-0.04063		-0.2006	0.15
714	1	0.6038	1.617	-0.205		-1.903	-0.3256	-0.795	-0.6756	-0.475
715	1	-0.07125	0.5919	-0.65	-0.8806	0.8819				
716	1	0.6369	0.88	-0.4519	-0.3925	-2.79E-10	-0.6225	-0.3019	-0.3525	-0.1519
717	1	-0.6363	0.2669	-0.575	0.1644	1.147	0.2044	1.055	0.2744	-1.165
718	1	0.03938	0.6525	0.07062	-1.87	0.7025	0.7094	1.811	2.76	-0.03938
719	1	-0.2213	-0.3881	-0.56	0.1894	1.432	-1.431		1.669	2.4
720	1	-0.5663	2.587	-1.025	-0.5256		-0.8256			
721	1	-1.036	-0.6131	-0.245	3.284		0.8844	5.445	0.7344	
722	1	-0.4862	1.417	-0.235	-0.2456	0.6469	-0.3756	3.525	2.014	-0.625
723	1	-0.06563	0.9875	-2.524			-2.205			0.06562
724	1	-0.3412	0.01188	-0.68	-0.000625	0.3619	-1.921		-1.961	-0.93
725	1	-2.321						-1.97	1.299	
726	1	0.1388	0.1319	-0.13	-0.3706	0.5919	0.4794	-0.57	-0.4706	-0.77
727	1	0.2087	-1.888	-1.12	0.09937		0.7094			
728	1	-2.26E-09		0.2612	-0.8294	0.7831	0.2806		-1.239	0.06125
729	1	-0.9212		-1.7					0.6494	
730	1	-0.8006		-1.349	-2.49				0.38	
731	1	-0.2112	-0.4881	-0.27	-0.6606	-1.408	-1.031	0.08	1.529	-1.01
732	1	-0.2662	-0.3431	-0.045	-0.05562	-1.263	0.1744			
733	1	0.2688		-0.17	-0.000625				0.9894	-0.52
734	1	2.758	0.7709	0.7391	0.008437	-0.009062	-0.6016			-1.751
735	1	0.2688	0.1919	0.69		1.082	-0.1606	-1.2	-1.311	0
736	1	-0.2712	1.022	0.27	1.319		1.209	-4.13	-1.951	-0.76
737	1	0.7288	0.6019	1.39	0.6794	0.3819	1.569	-1.59	-1.291	-2.05
738	1	0.6128	0.4459	1.224	1.333	0.3659	1.043		-3.177	-0.3659
739	1	-0.2212	-0.01812	1.5	0.7894	0.5719	2.679	-0.38	0.2594	-0.83

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
740	1	-2.586		-2.195	0.9644	1.687	1.284	-3.845	-1.146	-2.525
741	1	0.06875	-1.128	-0.2	0.1594	0.9219	1.299	-2.17	-0.4606	-0.51
742	1	1.499	1.242	0.88	2.539	0.7719	2.699	-2.61	-3.911	-1.22
743	1	-2.081	1.202	1.5	0.7894	0.5219	0.4294	-3.06	-3.281	0.21
744	1	-0.08125	-0.2781	0.11	1.579	0.7619	1.349	-4.31	-1.971	0
745	1	0.3769	-2.78E-17	-0.1119	0.6475	1.87	2.207	-1.792	-3.023	-0.2519
746	1	-0.97		0.1712	0.9606	-0.6469	0.000625	-0.7388	-0.9194	-0.05875
747	1	0.4088	-0.08812	-0.15	0.1894	0.5919	1.599		-0.2106	-0.25
748	1	-0.6312	-0.8881	-2.91E-09	0.1694	1.742	1.659	-0.92	-1.011	-0.77
749	1	-0.1113	-1.058	0.56	1.069	2.192	2.529	-1.599	0.6694	-2
750	1	-0.89	0.6131	-0.5788	1.161	2.163	1.971	-0.88	0.000625	-2.719
751	1	-1.881	-0.2381	-2.91E-09	4.159	4.322	4.129	-1.252	2.339	
752	1	0.1069	0	0.3281	1.177	0.74	1.157	-0.88	-0.8125	-0.5319
753	1	0.3228	0.1959	0.8441	1.893	1.236	2.323	-1.1959	-0.3266	
754	1	0.1	-0.5869	2.831	1.471	0.5131	-0.1694		0.000625	-0.7087
755	1	0.3088		0.41	0.6894	0.5619	0.1994	0.42	-0.06062	
756	1	-0.6688	-0.6156	-0.4375	-1.108					-0.1075
757	1	-0.2662		-0.135	-1.296		-0.7356	0.385		-1.785
758	1	-0.2113	-0.7381	0.47	1.289	-0.2281	-0.6806	-0.15	-0.7606	0.84
759	1	0.04875	0.1719	-2.91E-09		-0.1281	0.2394	-0.12	-1.101	-0.94
760	1	0.1894	0.8925	-0.7194	-0.41	-0.2075	-0.47		-0.57	-1.369
761	1	-0.06125	1.012	0.17	-0.5106	-0.3081	0.04937	-0.2	-0.5606	-0.42
762	1	0.1988	-0.4581	-0.51	-0.4506	-0.4181	-0.7806	-2.2	-0.2006	0.15
763	1	0.05781	0.02094	0.7691	-0.5316	1.031	1.748		-0.9216	-0.3309
764	1	-0.1512	-0.8981	-0.41	-0.05062	0.1219	-1.291	0.13	0.2694	-0.12
765	1	0.4588	-1.748	-1.21	-0.000625		-2.301		0.3994	-0.44
766	1	-0.4756	-0.5025	-0.5344	-0.965	0.2375	-0.495		-0.155	1.806
767	1	-0.1062	-0.4231	-1.345	-0.6656	-1.303	0.2744		-0.2556	-0.085
768	1	0.06875	-0.1681	-0.32	-0.4506	-1.028	-0.1706		-0.5606	-0.39
769	1	0.3538	-0.4031	-1.225	-0.4356	-1.573	-1.706			0.785
770	1	0.9087	0.1919	-0.77	-0.8906	-1.568	-1.091	0.13	0.5194	0.71
771	1	-0.3812	-0.7481	-0.86	-0.000625	-0.7381	-1.121	1.29	1.979	1.58
772	1	-0.01125	-0.2181	0.16	-0.8806	-0.8481	-0.9506	-0.82	0.01937	0.56
773	1	-0.15		-1.509	-0.7894		0.1506			0.6412
774	1	-0.8262	-0.9931	-0.335	-1.226	0.08688	-0.3656	2.285	-0.4956	0.345
775	1	-0.7212	-0.5581	-1.68	-1.121	-1.018	-1.041		0.3394	1.71
776	1	-1.33		-2.349	-0.8594	-1.697	0.000625		0.9806	-0.7387

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
777	1	-1.951		-2.22	-2.511	-2.798		2.18	2.949	-0.2
778	1	-1.621		-1.43			0.4194	4.08	2.629	-0.26
779	1	-2.26E-09	-0.05687	-1.709	-0.4394	-0.6669	-0.9694		0.7806	0.5912
780	1	-0.6013	0.7919	-0.35	-1.091	0.06187	-1.251		-0.3006	-0.25
781	1	0.35	-0.1869	0.07125	1.031	-0.2269	0.04062	-0.9388	0.000625	-0.06875
782	1	-0.8912	-1.258	-1.13	0.5194	0.6619	0.3094	-0.23	0.03938	-0.46
783	1	-0.09125	-0.1681	-0.07		1.472	1.389	-0.65	-0.2206	-1.49
784	1	-0.405	-0.8619	-1.444	-0.07438	-0.1819	-0.9344	0.3562	0.1056	0.4162
785	1	-0.5613		-2.11	-0.8006	-2.068	-1.111	0.15	1.439	1.22
786	1	-0.5012	-0.7281	-0.7	0.2594	-0.3681	0.4294	-0.16	0.009375	0.92
787	1	-0.6512	-0.01812	-0.39		-1.048	-2.191	0.48	0.3294	0.14
788	1	0.08438	-0.5725	-0.7544	-1.185		-0.315		2.975	-0.4044
789	1	-0.6912	-1.168	-0.58	-1.341	-0.9181	-2.701	-0.81	0.8094	2.72
790	1	-0.2012	1.022	0.93	-1.861	-0.8081	-1.721	-0.77	1.329	-1.77
791	1	0.6469	0	-0.03188	-0.2225	-0.19	-0.0325	-0.8019	0.0375	0.2281
792	1	-0.1612	-0.1081	-0.03	-0.000625	-0.7581	-0.1006	-0.1	0.3094	1.35
793	1	-0.8312	-2.288	-3.06	-0.000625	-1.638	-3.381	0.66	2.179	0.26
794	1	-2.011	-3.058	-2.6	-0.1206	2.312	-1.091	-0.47	0.8794	
795	1	-0.00125	-0.6681	-0.29	0.03938	-1.298	-0.2506	-4.72E-16	-1.981	0.26
796	1	-0.6812	-1.508	-0.59	-0.000625		-0.6806	-1.54	-0.02063	0.58
797	1	-0.01125	-0.7181	-0.45	0.1394	-0.01812	0.03938	-0.45	-0.02062	0.75
798	1	-1.141	-1.848	-1.77	-1.381	-1.278	-0.5306	2.46	1.539	1.32
799	1	-0.1312	-0.8281	-1.6	-0.2806	0.01188	-1.311	0.41	0.7594	1.03
800	1	-0.2212	-0.07812	-0.91	-0.4106		-0.8306	1.06	2.789	0.6
801	1	0.09	-0.3569	-1.559	-0.2994	-0.6869	0.000625	2.491	3.081	2.511
802	1	-0.2312	-0.3781	0.06	-0.8606	-1.368	-1.591	0	0.1494	0.48
803	1	-0.04125	-1.178	-1.43	-0.2806	-0.4281	-0.6306	-0.92	-0.05062	0.08
804	1	-0.5213	-1.278	-1.89	-0.2006	-0.04813	-1.411	-0.2	0.04937	0.92
805	1	-0.7412	-1.758	-1.05	-0.7306	-0.3181	-0.7606	-0.18	0.2194	0.28
806	1	-0.7662	-0.8131	-0.545	-0.5956		-1.326	-0.125	0.3844	0.755
807	1	-0.5412	-1.058	-0.98	0.1694	0.2419	0.3594	-0.02	-0.03063	-0.58
808	1	-0.7812	-1.088	-0.74	-0.2906	0.5019	0.09937	-0.23	-0.06062	0.39
809	1	-0.6762	-2.093	-1.705	-0.02562	0.1769	0.5444	0.345	0.4944	-1.125
810	1	-0.2912	-1.808	-1.4	-0.000625	-1.118	0.3694	-0.37	0.1294	0.11
811	1	0.1588	-0.6081	-0.57	-0.6206	-2.868	-0.3506	-0.42	-0.000625	1.39
812	1	-0.4312	-1.758	-0.81	0.05938	-0.2881	-0.5806	-0.2	0.08938	-0.55
813	1	0.1128	-1.704	-0.7159	-0.9266	-0.06406	-0.2766		0.5134	1.074

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
814	1	-0.45	-1.387	0.06125	-0.9894	-0.1069	-0.3294	-0.1888	0.000625	0.6613
815	1	-0.2144		-0.8431	-0.3837	0.4488	-0.7738	-0.3631	0.00625	0.6369
816	1	-1.071		-1.929	-0.54	-0.1775	0.24	-1.579	0.16	0.8006
817	1	0.17	-1.147	-0.6388	-0.07937	-0.6869	-0.8494	-0.7188	0.000625	0.8512
818	1	-0.8912	-1.778	-1.18	-0.9706	0.2119	-0.3306	-1.2	0.02938	0.28
819	1	-1.221	-2.798	-2.66	-0.3106	-1.178	-1.581	0.34	0.1194	0.51
820	1	-0.7413								-1.51
821	1	-1.141	-2.938	-1.95	-1.451	-1.468	-2.371	0	0.6994	-0.71
822	1	-1.141	-1.748	-2.04	-0.3606	-0.6281	-0.8606		-0.5706	-0.06
823	1	-0.48	-2.207	-1.129	0.1006	-0.3769	0.000625	-0.5688	0.07062	0.7213
824	1	-2.26E-09	-2.037	-1.719	-1.029	-0.9969	-1.519	0.4312	0.4306	1.131
825	1	-0.3513	-1.418	-1.34	-0.5106	0.06187	-1.101	-0.64	-0.07063	1.23
826	1	-0.1172	-0.9141	-0.7159	0.02344	-0.02406	-1.257	-0.7359	-0.1566	1.024
827	1	-0.9912	-0.5581	-1.74	-0.4206	0.5819	-0.6606	0	0.1694	0.24
828	1	-0.06125	-0.8981	-0.77	-0.07062	-1.298	-0.9606	-0.03	0.06937	0.46
829	1	0.06875	-0.7181	-0.51	-0.1406	-1.598	-0.03062	-0.23	-0.07062	1.56
830	1	-0.6713								0.25
831	1	-0.6612	-1.828	-1.6	-0.000625	-0.2781	-0.5006	-1.5	0.3894	0.66
832	1	-0.7913	-2.518	-2.44	-0.3506	-0.2181	-0.06063	-0.49	0.5994	1.18
833	1	-0.6931	-1.58	-1.502	0.1575	-2.79E-10	-3.003	-0.6819	-0.3825	0.7981
834	1	-1.411	-3.238	-2.42	-0.3306	0.4519	-0.6906	-0.64	0.04938	1.06
835	1	-0.8112	-2.538	-2.12	-0.4206	-0.3319	-1.461	0.4	1.079	1.36
836	1	0.3688	-1.618	-1.44	-0.1006	-0.3981	-1.391	0.15	0.7994	1.03
837	1	-0.2913	-2.828	-2.26	-0.7306	-1.678	-1.441	-0.08	0.1894	1.11
838	1	-0.7813	-2.078	-1.06	-0.3006	0.1619	-0.2406	-0.8	-0.1406	0.7
839	1	-0.5812	-1.238	-1.7	-0.2706	-0.1881	-0.6806	-0.52	0.1394	0.82
840	1	0.15	-0.8569	-1.159	-0.4894	-1.537	-1.379	-1.229	0.000625	0.6713
841	1	-0.5512	-0.6981	-1.72	-0.5606	-2.208	-1.761	-1.06	-0.05063	1.26
842	1	-0.3912	-1.428	-1.03	-0.6206	-1.518	-1.361	-0.5	0.06938	1.1
843	1	-0.3412	-1.358	-1.46	-0.3106	-0.8081	-1.201	-0.19	0.4794	0.75
844	1	-2.26E-09	-0.8669	-0.6688	-1.269	0.6131	-1.329	-0.8088	-0.4594	0.5812
845	1	-2.26E-09	-0.9869	-0.5588	-1.399	-1.577	-1.209	-1.719	-0.3794	0.7412
846	1	-0.2412	-1.968	-1.89	-0.3706	-1.388	-1.911	-0.46	0.2494	0.51
847	1	-0.1212	-1.208	-1.06	-0.5606	-1.328	-1.401	-0.52	0.09938	1.01
848	1	-1.021	-2.508	-2.23	-1.301	-2.128	-1.421	-0.99	0.2594	0.96
849	1	-0.9712	-2.008	-1.7	-1.001	-0.7381	-1.351	-2.3	-0.03062	0.99
850	1	-0.8062	-2.563	-1.985	-0.6256	-1.623	-2.126	-3.415	-0.4456	0.955

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
851	1	-2.001	-4.068	-3.09	-2.411	-1.538	-3.011	-0.84	0.04938	-1.94
852	1	-1.011	-1.878	-2.57	-0.1506	-0.1081	-1.751	-0.06	0.5794	0.78
853	1	-1.05	-3.067	-2.209	-0.3594	0.3831	-1.289	-0.2888	0.000625	1.511
854	1	-1.16	-2.177	-2.309		0.3831	-1.229	-0.1588	0.000625	1.351
855	1	-1.089	-3.146	-2.108	-0.1481	0.1944	0.1919	-0.6275	0.1219	1.212
856	1	-0.9412	-2.108	-1.5	-0.7706	0.3819	-1.251	-0.66	-0.3506	1.06
857	1	-2.26E-09	-1.067	-1.269	-0.5194	-0.1669	-1.349	-1.599	0.2606	1.201
858	1	-0.9412	-1.698	-2.26	-1.271	0.07188	-1.211	-1.83	-0.2106	0.07
859	1	-0.4313	-1.758	-1.68	-0.5106	0.8419	-0.8306	-0.23	0.3794	0.55
860	1	-0.6672	-2.454	-1.956	-0.1866	0.08594	-1.757	0.1641	0.7634	0.2041
861	1	-0.5912	-2.088	-1.8	-0.7906	-0.5881	-1.321	-0.2		0.33
862	1	-0.2813	-1.648	-1.53	-0.6006	-0.6181	-0.1706	-0.27	0.4594	1
863	1	-0.5012	-2.048	-1.84	-0.000625	-0.09812	-0.9106	0.64	0.7394	1.41
864	1	-0.3412	-1.998	-1.74	-0.1806	0.7219	-0.6206	-0.65	0.7294	0.92
865	1	-0.6112	-2.298	-2.04	-0.2206	0.3319	-0.5406	0.3	0.5794	1.13
866	1	-0.88	-2.607	-2.189	-0.5394	0.4131	-1.129	-0.6588	0.000625	1.061
867	1	-0.8988	-2.116	-2.318	-0.7181	0.7744	-0.9981	-0.4775	0.4319	0.2625
868	1	-1.011	-2.348	-2.13	-0.5606	0.8319	-0.7206			0.24
869	1	-1.151	-1.868	-3.05	-0.7306	0.3419	-1.321	-0.09	-0.1706	1.35
870	1	-0.09125	-1.768	-1.76	-0.2606	0.4319	-1.151	-0.54	0.4594	1.92
871	1	-0.7312	-1.238	-1.58	-0.2506	0.09188	-1.131	-0.41	-0.1906	0.91
872	1	-0.6913	-2.668	-2.52	-0.9506	-0.9881	-1.911	-0.96	-0.2306	0.7
873	1	-1.15	-2.757	-2.159	-1.519	-1.267	-2.819	-1.049	0.000625	1.461
874	1	-1.271	-2.728	-2.45	-1.301	-0.7581	-1.531	-0.48	0.1994	0
875	1	-0.9512	-2.498	-2.5	-1.291	0.7019	-0.7406	-2.42	-0.1506	1.38
876	1	-1.16	-2.157	-1.819	-0.9994	0.3831	-0.5694	-0.7788	0.000625	0.3712
877	1	-0.6712	-2.968	-2.04	-0.000625	0.1119	-0.6906	-0.5	-0.1306	0.38
878	1	-0.6531	-3.07	-1.612	0.1175	-2.79E-10	-0.7625	-0.7419	-0.2125	0.4781
879	1	-0.9862	-2.323	-2.245	-0.6856	-1.143	-1.106		-1.006	0.925
880	1	-0.7212	-1.918	-1.78	-0.3606	0.3619	-0.1506	-0.5	-0.06063	0.35
881	1	-0.5506	-1.867	-1.469	-0.33	-0.9375	-0.42	-0.3794	0.01	0.2906
882	1	-0.1	-1.477	-0.8988	-0.03937	-0.4469	0.000625			-0.1787
883	1	-0.72	-2.007	-1.429	-0.1094	-1.567	-0.8494	-1.079	0.000625	0.9913
884	1	-0.2412	-1.298	-1.19	0.2594	-0.2781	-0.3406	-0.17	0.009375	0.96
885	1	-2.011		-2.85	-2.551	-0.1381	-1.521	-1.57	0.01938	-0.03
886	1	0.1712	-1.656	-1.458	-1.188	-1.086	-2.258	-1.428	-0.9781	-0.2225
887	1	-0.4212	-1.698	-1.3	-0.9406	-1.108	-1.131		-0.1806	

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
888	1	-0.5612	-1.388	-1.31	-0.000625	-0.4281	-1.111	-0.22	0.2294	0.81
889	1	-0.5812	-2.448	-2.15	-0.4006	-0.6281	-1.671	-0.38	0.1994	0.87
890	1	-1.071	-1.278	-2.13	-0.7006	-0.5781	-1.321	-1.42	-0.3506	0.28
891	1	-0.7112	-2.128	-1.54	0.3694	0.4819	-0.1106	-0.07	0.1494	0.28
892	1	0.1044	-1.232	-1.004	-0.155			-0.1544	0.515	1.246
893	1	-0.1012	-1.698	-1.03	0.1594	-0.6181	-0.5006	0	0.6194	1.66
894	1	-0.7012	-2.428	-1.61	0.04938	-0.1681	-1.251			0
895	1	-2.26E-09	-1.587	-0.6088	-0.5294	-0.9169	-1.529	-0.2588	0.02062	1.361
896	1	-0.9856	-1.342	-1.634	-0.955		-1.045	-0.4544	0.005	1.546
897	1	-0.5	-1.667	-0.7488	0.2106	1.153	0.000625	-0.6688	-0.5494	-1.219
898	1	-0.67	-2.747	-1.909	0.1306	1.303	0.000625	-0.3888	-0.2194	-1.369
899	1	-0.1012	-1.168	-1.66	-0.5006	-0.06812	-1.361	0.26	0.9594	-0.24
900	1	-1.25	-1.227	-1.099	-0.4794	0.3731	-0.4794	-0.1588	0.000625	1.011
901	1	0.2888	-0.3681	-0.51	-0.09062	-0.5781	-1.801			0.55
902	1	-0.1712	-1.148	-1.29	0.1894	0.07188	-0.4106	-0.23	0.3294	0.33
903	1	-0.1831	0	0.1681	-0.3025	-0.76	-0.7725	0.1381	0.5775	-0.08188
904	1	-0.4112	0.03188	-2.92E-09	-0.3806	-1.418	-0.9806	-0.4	-0.1306	1.63E-11
905	1	-0.000625		-1.349	-0.2	0.0725	-0.67	-0.8694	0.01	0.000625
906	1	-0.4112	-0.7281	-1.8	-0.000625	-0.1081	-0.3506	-0.22	0.2694	1.96
907	1	0.2988	-0.05812	-1.22	0.1194	-0.9181	-1.131	-0.31	0.3094	0.02
908	1	-0.7612	-1.328	-1.71	-1.121	-0.7781	-0.5906	-0.73	-0.1706	0.26
909	1	-0.075	-0.6019	-0.7338	-0.5544	-0.9319	-1.144		0.07562	0.5862
910	1	-1.196	-3.993	-2.235	-1.356		-1.986	-1.01	-0.4656	
911	1	-1.071	-0.4181	-0.4	-0.8506	-0.5781	-0.8606	0.1656	-0.4506	0.75
912	1	-0.1656		-0.8344	-1.395		-0.955	0	-0.425	
913	1	-0.5112	-1.708	-1.57	-0.6706	-0.4981	-1.251		0.04938	1.09
914	1	-1.219	-0.8556	-0.7975	-0.1981	1.184	0.3419	0.1825	-0.1781	-0.4775
915	1	-1.076		-0.225	-1.076	0.8969	0.2644			-0.465
916	1	-0.9912	-1.748	-1.05	0.08938	0.3919	0.2594	-0.93	-0.2006	-0.27
917	1	-0.00125	-0.6181	-0.19	-0.1606	-0.6681	0.2194	-4.72E-16	-0.1906	1.47
918	1	0.6588	-2.578	-0.79	-1.311	0.1619	-0.4706	-0.74	-1.231	0
919	1	-0.5088	-0.7656	-0.0975	0.03187	0.4444	0.2919	-0.6275	-0.3281	0.8125
920	1	0.3388	-0.2081	-0.35	-0.000625	-0.2181	-0.3306	-0.58	-1.011	0.29
921	1	-0.7212	-1.838	-2.27	-0.9006	-0.2481	-1.071	0.13	0.1094	1
922	1	-0.9	-1.577	-2.659	-1.039	-0.8469	-2.219		0.000625	0.7512
923	1	0.6087	-0.4681	-0.32	0.3894	0.06188	-0.5106	1.82	0.7494	0.05
924	1	1.071	0.06438	-0.0075	1.482	1.324	-1.408	3.022	1.772	

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	18485 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
925	1	0.4569	0.15	0.1181	1.067	-2.79E-10	-3.213	0.1081	-0.0225	0.9081
926	1	1.339	0.4119	1.53	0.6294	-0.6681	-0.5106	0.09	-0.4006	0.87
927	1	0.4228	-0.6441	-0.01594	0.8534	0.01594	-0.3766	0.9141	1.343	0.1841
928	1	0.00125	-1.176	-0.6575	0.5419	-0.7056	-0.2881	0.8325	0.3819	0.2825
929	1	1.259	-0.09812	0.77	0.6194	0.4719	0.7794	0	-0.2106	2
930	1	0.3788	-0.1481	-0.03	0.02938	0.8919	0.6594	0.09	0.4694	-0.41
931	1	0.05062	-0.2163	-0.2481	0.6512	1.744	1.361	0.09187	0.3312	-0.07813
932	1	-0.4712	-1.228	-2.91E-09	0.2594	0.5119	-0.2606	1.08	0.3994	0.28
933	1	0.3769	0	-1.892	-2.773	-0.79		0.1681	-1.683	0.6981
934	1	-0.9013	-2.148	-2.55	-1.731	-0.1481	-1.591	-0.62	0.09937	0.74
935	1	-2.001	-1.538	-2.46	-3.201		-2.741	2.49	1.649	1.43
936	1	0.4788	-0.3781	-0.7	-0.000625	0.7719	-0.4706	2.28	1.339	1.22
937	1	0.1912	-0.8856	-1.028	-0.3081	0.4244	-0.5481	1.972	0.8919	1.102
938	1	-0.4356	0.2175	-0.01438	-0.335	0.5275	0.015		-3.695	-0.9444
939	1	0.03438	-0.3125	0.08562	-0.665	0.1975	0.025	-1.964	-2.035	-0.02437
940	1	-0.02062	-1.697	-0.9094	-0.64	0.6925	-0.04		2.29	0.3206
941	1	-0.9306	-1.117	-1.219	-0.38	0.3625	0.2	1.581	1.62	
942	1	-0.2131	-1.03	-0.6119	0.2375	-2.79E-10	0.0175		-0.0125	-0.4619
943	1	-0.1922	-1.229	-0.9209	-0.3716	0.07094		0.09906	-0.3016	0.2291
944	1	0.4487	-0.2681	0.19	-0.2006	-0.2181	-0.1506	-0.02	-0.000625	0.02
945	1	-0.47	0.3731	0.01125	0.07063	-0.3369	0.7206	-0.5788	0.000625	0.2713
946	1	-0.6912	-0.6381	-0.11	-0.7706	-0.1381	-0.3206	0.44	0.02937	0.04
947	1	-0.1912	0.7019	-0.31	-0.000625	-0.4381				0.63
948	1	-0.3472	-1.204	-0.8959	-0.1566	0.06594	-1.127		-0.2766	0.6041
949	1	-0.2312	-0.9781	0.1	-1.841	-1.858	-1.381		-2.051	
950	1	0.1088	-0.2981	-0.51	-1.621	-1.638	-1.481	-1.53	-1.831	0.37
951	1	-2.26E-09	-0.1669	-0.07875	-0.2594	-0.09687	0.06062	-0.6188	-0.2394	0.05125
952	1	0.7988	0.2119	0.93	1.099	1.452	0.9394	-1.08	-1.631	0.03
953	1	-2.26E-09	1.223	0.9312	1.191	-0.01687	2.761	-0.4088	-0.2294	0.6912
954	1	0.5169	0	0.1281	-0.2825	0.72	-0.8525	-0.1219	-0.3725	-0.1219
955	1	1.059		0.27	-0.6306	0.3719	-0.1906	-1.92	0.3194	-0.82
956	1	-0.1312	-0.5081	0.03	-0.09062	0.2119	-1.701	-0.03	0.3594	0.4
957	1	-0.9131	0.33	-0.3719	-0.7925	-2.79E-10	-0.8025			1.258
958	1	0.03875	1.462	-0.78	-0.7206	0.5519	-1.431	1	0.1194	0
959	1	-0.2112	0.06188	-0.02	0.5394	1.692		0.57	1.449	
960	1	-0.4112		-0.23		0.6419	-0.3006			
961	1	-0.2631	1.22	0.8381	-0.7825	-2.79E-10	0.1575			

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
962	1	0.5438	0.2969	0.505	0.5244		0.9794	-1.51	-1.511	-1.39
963	1	1.149	0.4019	1.59	1.259	-0.4981	0.8294	-0.07	-0.8506	0.43
964	1	0.08875		0.11	0.4494	-0.1981				
965	1	0.2237	0.3969	-0.075	-0.05563					0.35
966	1	0.2888	-0.1981	-0.8	-1.061	-0.4981	-0.9206		-1.851	
967	1	-2.26E-09	-1.167	-1.509	-2.029					0.29
968	1	0.4688	-0.07812	-0.74	-1.681	-1.698	-1.121		-1.521	1
969	1	-0.5312	0.03188	0.01	-1.151	-0.5781	-0.7906	-1.64	-0.4488	1.932
970	1	-0.03938	-0.7963	-1.298	-1.239	1.444	-0.7788	-1.148	-0.3106	0.05
971	1	0.2688	0.8219	0.68	-0.8706	-0.2581	-0.5106	0		
972	1	-1.271		1.681	-2.42		0.04	-0.5894		-0.1
973	1	-0.6712		-0.76	-1.291	1.132	-1.491	0		0.3869
974	1	-0.1644	0.5787	-0.2531	0.2362		-0.03375	-0.3831	-0.7038	0.02062
975	1	-0.02062		-0.06938	0.06	-0.6975	-0.76	0.1406	0.31	
976	1	-0.08125	-0.2181	-0.07	-0.4806	0.5619	-0.9706	-0.26	-0.2906	2.23
977	1	-0.6312	-0.6581	-0.98	-0.4906	-0.8481			0.1994	0.44
978	1	-0.1762		0.095			0.7844	-0.785		0.805
979	1	0.03781	0.0009375	-0.0009375	-0.1216		-0.4716		-1.542	0.7691
980	1	0.09875	0.5419	-0.07	-0.03062		0.2294	-0.88		-0.28
981	1	-0.2112	-0.3781	-0.78	-0.9606	0.8419	-0.6606	0	-0.3706	0.9
982	1	-0.9962	0.4269	-0.425	-1.436	0.9269	-0.2256	1.235	-1.596	-0.435
983	1	0.2038	-1.393	-0.365	0.03438	-0.3531	-0.2156	1.515	0.8044	0.545
984	1	-0.6731	0	-1.182	-0.6125	-0.79	-1.173	0.2681	0.5175	1.738
985	1	-0.1012	-0.5981	-0.81	-0.000625	-0.09812	-0.6106	1.22	1.369	2.86
986	1	-0.4662	-1.633	0.355	-0.4256	-1.323	-2.166	1.595	2.754	-0.185
987	1	0.00875		-2.91E-09	-0.08062	-1.738	-0.4106		3.889	-0.17
988	1	-0.3612	-0.7381	-1.13	-0.2206	-0.4081	-1.461	1.76	1.049	1.14
989	1	-0.1012	-0.8781	-0.8	-0.05062	0.2719	-0.1706	1.67	1.969	2.23
990	1	-2.26E-09	-0.7069	-0.8188	-0.05938	0.3131	-0.9194	-0.1488	-0.1594	1.201
991	1	-2.26E-09	-1.207	-0.7188	-0.3694	0.2631	-0.9794	-0.3088	-0.3394	1.021
992	1	-1.111	-1.208	-0.31	-1.531	-1.028	-1.691	0.36	0.5294	1.44
993	1	-0.9206		-0.4894	-0.75	0.7825	-0.44	-1.339	0.07	
994	1	-0.8612	0.06188	-2.24	-0.000625	2.992	1.549		-1.971	5.19
995	1	-0.1563	-0.3231	-0.025	-0.03563	0.3469	0.5344		-0.7556	-0.135
996	1	-1.063	0	-1.152	-1.293	0.57	-0.3325	-0.7319	-0.7025	-0.3819
997	1	0.7488	1.192	0.79	-0.02062	-2.098	-1.701	-0.03	-0.3306	0.5
998	1	0.2878	0.1609	1.199	-0.2216	-0.4191	-0.1716		-0.4416	

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
999	1	0.2188	0.6019	0.17	-0.5206	-1.098	-0.6306		-1.371	-1.75
1000	1	-0.2712	0.7519	0.32	-0.1606	-0.9981	-0.8706	2.23	1.109	-0.29
1001	1	-0.4272	-0.1141	-1.036	-0.7766	-1.474	-0.4666	2.094	-0.5666	0.7041
1002	1	-1.091		-0.92				2.81	0.6394	
1003	1	-0.1813	-0.1481	-1.49	-2.011			6.16	3.549	-0.63
1004	1	-0.2112	-0.2781	0.54	-1.721	-1.058	-0.9006	5.2	2.589	
1005	1	0.1287		-0.03	-0.3306	-1.438	0.5694			-0.33
1006	1	0.1687	-0.5181	-1.05	0.6594	-0.4481			1.149	-0.54
1007	1	-0.1106		1.711	-0.53		-0.05			
1008	1	0.085		0.05625	-1.144			0.2962	-1.554	-1.134
1009	1	0.1144	0.6575	0.9456	-0.715	0.6775	-1.055	0.4056	0.105	-0.6844
1010	1	-0.1262	1.757	0.225		-0.2631			-0.7956	
1011	1	-0.2913	1.672	0.82	-1.671	0.7219	-0.6206	0.1		-0.58
1012	1	-0.4112	0.2819	-1.1	-0.9106		-1.041			
1013	1	-0.2106	0.1725	-0.5694	-0.24	0.9625	-0.27	2.151	0.08	1.001
1014	1	-0.1612	0.8219	-0.62	-0.7806	0.7019	2.299	-1.69	1.799	-0.95
1015	1	-0.4462	-0.2331	0.225	0.004375	1.227	-1.076	-0.385	-0.7856	-0.005
1016	1	-0.2663	-0.4331	1.495	-1.196	0.2269	-0.2756	-0.445	-1.786	
1017	1	0.07875	-0.8681	-0.01	0.009375	-0.6781	-0.4606		-0.4506	0.34
1018	1	-0.7712	-0.6881	-1.04	-1.041	-0.8181	-1.281	0.05	0.09938	0.07063
1019	1	0.009375	-1.477	-1.399	-1.34	-0.0375	-1.2		-1.13	-0.9994
1020	1	0.1594	-0.2275	-0.7294	-0.67	0.7725	0.05		-1.46	0.07
1021	1	0.00875	-0.3981	0.14	-0.3606	1.002	0.7294	-0.47	-0.3506	-0.4519
1022	1	-0.5131	0	-0.9219	-1.543					-0.35
1023	1	-0.1512	-1.318	-1.82	-2.761	-0.7781	-2.621			-0.23
1024	1	0.2187	0.1519	-0.19	-1.251	0.1719	-0.5706		-0.04063	0.48
1025	1	0.9387	-0.04813	0.01	-0.8306	0.3219	-0.6906	-1.37	-1.421	
1026	1	-0.3588	0.9144	-2.108	-1.848	0.7444	-2.388			
1027	1	-0.3422	0.03094	-0.7209	-0.03156	-1.149	-0.9916	-1.741		
1028	1	-0.4213	-0.01813	0.37	-1.291	-0.7881	-1.051	-0.42	1.439	0.78
1029	1	-0.3112	1.752	-0.1	-1.241	1.292	-0.2006	-0.95	-2.251	-0.95
1030	1	0.1078	-1.419	0.2991	-0.1816	0.0009375	-0.7816		0.2284	-0.77
1031	1	-0.5612	0.6219		-0.1506	0.5619	-0.4506	-1.21	-1.031	
1032	1	-2.73		-1.919			1.611		0.000625	
1033	1	-0.1672	-0.1841	-1.006	-0.4266	0.03594	-0.3466	-2.856	-0.2166	-0.05594
1034	1	0.4088	-1.078	-2.91E-09	-0.1206	-0.3381	-1.361			1.01
1035	1	0.2588	1.282	-0.1	-0.6206	1.362	2.369	-3.53	-0.09063	-2.21

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1036	1	-2.881			1.289	-0.1181				
1037	1	-1.761		-3.85	3.209	1.742	-2.651	-2.7		-1.7
1038	1	-1.282	0.01156	-0.5903	0.3591	-0.01844	-0.01094		-2.691	-2.03
1039	1	-2.26E-09		-0.00875	-0.3094	1.143				
1040	1	-2.26E-09	1.923	-1.239	-0.1094	-1.047	1.181		-1.511	-0.4588
1041	1		1.252	0.37	0.02938	-0.4981	0.4494			
1042	1	-1.512	0.3709	-0.4509	-1.542	0.2009	-0.6416	0.2391	0.2484	-0.2009
1043	1	0.06937	-0.9975	-0.5294	-0.11		-1.4	0.4406	0.96	2.811
1044	1	-1.092	-1.359	-1.721	-1.042	-0.05906	-0.9816	0.5491	0.1284	1.249
1045	1	-0.004375	0.6288	-1.093	-0.7138	-1.471	-1.894	4.277	4.436	4.067
1046	1	-0.5912		-1.22	0.01938	-0.9381	-1.901		-1.831	4.1
1047	1	0.3538	0.2669	-0.685	-0.03562	-0.8631	-1.966		0.2044	2.805
1048	1	-0.03562	-0.3225	-1.504	0.035	2.188	-1.305	4.446	2.905	1.026
1049	1	-0.2412		-1.06	-1.171	-0.7281	-0.5706	1.05	1.499	1.89
1050	1	-2.26E-09	1.223	-0.8688	-0.2294	-0.6069	-1.669	1.951	2.161	2.681
1051	1	-0.1822	0.07094	-0.8809	-1.762	-1.202	-1.202			
1052	1	-0.4306		-0.6394	-1.3	0.4925	-0.21	1.931	3.68	
1053	1	-2.26E-09	1.393	-1.409	-1.129	-1.367	-0.3294	3.411	3.881	
1054	1	-0.3912	0.2419	0.58	-1.621	-1.058	-1.221	2.74	2.939	-0.95
1055	1	0.8269	0	-0.3319	-0.2025	-1.46	-1.503	3.568	2.047	-1.352
1056	1	-0.9112	1.712	-2.91E-09	-1.841	-0.1981	-0.6006	3.3	2.059	
1057	1	-0.7812	1.092	-0.48	-2.811	0.3419			1.299	-1.14
1058	1	-0.1562		-0.505	-0.5956					
1059	1	-0.2212		-0.97	-1.391				-3.501	-1.3
1060	1	-0.3412	2.452	0.15		1.372	-0.09063	-0.6	-0.1606	-0.8
1061	1	-1.241	1.392	-1.15	-1.271					0.1
1062	1	-0.5156	0.7575	-0.08438	-0.345	0.6775	0.035		-1.135	-0.9344
1063	1	0.1238	-0.4531	0.585	-0.5856	0.4469	0.1144	0.065	-1.276	-0.075
1064	1	0.3888	-1.018	-1.36	-0.4206	0.1819	-1.741	-0.33	-0.8706	-0.62
1065	1	0.1669	0	-0.2419	-0.9625	1.39	0.0775		-0.5525	
1066	1	-0.6062	0.8569	0.305	-0.9556	1.197	-1.016	-0.165	-0.9456	-0.545
1067	1	0.02375	-0.4131	-0.155	-1.376	0.1969	-1.716		-1.646	0.155
1068	1	-0.5313	2.632	-0.33	-1.411	0.8319		-3.64	-2.521	1.16
1069	1	-0.3731	0.91	-0.04188	-0.8425	-2.79E-10	-0.8425	-1.212	-1.093	1.308
1070	1	-0.9412	0.5119	-1.03	-1.671	1.212	-1.361	0	-1.291	-0.78
1071	1	-0.6962		-0.435		-0.5231	-0.3656	-0.635	-0.9856	
1072	1	-0.4412	2.492		-0.7106	-1.018	-3.031			

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRYOX	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1073	1	-1.951			-2.761			2.75	1.369	
1074	1	-0.6512	-2.098	-1.82	-0.7606	-0.4581	-1.041		3.499	0.08
1075	1	-0.4312	-0.5481	0.01	-0.6306	-0.7681	-0.4306	0.73	1.539	-0.66
1076	1	-0.4313		0.69	-1.031	-0.4481	-2.361			-0.37
1077	1	0.1044	2.378	-0.1044	-1.185	0.4775	-0.365	-0.8344	-1.715	-0.4144
1078	1	-0.5812	-1.128	-0.85	-0.7906	1.142	-0.4706	-0.9	-0.6406	0.1
1079	1	2.24E-09	0.2831	-0.4188	-0.2594	-0.5369	-0.1694		0.000625	1.601
1080	1	-0.6262	0.8469	0.575	-0.8756	-0.6731	-0.2256			
1081	1	-0.3163	0.4569	-0.345	-0.5256	-0.6831	-0.9456		2.964	-0.375
1082	1	-0.7912	-1.038	-1.14	-0.01052	-0.7281	-0.1706	1.65	1.359	0.14
1083	1	-0.8912	-0.8281	-1.5	1.389	-0.06812	-0.9806	-1.18	-1.151	0
1084	1	-0.5012	1.152	-1.12	-0.7706	-0.3481	-0.7706	0.99		0.32
1085	1	-1.011	-1.278	-0.78	-1.341	-1.358	-0.8206	-1.63	0.9694	0.75
1086	1	-1.551		-1.06	-2.141	0.3619	0.1394	0	-0.1306	0.42
1087	1	0.02844	0.01156	-0.3803	1.319	-0.3184	-0.05094		-0.01094	-0.3203
1088	1	0.4294			0.27				-0.15	-0.6094
1089	1	-0.3831	0	0.2981	-0.3125	-0.18	-0.1725			0.6281
1090	1	0.07	0.003125	0.3612	-0.7694	0.2031	0.000625		0.5906	-0.4987
1091	1	-2.26E-09		0.1612	-1.179					
1092	1	-0.5672	0.3159	1.064	-0.3266	-0.1441	-0.9566		-0.5166	-0.9
1093	1	0.2987		0.42	-1.191		0.3194			
1094	1	0.4188	-1.338	-1.84	-2.781	-0.7981	-2.641	0.11	3.229	-0.11
1095	1	0.1656	-1.421	-1.343	-2.864		-2.724	0.2269	3.386	-0.4531
1096	1	0.5037	0.6769	-1.025	-1.766	-0.9831	-1.306	-0.215	2.224	-0.875
1097	1	-0.1612	-0.9481	-0.13	-0.5406	-2.408	-1.251	0.13	1.539	0.38
1098	1	0.2038	1.357	-0.565	-0.8256	0.9569	-1.106	-0.735	-2.616	-0.155
1099	1	-0.1962		-0.425			-1.546		-2.476	-0.275
1100	1	-0.2513		0.9	-1.421	1.092				-0.48
1101	1	-0.3163	-0.1931	-0.865	-0.3156	0.2369	0.2844		-0.7456	0.365
1102	1	-1.571	-1.398	-1	-2.141	1.122	-2.701	1.95	0.2194	3.14
1103	1	-0.49		-0.06875	-0.9794	-0.1969	0.000625			3.251
1104	1	-2.26E-09	0.2831	-0.2488	-2.349				1.981	-0.5488
1105	1	0.3178	-0.009062	0.5691	-0.6316		-0.3516			-1.061
1106	1	-0.4612	-1.028	-0.86	0.6894	1.742	1.879	0.16	-0.3906	-0.11
1107	1	1.043	-0.2141	-0.01594	1.493	-0.01406	2.233	0.9641	0.3234	-0.2859
1108	1	-0.5412		-0.03	0.3894	1.172	0.1694	-1.62	-0.5506	-0.24
1109	1	0.3488	-0.3281	-0.19	0.7794	0.2819	0.01937			-0.32

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1110	1	-2.24E-09	0.7731	-0.4488	0.4506	-0.3369	-0.1094	-0.2288	-0.01938	0.8012
1111	1	0.45	-0.2669	0.1712	0.9806	0.3331	0.03062	-0.1788	0.000625	1.001
1112	1	-0.4862	-0.1231	-1.375	0.6244	-0.1431	-1.456	0.445	0.1844	
1113	1	0.3388	-0.6881	-0.78	0.4594	-0.7681	-0.4106		-0.04062	-0.14
1114	1	0.00875	-0.4681	-0.79	0.2594	-0.3881	-0.5106	0.32	-0.1006	-0.4
1115	1	0.4687	-0.4181	-0.27	0.2394	-0.5281	-0.6706	-0.19	0.3194	0.14
1116	1	-0.3513	-1.208	-0.72	0.2694	-0.7681	0.2494	0.14	0.2994	-0.31
1117	1	-0.05125	-0.6181	-0.54	0.5494	-0.8281	0.6094	0.04	0.2594	0.09
1118	1	0.4888		0.37	0.02938	-0.1581	-0.5406			-0.47
1119	1	0.6812	0.9744	0.6825	1.062	0.1944	-0.1181	0.9425	-0.4181	-1.398
1120	1	0.5669	0	0.1881	1.317	0.14	0.9775	0.7181	0.6875	0.7181
1121	1	0.01875	-0.5981	-0.19	0.1994	0.1219	0.5994	0.22	-0.2106	0.34
1122	1	-0.2312	-0.2781			0.7619				
1123	1	-0.1006	-0.5475	-0.5594	0.99	0.5825	-0.48		-0.43	-0.7994
1124	1	-0.1088	-0.5156	-0.1675	1.522	0.1444	0.01187	2.052	0.8819	-0.8075
1125	1	-0.3912	-1.408	-1.64	0.4694	-0.7181	-0.06063	-0.02	0.1694	-0.13
1126	1	-0.3012	-0.8781	-0.83	-0.09062	0.001875	-1.371	0.48	0.02937	0
1127	1	0.1088	-0.3181	-0.01	0.9794	0.1719	0.1394	0	0.4894	0.8
1128	1	-0.05125	-0.3881	-0.16	1.889	0.7919	0.05937	1.17	0.6194	0.18
1129	1	0.1194	-0.3275	-0.2994	0.35		0.05	-0.1294	-0.19	0.9106
1130	1	-0.21	-0.9669	-0.9288	0.6706	0.09313	-0.06938	0.3512	0.000625	-0.9487
1131	1	-0.3012	-1.468	-1.03	-0.4506	-0.7481	-1.311	0.09	0.3194	1.32
1132	1	-1.066	-2.083	-2.005	0.02438		-1.576	-0.355	-0.5056	0.015
1133	1	-0.6662	-2.483	-1.245	0.1444	-0.3131		0.685	0.4044	-0.975
1134	1	-1.32	-1.557	-1.579	0.1006	-0.3369	0.000625	-0.5512	0.2706	-1.169
1135	1	-0.2712	-0.8981	-1.12	0.06938	-0.1219	-0.1306	-0.15	-0.2006	0.12
1136	1	-0.4612	-1.168	-0.94	-0.000625	-0.8681	-0.2406		-0.1306	-0.74
1137	1	-1.071	-1.678	-1.18	-0.000625	-1.938	-0.5306	0.19	0.2294	-0.02
1138	1	-0.4112	-1.308	-0.99	0.4194	-0.5081	-1.431	-0.09	0.09938	0.21
1139	1	-0.1013	-0.5381	-0.79	0.5294	-0.4681	-0.4906	0.92	0.6094	0.29
1140	1	0.08875	-1.348	-0.98	0.5194	-0.2181	-0.3206	0.76	0.5894	0.33
1141	1	-0.4506	-0.3475	-1.009	0.22	-0.2275	0.04	-0.4994	0.06	0.2006
1142	1	-0.9931	-1.35	-1.342	0.5075	-2.79E-10	-0.4125	-0.2019	0.2575	0.8181
1143	1	-0.4612	-1.088	-0.75	0.2694	-1.468	-0.7606	0.04	-0.1806	0.19
1144	1	-0.1812	-0.8381	-0.86	0.4794	-1.398	-0.06062	0	-0.2706	0.46
1145	1	-0.64	-1.137	-1.609	-0.1594	-0.4169	-0.7394	-0.2488	0.000625	0.8113
1146	1	-0.9706	-1.137	-1.209	0.56	-0.6275	-0.7	0.2506	0.08	-0.08937

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1147	1	-0.3962	-0.9231	-0.615	-0.1656	0.2769	-0.1556		-0.08563	-0.115
1148	1	-0.2512	-1.488	-1.27	0.009375	0.3419	-0.4306	0.18	0.5094	-0.03
1149	1	-1.019	-1.616	-1.248	0.8119	-0.1356	-0.05813	0.1425	-0.1281	0.7425
1150	1	0.4238	-0.2631	-0.285	0.09438	-0.4131	-0.3056	0.105	-0.6056	
1151	1	0.5788	0.4819	0.41	0.5994	0.8319	-0.07062	-0.49	-1.161	-0.77
1152	1	-0.2912	-1.358	-0.79	0.2194	0.2719	0.3194	-0.46	-0.4406	0.23
1153	1	0.4888	-0.6881	-0.34	0.8994	1.002	1.309	-0.61	-0.8506	-1.77
1154	1	-0.12	0.003125	-0.5688	0.3906	-1.097	-0.4294	0.4212	0.000625	1.101
1155	1	-0.06125	-0.8081	-0.27	-0.5006	-0.6881	-0.7306	-0.78	-0.8806	0.66
1156	1	-0.2712	-0.04812	-2.91E-09	-0.2706	-0.4181	-0.9006	-0.12	2.199	0.71
1157	1	-0.07125	-0.4681	-0.28	-0.2606	-0.02812	-0.2606	-0.04	2.029	0.93
1158	1	-0.1113	-0.7581	-0.4	-0.5006	0.2619	-0.1206	-1.01	1.289	0.88
1159	1	-0.02063	-0.8875	-0.9294	0.85	0.2425	0.49	1.391	-2.79	
1160	1	-0.09125	-0.5181	-0.51	0.5994	-0.3281	0.2394	0.22	0.2194	-0.05
1161	1	0.4544	-1.392	-1.134	0.795		0.195	0.1156	-0.005	-0.8544
1162	1	-0.003125	0	-0.2419	0.0775	-0.31	1.347	-0.3119	-0.9125	0.7981
1163	1	0.4087	-0.2681	0.49	0.6194	0.1919	0.7094		-1.521	-1.08
1164	1	-0.3013	-0.4581	-1.28	-0.7606	0.4819	0.5794			0.56
1165	1		1.102	-1.02		-0.1581	-0.09063		-0.1706	0.12
1166	1	0.1478	0.9709	-0.05094	0.008437	-0.009062	-0.2416	1.869	1.918	-1.371
1167	1	-0.5031	-1.12	-0.8919		-2.79E-10	-1.183	-0.3119	-0.4925	1.028
1168	1	-0.6212	-0.6381	-1.06	0.1694	-0.3481	-0.9506	-0.09	-0.5106	0.97
1169	1	0.29	-0.5269	0.3812	1.311	-0.2269	-0.06938	0.8412	0.000625	
1170	1	-0.2712	-0.7781	-1.19	-0.03062	-0.9781	-0.000625	0	0.4494	0.11
1171	1	-0.08	-0.9169	-0.8888	0.1106	-0.2769	-0.1194	0.2912	0.000625	0.4913
1172	1	-0.2212	1.122	-2.91E-09	-0.5706		1.529		-0.1606	
1173	1	-0.4712	-0.1681	-0.39		0.1619	-0.09063		0.6794	-0.09
1174	1	-2.26E-09	-0.2369	-0.08875		-0.2269	-0.009375		0.8406	0.03125
1175	1	1.089	0.2919	0.99	-0.9606	-1.218	0.08937	-0.59	-0.06063	0
1176	1	-0.3631	-0.67	-0.8119	-1.183	-2.79E-10	-0.4225	-2.332	-0.6325	2.728
1177	1	0.1488	0.2519	-2.91E-09	-0.4906	-2.108	-0.2406	-0.31	0.1994	-0.68
1178	1	-1.051	-0.9681	-0.26	0.06938	-0.5881	0.3994	-0.65	1.129	-0.65
1179	1	-0.3313	0.7619	-0.8	-0.3306		1.529			
1180	1	0.4588	-0.3481	0.51	1.129	1.942	-2.351	0	0.5594	2.12
1181	1	0.7	-0.6469	1.151	-0.06938		-0.7594		-1.439	1.171
1182	1	0.03875	-0.7481	-0.19	-0.000625	0.7919	-0.4706		-0.4506	0.66
1183	1	-0.7188	1.724	2.662	-0.1781	-0.4156	0.06187	2.432	2.142	2.072

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1184	1	-2.26E-09		0.5212	0.2106	-0.3869				-0.4988
1185	1	0.03	0.6631	0.8112	-0.1794	-1.407	-0.3194	0.07125	0.000625	-0.7988
1186	1	-0.8512	1.862	1.71	-0.000625		2.249			
1187	1	-0.6012	2.412	2.41	0.08938	1.412	2.629	-1.6	-1.771	0.94
1188	1	-1.237	0.05594	-0.1859	-0.6366	1.576	0.4234		-1.177	1.094
1189	1	-4.251	0.7619	0.32	-6.861	0.1219	-0.2006	-3.97	-1.771	0.19
1190	1	0.2744	1.438	1.796	0.005	0.2475	-0.005		-0.315	1.806
1191	1	0.5388	1.502	2.28	0.1694	-0.5981	-0.8206	0.93	-0.3006	1.61
1192	1	0.1338	1.637	1.465	0.004375	-0.3731	-0.2756	1.185	-0.7356	1.885
1193	1	-0.05	2.173	2.301	-0.09937	-0.1369	0.000625	0.7312	-0.7794	1.901
1194	1	-0.1056	1.638	1.706	-0.275	-0.4225	-0.385		-0.955	1.596
1195	1	-0.3112	1.212	1.32	-0.8006	0.07188	-0.5506	0.87	-0.1806	0.36
1196	1	-0.3212	1.542	1.46	0.1694	0.6019	1.329	-0.3	-0.7106	-1.48
1197	1	-2.26E-09	3.723	3.431	-1.149	0.07313		-0.5688	-3.819	
1198	1	-0.7331	1.91	1.508	-0.5325	-2.79E-10	0.3575	0.1381	-0.9625	-0.7019
1199	1	-0.3356	1.498	2.006	-0.475	0.3475	0.145	0.6656		-0.1544
1200	1	-1.46	3.393	2.771	-1.549	1.043	0.6906	-0.00875	0.000625	-0.02875
1201	1	-1.571	4.142	3.21	-2.351	-0.1481	-0.4106		-1.851	0.11
1202	1	-0.29	2.263	0.8312	-0.4994	-0.6369	-0.5094	-0.3888	0.000625	0.7712
1203	1	-2.26E-09	3.693	3.651		1.163	0.3006	-1.489	1.551	1.401
1204	1	-1.046	4.817	6.285	0.6644	2.677	1.674		-0.3256	0.065
1205	1	-0.4262		3.525	-0.9356	1.037	0.2144	-0.625	-0.3356	1.545
1206	1	-0.96	2.143	3.671	-0.8394	0.6531	0.5706		-1.039	1.701
1207	1	-0.06	1.563	2.361	0.09063	1.773	0.6106	-0.02875	0.000625	-0.5587
1208	1	-1.339	5.224	5.802					-2.208	
1209	1	-2.201	3.732	3.86	-1.891	2.512	0.1994	-0.16	0.1994	1.57
1210	1	-0.9362		3.705	-1.076	2.587	0.6244	0.205	0.6744	1.675
1211	1	-0.1106	2.853	2.451	-0.61			-0.9694	-1.09	0.1106
1212	1	-0.7712	2.282	2.67	-0.6406	1.742	0.5294	0	0.08938	-0.25
1213	1	-1.589	2.824	3.892		3.064	0.3419	-1.978	-0.1681	-2.308
1214	1	-0.3812	2.752	2.63	-0.000625	1.002	0.09937	-0.02	0.2994	-0.34
1215	1	-0.7712	2.292	2.43	-0.000625	1.122	0.09937	0.12	0.2394	-0.31
1216	1	-0.8556	2.428	2.286	0.065	1.088	-0.065	0.08562	0.155	
1217	1	-0.5613	2.512	2.55	0.01937		-0.4106	-0.09	0.1994	0.2
1218	1	-0.1312	1.702	1.82	0.01938	-0.6381	1.169	-0.6	-1.881	0.71
1219	1	-0.3612	3.322	1.74	-0.3306	0.7419	-0.8006	0.34	-1.561	1.73
1220	1	-0.2912	2.582	3	-0.3906	-0.2781				0.34

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Table 2

	GWEIGHT	HMEC-C	HMEC+INFA	HMEC-C_CONFL2	184AA	184A1-LATE	184B5	HMVEC	HUVEC	MDA-MB-321
		ARRY2X	ARRY4X	ARRY3X	ARRY5X	ARRY1X	ARRYOX	ARRY7X	ARRY6X	ARRY11X
1221	1	-1.4	-0.2769	-0.1988	-0.6594	0.2731	0.000625	0.2512	-0.2394	0.5013
1222	1	-1.263	0	-0.1019	-0.1825	0.53	0.6375	0.008125	-0.2125	1.438
1223	1	-0.6512	0.3619	-2.91E-09	0.07938	-0.008125	1.009	-0.1	-0.1306	0.28
1224	1	-1.79	1.013	0.7412	0.04063	1.693	0.000625	-0.8788	-1.609	-1.349
1225	1	0.04125		0.9325	0.3619	-0.3256	0.6819	0.1825	0.2319	0.4925
1226	1	-0.3906	-0.4875	-0.2494	0.43	0.2525	0.06		0.03	-0.3294
1227	1	0.06875	0.7019	-0.02	-1.551	0.3819	-0.7506	5.11	-2.141	-0.05
1228	1	0.01438	0.8575		-0.015	0.0375	2.095			
1229	1	0.2788	0.3119	0.02	0.07938		-0.01062	0.7		
1230	1	-0.3056	1.697	1.856	0.305	1.627	0.725		-5.165	1.016
1231	1	-2.26E-09	2.163	2.411	1.021	2.283	1.541	-3.289	-3.489	1.401
1232	1	-2.26E-09	1.883	2.041	0.7906	1.873	1.041	-2.159	-2.139	1.271
1233	1	0.9088		1.25	-0.7506					
1234	1	0.6738	1.197	0.705		0.5269		-1.035	-0.3756	-0.255
1235	1	-0.01062		0.2406	-0.56					-3.519
1236	1	1.131	1.514	2.302	-0.008125	-0.6256	-0.7981	0.3525	0.1219	-2.988
1237	1	0.06875	0.1119	1.37	-0.1606	0.1619	-0.2106		-1.841	-2.92
1238	1	-0.08219	0.03094	0.8791	-0.8016	-1.159		1.899	-0.7916	0.1291
1239	1	-2.26E-09	-0.5069	-0.5388	0.2306	0.4431	0.7606	0.5312	0.8106	0.9312
1240	1	-0.8012	-0.4981	-1.12	-0.7006	0.3919	-0.6906	0.99	0.8394	0.14
1241	1	0.1688	-0.06812	-0.35	-0.6806	0.7319	0.8394	-0.73	-0.8906	-0.63
1242	1	0.09125	-0.1556	-0.9075	-1.218		-0.7081		-0.8081	2.482
1243	1	-0.4831	-0.59	0.2181	-0.6525	-2.79E-10	0.9175	-1.832	1.427	2.118
1244	1	-0.8562		-0.235	-0.2156	0.3869	-0.3656	-0.305	-1.186	2.285
1245	1	0.4237	-0.7431	0.595	0.4044		1.344	-0.825		0.025
1246	1	-0.8862	0.4669	-0.215	-1.016		1.384			0.215
1247	1	-0.8362	-0.6931	-0.025	0.2544	0.05688	1.934	0.655		0.025
1248	1	-0.4612	1.822	1.94	-0.7506	1.552	1.984		-2.601	0.02
1249	1	-0.3863	-0.1431	0.025	0.004375	0.3269	2.149		-1.346	-0.465
1250	1	0.2488	0.2919	0.65	-1.271	1.092	0.6894	-1.41	-1.231	0
1251	1	-0.1413	1.642	-0.12	-0.5006	0.3119	1.359			-3.36
1252	1	0.01875	0.2219	0.53	0.1294	0.8819	1.249	0.12	-1.251	-0.23
1253	1	-0.5612	0.5419	-0.21	-1.351	1.532			-0.9106	-1.98
1254	1	-0.05	0.2731	-0.4288	0.1406		0.000625		-0.7794	-0.4687
1255	1	-0.05125	0.3019	-0.2	-0.8006	-0.1581	-0.4606			-0.34
1256	1	-0.3813	0.8919	-0.32	-0.8706	0.1619	-0.2706			
1257	1	0.5288	0.3819	0.37	-0.6806	-0.2681	0.3494		-2.541	-0.34

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	18485 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1258	1	-0.07125	-0.7681	-0.03	-0.8206		0.1394		-0.5606	-0.23
1259	1	0.1534	-0.1534	-0.3653	-0.3059		0.2941	-0.8653	0.1541	0.4847
1260	1	0.3688	1.542	-0.42	-1.041	-0.05812	-1.641		-1.571	
1261	1	0.3088	0.4219	0.22	-0.2606	1.952	0.6294	-0.32	-0.9406	2.34
1262	1	-1.019	1.444	-0.6875					-1.838	-0.9575
1263	1	-0.1612	1.192	-0.45	-2.011	2.172	-1.051			1.67
1264	1	-2.007	-1.254	-1.856	-2.417	-0.8541			-0.9566	-1.326
1265	1	-0.01656	0.01656	-1.275	-2.796	-1.033	-2.116	-2.265	-1.966	-1.265
1266	1	0.4988	-0.8581	-0.58	-1.251	0.3819	-0.1106	-3.71	-4.811	-1.23
1267	1	0.5837			-0.6256	0.8969	0.1344			-0.415
1268	1	-2.26E-09			-3.029	-0.3869				
1269	1	-0.01562	1.238	-0.2244	-1.625	-1.062	-1.165		-1.835	-0.3644
1270	1	0.38	-0.5869	0.1512	-0.6094	-0.03687	0.000625			
1271	1	-1.386	-1.963	-1.955	0.2844	1.517	1.514		-1.486	-0.195
1272	1	-0.8388	1.164	0.0725	-1.288	-0.3056	-1.728			-0.4575
1273	1	-0.7912	0.6919	-1.2	-1.341	-0.5181		-1.88	-0.3506	-0.41
1274	1		0.2869	-0.355	-0.03562	-0.5031	2.064		-0.4056	-0.445
1275	1	0.04687	1.14	-0.5619	-1.723	-2.79E-10	-2.163	0.1781	-0.7725	-0.1319
1276	1	-0.1763		-1.345	0.04437		2.174		-0.9656	0.015
1277	1	0.1138	0.8769	-0.585	0.08438	-0.2131		-0.565	-1.036	-0.955
1278	1	-0.2112	-0.1481	-0.45	-0.6206	0.4219	-0.3606	-0.53	-0.4706	-0.1
1279	1	-1.101	-1.538	0.57	-0.7406	-0.1181	-1.141	2.92	3.399	-0.14
1280	1	-0.08062	-0.3875		-0.87	-0.4175	-0.63	-0.3094	-0.04	0.04062
1281	1	-0.000625	1.173	-0.3794	2.56E-11				-1.29	2.091
1282	1	0.04437		-0.04438	0.585	-0.8225	-0.515		-0.875	0.08562
1283	1	-0.3512	0.2119	0.64	-0.4006	1.822	1.099	0.74	0.3494	
1284	1	0.1484	0.4716		0.6291	-0.1484				0.5997
1285	1	0.765	-0.5619	0.1562	0.8556	0.2181	1.396		1.466	0.6863
1286	1	0.6669	0.06	0.9381	0.4475	-2.79E-10	2.547	1.558	2.747	-1.612
1287	1	0.7912	-0.1656	0.0625	0.09187	0.3344	1.492	0.0925	-0.1581	1.042
1288	1	-0.09062	-0.4975	0.3806	0.35	0.1425	1.06	-0.2594	0.1	
1289	1	0.00875	0.8019	0.57	-0.000625	-0.1381	0.3794	0.97	0.2494	-1.08
1290	1	1.097	-0.34	-0.1019	0.2975	-2.79E-10	1.387	-0.2019	-0.1625	-0.07188
1291	1	0.01875	-0.08812	0.83	-0.000625	-0.6681	2.549		-0.7506	0.93
1292	1	0.5888	-0.1281	0.45	-0.4606	-1.668	-0.1006	-0.02	0.5094	0.05
1293	1	0.7769	0	0.5781		-1.25	-0.3225	1.628	0.9775	-0.07188
1294	1	0.5538	-0.4831	0.515	1.004	0.3969	1.054	0.835	0.7844	

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1295	1	1.319	0.2519	1.62	1.039	0.2819	1.969	0.1012	0.3194	-0.68
1296	1	0.05	-0.4769	0.07125	0.000625	0.5531	-0.3794		0.000625	0.4513
1297	1	-0.3488	0.1944	1.002	0.01187	-0.2256	1.472	0.7725	-0.7281	-0.1175
1298	1	-0.5488	0.2444	0.9525	0.08187	-0.7956	1.192	0.7525	-0.7281	-0.2575
1299	1	-0.5031	0	0.2981	0.4975	0.65	0.6575		-1.923	-1.012
1300	1	-0.3313	-0.5381	1.32	-0.1206	-0.3081	-0.9006	-0.2		
1301	1	-0.7988		-0.2775	0.1019	0.1544	1.022		-1.308	-1.668
1302	1	-0.4512	-0.02812	0.34	-1.061	1.442	2.209			-0.51
1303	1	-0.5012		0.91	0.2994	1.462	4.299	-1.69	-1.171	0
1304	1	1.197	0	-0.1719	0.2275	-0.82	-0.2125	-2.182	-0.9325	0.9581
1305	1	0.9234		1.995	1.554	-0.05344	0.05406		-2.356	-0.5553
1306	1	-0.3512	0.3719	0.22	0.1994	3.182	3.569		-2.541	2.56
1307	1	1.699	0.2719	1.21	0.7594	0.5019	1.009	-0.85	-1.471	-1
1308	1	1.373	-0.3941	0.3941	0.7534	0.4559	0.8034		-1.817	-1.306
1309	1	0.1369	0	0.4581	0.1875	-0.08				-0.09188
1310	1	-0.1312	-1.898	-2.91E-09	0.1494	1.672	2.389	-2.59	-0.1406	-0.91
1311	1	-1.401	-0.5081	0.8	1.119	-0.3781	0.7094		-3.231	2.1
1312	1	-1.95	-0.6369	0.3312	0.8506	-1.087	0.4906		-3.119	1.981
1313	1	-0.4262	-1.343	0.685	0.6244		0.1944		-1.966	2.865
1314	1	0.2912	0.1844	0.6425	0.07187	0.5544	0.4319		-4.008	-4.048
1315	1	0.6388	-0.5181	0.07	-0.1806	1.312	2.399	0	-0.1806	-2.83
1316	1	-0.38	0.4131		0.1806	0.4731	0.4206		-0.5394	
1317	1	3.419	4.192	6.21	5.259	2.962	4.239		-4.051	-1.71
1318	1	0.725	1.298	2.076	1.756	0.5981	1.896		-0.3944	-0.05375
1319	1	0.1812	1.304	-1.498	0.2394	-3.036			-2.808	-1.348
1320	1	0.6688	0.5619	0.99	2.289	-0.3381	1.249		-0.8806	0.02
1321	1	-0.2513	0.8819	1.39	0.4506	-0.9869	-0.5706	0.1112	-0.6306	0.61
1322	1	0.6	-0.1669	0.5112	-0.01062	-1.748	0.1406	0.19	0.02062	-1.759
1323	1	0.4688	-0.1981	-0.44	0.4275	2.65	-0.7406		0.3594	-0.6
1324	1	0.3469	0	3.478	-1.679	2.073	1.137		-2.113	-2.912
1325	1	-0.45	-0.2769	0.8812	-0.000625	-0.6581	4.231	1.251	0.000625	-2.079
1326	1	1.409	-0.2381	0.77	-0.000625	-0.2981	-0.2206		-2.961	-0.36
1327	1	0.3788	1.212	0.7	-1.571	-2.908	0.9994		-0.9306	
1328	1	0.9888	1.102	0.51	-0.07062	-1.228	-2.171	0.48	0.4894	0
1329	1	0.4288	0.2119	-2.91E-09	0.35	-0.4975	-2.891	-0.34	0.6094	0.68
1330	1	-0.04062	-0.1375	-0.8394	0.9894	2.392	0.3	0.2506	-0.01	-0.1394
1331	1	-1.571	-1.048	-1.63			2.279			-0.07

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1332	1	-1.536	1.247	0.015	-1.566	-0.2631	0.4244	-0.015	0.3944	0.655
1333	1	-2.971			-2.281	-2.648				1.65
1334	1	-1.492	-0.02906	-0.8309	0.4084	-0.4691	-0.1606		0.2784	0.6491
1335	1	-1.111	-1.308	-1.07	-0.4906	-0.3181		0.41	0.2194	0.04
1336	1	-1.101	-1.518	-1.17	-0.4606	-0.6481	-0.2506	0.47	0.05938	-0.03
1337	1	-1.311	-1.158	-1	0.07937	0.3419	0.5694	-0.76	-0.6106	0.03
1338	1	-0.9412	-0.8881	-1.18	-0.4606	0.8919		-0.14	-0.1806	0.19
1339	1	-0.6812		0.49	0.8694	0.8319	2.119		1.539	-0.3
1340	1	-1.625	0.1181	-1.054	-0.09438	-0.9119	2.086	-1.104	1.496	
1341	1	0.6288	0.06188	-2.91E-09	0.6994	-0.5081	0.7794		0.3594	-0.48
1342	1	0.07687	-0.17	0.3481	-0.5525	-2.79E-10	0.7775		-0.3025	-0.2519
1343	1	-0.3666	-1.253	-0.9253	0.4141	0.2566	-0.2559		3.034	0.3747
1344	1	-1.201	-0.6181	-0.59	0.3394	0.9019	0.4994			-1.76
1345	1	-0.5012	-0.3181	0.14	0.4394	0.4019				0.25
1346	1	1.554		1.806	0.495		0.485		-1.745	-1.794
1347	1	0.1488	1.452	-0.26	-1.201		-0.6406	-0.52	-1.111	1.44
1348	1	0.09781		-0.3909	-2.132	0.01094	0.2084		-0.9216	-0.01094
1349	1	-0.2512		-0.47	-0.5006	0.1319	-0.4206		-0.4806	0.7
1350	1	0.5988		0.75	0.9594		-0.9706		-0.9006	-0.76
1351	1	-0.9262	-1.853	-1.065	-0.5656	1.057	-0.8156	0.455	0.8944	-0.115
1352	1	-1.621	-1.588	-1.71	-0.7806	0.4219	0.1094	-0.34	-0.4106	0.39
1353	1	0.04562	0.4587	-0.6631	1.616	1.539	4.236	-2.653	-2.414	1.177
1354	1	-1.161	-0.9081	-0.64	0.3794	1.662	2.579	-0.88	-0.6506	0.36
1355	1	-0.9012	-1.758	-1.14	0.2294	1.462	1.639	-1.06	-0.8506	
1356	1	-1.141	-1.788	-1.05	0.1694	1.572	1.689	-1.12	-0.9606	0.41
1357	1	-0.7309	-0.007813	0.3803	1.02	1.642	3.6		-2.29	-2.41
1358	1	0.1387	1.262	-0.01	-0.9506		0.4694		-1.091	
1359	1	0.3028	0.04594	0.4541	-0.04656			0.2141	-0.3966	
1360	1	0.1112	0.1544	0.0225	0.6919	0.4744	-0.4081	-1.328	-1.208	-0.2575
1361	1	-2.26E-09	0.05313	0.01125	0.5406	0.3631	-0.4094	-1.419	-1.379	-0.3188
1362	1	0.4988	-0.7481	-2.91E-09	0.4694	0.6919	0.9694	0.61	-0.5306	0.8
1363	1	-0.07	-0.1869	-0.2988	0.7006	0.3531	1.161	-0.5888	0.000625	-1.119
1364	1	0.07687	-0.84	-0.3119	0.3875	-2.79E-10	1.277	-0.5719	0.0775	-1.222
1365	1	1.191	1.034	1.562	1.522	0.7444	2.092	-4.808	-0.6381	-4.278
1366	1	-0.6012		-0.08	-1.491		0.4694		-2.721	-0.81
1367	1	1.089		1.27	1.569		1.969		-3.681	-1
1368	1	-2.26E-09	0.4131	0.4312	-0.7394	-0.9869	-0.06938			-0.5288

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1369	1		1.512	-2.91E-09	-0.9606					-0.91
1370	1	0.4288	-0.008125	-2.91E-09	0.8294	-0.2781	0.2394		0.3794	0.35
1371	1	0.4794	0.0625	0.3106	0.03	-2.247	-0.03			0.4106
1372	1	1.411	0.5344	0.6525	0.02187	0.1744	-0.1981	-1.588	-0.5781	0.0425
1373	1	0.4828	-0.2641	0.8241	1.643	0.1659	1.923	0.3841	-1.347	-1.926
1374	1	1.029	0.08188	-2.91E-09	1.679	0.3119	1.709	-1.46	-0.5606	-1.62
1375	1	1.217	0	0.01812	2.247	0.51	2.197		-0.3825	-2.632
1376	1	0.2	0.1331	0.5212	0.8406		-0.6894	0.2412	0.000625	
1377	1			0.995	1.264	0.1969	0.04438	-1.345	-1.066	0.395
1378	1	-0.3588	-1.326	-0.1575	0.7519	0.6644	0.6919	-0.5975	-1.428	-1.988
1379	1	-0.1406	-1.687	0.1406	0.91	0.9125	1.24	-3.039	-1.54	
1380	1	1.283	-0.2241	1.184	1.123	-0.9941	2.493		-4.897	-4.216
1381	1	0.5912	0.8644	1.332	1.102	0.5644	0.9819	-2.788	-2.488	-1.298
1382	1	1.819	1.252	1.38	0.7394	0.1119	-1.081	-4.54	-6.221	-1.67
1383	1	1.459	0.7119	2.09	0.6694	0.08188	0.7694	-2.22	-2.541	0
1384	1	1.167	0	0.4081	1.727	0.71	2.817	-2.672	-1.753	-0.1519
1385	1	2.579	2.062	2.89	1.279	-0.4081	1.159			
1386	1	1.799	1.552	2.25	1.709	0.4719	1.389	-1.91	-6.141	-0.14
1387	1	0.3828	0.04594	0.5041	1.003	0.2159	1.803		-3.527	-2.066
1388	1	1.079			1.289	2.082	2.639			-2.12
1389	1	0.7878		1.529	2.228	-0.2291	0.6584			-1.191
1390	1	0.9488	1.232	0.94	1.039	1.852	1.499	0.05	-0.3106	-0.45
1391	1	1.859	0.7219	0.76	1.939	0.8319	0.5994		-1.501	-0.69
1392	1	4.159	3.202	3.96	3.489	2.342	2.369	-3.88	-3.301	-0.39
1393	1	1.209	0.5519	1.25	1.799	0.9219	0.2194	-0.36	1.079	-3.71
1394	1	0.5569	0	0.9081	0.2775	-0.8	0.4375	-0.1119	0.5075	-0.6319
1395	1	0.7344	0.7675	0.2356	0.195	-0.9125	0.645	0.08562	-0.085	-0.1944
1396	1	0.5488	0.5919	0.52	-0.000625	-0.8081	0.4994	0.07	0.08937	-0.19
1397	1	0.8088	0.7419	1.34	0.8994	1.132	1.909	-0.78	-0.2906	-0.77
1398	1	2.33	1.313	1.211	2.341	2.053	1.641	0.6812	0.000625	-0.8187
1399	1	0.09375	0.6069	1.485	-0.05563					
1400	1	0.6578	0.4109	0.5891	0.4484	0.1109	0.7584	-0.6909	-1.102	0.1591
1401	1	1.669	1.432	2.19	0.8994	-0.5981	1.019	0	-1.071	-0.04
1402	1	0.8588	0.9919	2.01	2.189	-0.03812	2.589	-0.69	-0.2606	-0.22
1403	1	0.09875	-0.7381	0.02	1.229	0.3619	1.879	-1.02	-0.5906	0
1404	1	0.4888	-0.1581	0.46	0.8494	0.9719	0.8894	-0.12	0.08938	-0.34
1405	1	0.5978	0.03094	0.6391	0.8884	1.041		-0.05094	-0.07156	-0.3209

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1406	1	2.019	1.312	1.78	2.519	2.142	2.099	-2.75	-2.751	-3.53
1407	1	1.419	0.9119	1.54	1.139	0.5219	1.339	-2.93	-2.051	-1.85
1408	1	1.827	1.09	1.478	1.487	-2.79E-10	1.197		-2.993	-1.672
1409	1	0.3387	-0.6081	0.11	1.449	2.232	0.4894	-4.6		
1410	1	0.2388	-0.6981	-2.91E-09	1.129	2.152	0.7094		-7.301	
1411	1	0.004375	-0.7025	-0.004375	1.345	2.358	0.995			-6.274
1412	1	0.5069	-0.08	0.9781	0.7375	-2.79E-10	1.587		-3.433	-2.102
1413	1	0.6888	0.9819	1.26	1.459	1.442	2.569	0	-0.1506	-1.11
1414	1	2.289	1.302	2.05	1.949	1.622	2.119	-1.48	-0.3006	-1.48
1415	1	2.609	1.932	2.62	3.249	2.812	3.769	-3.71	-3.881	-2.42
1416	1	2.229	2.562	2.26	2.499	1.502	2.319	-0.08	-1.201	0
1417	1	0.735	1.108	1.296	1.276	2.318	2.426			-0.6638
1418	1	2.989	2.642	3.63	3.259	2.212	3.509	-2.97	-1.971	0
1419	1	0.3669	0	1.128	0.8675	1.99	2.107	-2.732	-1.523	-1.612
1420	1	0.8888	-0.008125	0.86	-0.000625	0.1119	0.9194	-2.01	-3.041	0.01
1421	1	0.9387	0.3419	1.44	0.9194	0.5619	1.319	-0.38	-0.7006	-4.08
1422	1	0.7328	-0.01406	0.8541	0.4434	0.7759	1.433			-4.086
1423	1	0.3069	-0.02	1.388	0.8675	-2.79E-10	1.287	-1.792	-1.273	-2.412
1424	1	0.01938		-0.09938		0.1025	0.74		-1.92	-0.01938
1425	1	0.7278	-0.05906	0.4591	0.05844	0.1709	-0.08156	-4.311	-4.412	-4.311
1426	1	-0.055	-0.4619	0.5662	0.1556	-0.8519	0.05562			
1427	1	0.91	0.4831	1.161	0.3206	-0.2069	0.000625	-3.659	-3.539	-0.5987
1428	1	1.16	0.2531	1.331	0.2306	-0.06687	0.000625	-5.069	-5.529	-0.6087
1429	1	1.31	0.1631	1.421	0.4206	-0.1469	0.000625	-4.969	-5.109	-0.6687
1430	1	1.559	0.9519	1.56	2.069	1.752	2.429		-4.641	-2.24
1431	1	-2.26E-09	-0.1669	0.1812	1.111	-0.7031	1.311	-1.659	-0.8794	-2.079
1432	1	0.6544	-0.0725	0.6556	1.205	0.5375	0.275	-0.2344	0.065	-4.664
1433	1	0.4688	-1.158	0.19	2.439	1.502	0.5094		-1.521	-1.67
1434	1	1.029		1.14	-0.07063	0.8819	-0.1206			0.14
1435	1	0.31	0.4731	0.4212	0.7806	0.003125	-0.7794	-1.019	0.000625	-0.9587
1436	1	1	-0.4069	0.4712	0.9806	1.923	1.251	0.2212	0.000625	-0.4587
1437	1	0.2488	0.2019	1.4	1.199	0.1319	1.769	-0.33	0.5594	-0.89
1438	1	-0.5322	-0.4591		0.7184	0.1009				1.079
1439	1	1.108	0.2009	0.8191	1.118	-0.1691		-0.7909	-1.132	0.4191
1440	1	1.323	0.1359	1.324	1.303	-0.02406	0.5134		0.4034	0.02406
1441	1	0.5178	0.4809	1.609	1.738	1.491	2.288			-1.391
1442	1	1.681	1.784	2.452	2.532	1.764	2.972	-3.348	-2.698	-0.8475

Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1443	1	0.7778	0.03094	1.179	0.3484	-0.009062	1.088	-2.391	-3.232	-0.3909
1444	1	0.9637	0.6769	1.005	1.034	0.6369		-1.775	-3.596	-0.195
1445	1	0.09562	-0.4712	0.1369	0.8062	1.669	1.186	-2.913	-3.994	-2.683
1446	1	-0.1312	-0.1681	-2.91E-09	0.8994	1.792	0.8594			
1447	1	-1.267	-0.1241	-0.7759	0.1234	1.156	-0.5266		-3.237	-1.236
1448	1	-1.139	0.4644	-0.8875	-0.2581	1.154	-0.9581			-1.348
1449	1	0.3844	0.0175	0.3856	-0.855		-0.005	-3.064	-2.145	-1.644
1450	1	0.6088	-0.2181	0.31	-0.000625	-1.268	0.3994		-2.351	-2.25
1451	1	1.867	1.15	1.458	1.657	-2.79E-10	1.427		-5.063	-1.442
1452	1	2.099	0.9019	2.92	1.099	1.192	0.8694	-3.99	-2.651	0.55
1453	1	2.091	1.254	2.372	0.5119	1.054	1.562	-3.438	-3.388	-0.4575
1454	1	1.289	1.072	1.69	0.4294	0.9619	1.239	-1.95	-1.301	-0.13
1455	1	0.7937	0.06687	0.485	0.9344	1.027	0.5744		-0.8556	-0.385
1456	1	2.849	2.312	2.06	1.859	1.042	0.7594	-0.92	-1.101	0.52
1457	1	0.95	0.2331	0.8412	1.411	0.5331	0.000625	-0.6688	-0.8894	-0.05875
1458	1	0.4588	-0.5781	0.63	0.8794	-0.6781	0.3794	-1.33	-0.7106	0.16
1459	1	0.7837	0.08688	-0.025	-0.1356	-0.6831	0.7444	-1.495	-0.7656	1.675
1460	1	0.1344	-0.4425	0.2556	-0.005	0.0175	0.005	0.7556	0.615	
1461	1	1.159	0.1819	1.11	1.109	1.662	1.909	-0.82	-0.4506	-0.93
1462	1	1.809	1.542	2.25	1.719	0.8819	2.999		1.069	-4.42
1463	1	0.4288	-0.5381	0.03	0.01938	-0.2281	-0.1506	-0.02	-0.08062	
1464	1	-0.1612	-1.348	0.34	-0.2706	0.1319	0.09937		-1.861	-0.59
1465	1	-0.3212	1.082	-0.41	0.2994	-0.5881	0.6294		-2.321	0.43
1466	1	-1.441	0.6619	0.41	-0.5406		1.149		-4.701	1.34
1467	1	0.1037	1.227	0.765	-0.5656				-2.446	1.325
1468	1	0.6878	-0.1791	0.5091	1.048	3.871	2.958	3.249	1.208	-2.831
1469	1	1.019	1.122	1.53	0.4394	2.812	2.439		-1.111	-2.44
1470	1	-2.26E-09	0.003125	0.5812	2.371	2.913	3.231	0.9912	0.06062	-2.499
1471	1	0.03344	-0.03344	0.2447	1.024	-0.2834	0.9641	1.595	2.104	-1.195
1472	1	0.4384	0.01156	0.2597	0.5291	0.4716	0.7791		-0.01094	0.1897
1473	1	-0.003125	0	0.6981	0.3075		0.3075	-0.3319	0.2775	0.3981
1474	1	0.3487	-0.7381	0.33	0.2594	-1.488	0.1094	0.65	0.3194	-0.04
1475	1	0.01875	-0.6281	-0.51	0.1294	0.6319	0.03937	-0.36	0.9894	0
1476	1	0.4069	0	0.9881	0.5875	-1.82	0.4175	0.2881	-0.2425	-0.6719
1477	1	0.6988	-0.6981	-0.21	0.3794	-2.128	-1.011	1.39	0.5694	0.89
1478	1	0.39	0.5231	1.201	0.1506	0.6131	0.8306	-0.9588	0.000625	0.5412
1479	1	0.54	0.5331	1.421	0.2006	0.2431	1.131	-0.7688	0.000625	0.3813

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1480	1	0.98	0.4531	0.5812	0.6906	-0.3769	0.000625	0.8912	0.5406	-0.5087
1481	1	-0.2362	-1.073	-0.825	0.1444	-0.9831	-0.9356	1.075	0.4744	0.21
1482	1	0.3788	-0.4281	-0.19	0.9694	-1.998	-2.371	0.41	0.4094	0.31
1483	1	1.279	-0.4981	-0.09	0.6394	-1.368	-1.441	3.05	2.679	0.31
1484	1	0.5888	-0.4281	0.37	0.9894	-0.2181	0.6194	0.72	0.9394	-0.25
1485	1	0.04844	-0.04844	-0.3403	-1.831	-1.848	-0.2909		4.289	1.56
1486	1	1.209	-0.2081			-0.008125				1.33
1487	1	1.019		0.5	0.5194	-2.138	0.8394	0.54	1.269	-0.26
1488	1	0.7188				-0.7681				-0.43
1489	1	0.06437	0.1775	-0.07438	0.085	0.5075	-0.165	0.5956	1.935	-1.484
1490	1	0.7088	-0.02812	0.7	1.019	0.2419	0.6994	1.59	1.759	0
1491	1	0.9869	0	0.8181	0.0075	0.39	-0.2325	0.1181	1.477	-0.9919
1492	1	0.8187	1.192	1.27	2.739	1.712	0.5494	-1.31		-0.62
1493	1	1.61	0.9331	1.351	0.5106	-1.897	0.3606	-0.8788	0.000625	0.7113
1494	1	1.458	-0.1291	0.1291	0.8684					
1495	1	2.319		0.07063		-0.1475	0.83		0.03	
1496	1	1.441	0.9644	1.562	0.8719	-0.01563	0.2819	0.9825	0.5919	-1.508
1497	1	1.521	0.7244	1.122	2.602	0.4744	-1.138			-1.748
1498	1	1.369	1.142	1.32	1.579	-0.008125	0.8494	0.88	1.709	0.78
1499	1	0.2988		0.12	1.949	0.7019	-0.2206	-1.43	-0.3906	0.66
1500	1	-2.26E-09	0.7031	-0.1188	1.751	2.223	2.041	0.1812	-2.049	-0.6488
1501	1	-0.5762	0.4569	1.945	1.274	2.407	1.924		-5.796	-4.065
1502	1	-1.561	-1.468	-2.91E-09	0.4994	3.072	1.329	0.22	-4.751	-2.99
1503	1	1.015	0.9481	1.006	2.306	1.508	1.206		-5.834	0.03625
1504	1	1.239	2.582	3.06	1.479	0.5319	2.159	2.68	-4.641	-1.61
1505	1	-0.4112	-0.4878	-0.76	-1.021	-1.038	-1.561	2.15	4.549	-1.34
1506	1	-0.6009	-0.7581	-1.69	-1.63		-1.71	1.17	4.23	-1.02
1507	1	-0.1212	-0.5881	-0.16	-0.9706	-1.098	0.8194	1.26	2.299	-0.44
1508	1	-0.6113	-1.681	-0.61	-0.1206	-0.9381	0.01937		1.229	-1.293
1509	1	0.1256	-0.3412		-0.1338	-1.841	0.4462			0.6969
1510	1	-0.2044		-0.4531	-0.4537	-0.6912	-0.02375	-0.61	0.1462	-0.95
1511	1	-0.8112	-0.6781	0.09	-0.2406		-0.1906		2.119	0
1512	1	-0.5412	-0.5369	-0.76	-0.4806	0.04188	0.4594	-1.37	0.7994	-0.7388
1513	1	-1.04	-0.7181	-0.8088			0.04062	0.7512	0.000625	0.46
1514	1	-0.1112	-1.097	-0.2	0.2594	-0.4181	-0.5506	1.911	0.3194	-0.3987
1515	1	-0.93		-1.139	0.2906	-0.09687	0.000625		0.5006	-2.259
1516	1	-2.26E-09		-0.6088	1.861	-1.047	1.031		1.611	

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1517	1	-1.011	0.1919	0.35	-0.9006	-0.7481	-0.7606	-0.5	-0.9106	0.4
1518	1	-1.271	-2.108		-1.741	-2.378	-1.551	1.11	1.009	0.99
1519	1	-0.08313	-1.12	-1.022	-0.0925	-2.79E-10	0.4375	0.2881	1.837	0.6881
1520	1	0.38	-2.807	-1.969	-1.089		-0.08937		0.09063	-0.4087
1521	1	-0.1456		-0.5544					-1.385	-0.6544
1522	1	-2.351	-0.9281	-0.14	-2.911		-2.511	-0.86		0.2
1523	1	0.3087	-0.5681	-0.12	-0.2306	-0.2081	0.4094			1.51
1524	1	-0.8612	-0.2881	-0.76	-0.9606	0.4019	-0.2906	-1.29	-1.071	-0.44
1525	1	-0.3712	1.932	-1.05	-0.9306	-0.5481	-0.2206		-0.4606	-0.35
1526	1	-0.6406			-1.11	-0.4075	-0.1	-0.8194	-0.7	
1527	1	-0.315	-0.2819	0.8962	0.1056	-0.6219	-0.4144	0.9262	0.8756	-0.1238
1528	1	-1.991	0.9819	-0.66						
1529	1	-0.2872	-0.7741	0.2641	-0.8266	-0.004062	-0.09656	0.6741	-0.6166	-1.016
1530	1	-0.4412	-1.018	-0.48	-0.4206	-0.8681		0.12	-0.6006	-0.12
1531	1	-0.4112	-0.1581	-0.61	-0.6406	0.2119	-0.5806	0.2	0.7194	-2.79
1532	1	-2.26E-09		0.4912	-1.619	-0.4569	-0.7694			-0.1888
1533	1	-0.3412	-0.4581	-0.05	-1.291	-1.238	-0.3506	0.97	1.109	0.73
1534	1	-0.5913	-0.9481	-0.15	-1.501	-0.8081	-0.7406	0.88	0.8094	0.15
1535	1	0.36	-0.2269	-0.02875	0.07063	-0.9369	-0.8294	0.05125	0.000625	0.5213
1536	1	0.4888	-0.6181	-0.48	-0.1606	-2.038	-1.101		1.229	0.45
1537	1	0.6488		-0.42	-0.1106		-0.5406		1.179	0.99
1538	1	-1.283	-0.4781	-0.6519	-1.943	-2.79E-10	-1.513	1.558	1.587	-0.1219
1539	1	-0.7412		-0.22	-1.111	-0.9481	-1.071	0.78	0.4994	
1540	1	-0.03	-0.5769	-0.06875	-0.3694	-0.4869	0.000625	0.4612	0.7306	-0.1187
1541	1	-2.26E-09		-0.1288	0.3506	-0.6169	0.2106	-1.359	-0.6394	-0.7588
1542	1	-0.1212		0.68	-0.08062	0.2719	0.4094	0.08	-0.6406	-0.13
1543	1	-1.431	-1.948	-0.96	-0.1506	0.2419	0.03938	-3.31	0.009375	-0.57
1544	1	-1.931	-1.228	-1.87	-0.3006	0.4619	-0.3806	-4.46	-0.5306	0.3
1545	1	-1.352	0.02094	-1.661	0.03844	0.5609	-0.06156		-0.1116	-0.1709
1546	1	0.5888	-0.4781	0.12	0.1794	-0.05812	-0.09062	0	-0.01062	0.21
1547	1	-2.26E-09	-0.8269	1.581	-0.6894	-1.927	-0.5494		-3.279	1.551
1548	1	0.6869	0	0.2181	1.217	0.46		-0.8319	-2.793	
1549	1	-0.5312	-1.208	-0.94	-0.9606	0.04188	-0.3406		-1.991	0.04
1550	1	-0.55	-1.427	-1.349	-0.7094	0.5831	0.000625	-0.3088	-0.1494	0.9913
1551	1	-0.25		-2.339		-1.037	0.000625			-1.709
1552	1	-0.125	-1.102	-1.244	-2.184	-0.2919		-0.5438	-0.2044	-0.1238
1553	1	-0.5312	-0.3581	-0.5	-0.2406	-1.388	0.4294	-0.15	0.5194	0.79

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Table 2

	GWEIGHT	HMEC-C	HMEC+INFA	HMEC-C_CONFL2	184AA	184A1-LATE	184B5	HMVEC	HUVEC	MDA-MB-321
		ARRY2X	ARRY4X	ARRY3X	ARRY5X	ARRY1X	ARRY0X	ARRY7X	ARRY6X	ARRY11X
1554	1	-0.1106		-0.6194	0.53	3.183	0.91		-3.1	
1555	1	0.125	-0.2419	0.3162	-0.1144	0.8781	0.7956	-0.7238	-0.9144	-0.3838
1556	1	0.15	-0.1469	0.3212	0.1006	-0.08687	0.5706	-0.4788	0.000625	0.7613
1557	1	0.2644		0.5556	-0.585	0.5275	0.375	-0.4044	-1.455	
1558	1	0.7488	-0.5981	-0.33	0.9794	1.352	-0.1206	-0.11	-0.3406	0
1559	1	0.6088	-0.4781	-0.3	0.8294	1.132	0.1594	-1.54	-0.1606	-0.12
1560	1	-0.09219	0.03094	-0.03094	1.228	1.261	0.8184		-2.662	0.5691
1561	1	-0.6312	1.142	-0.72	0.8594	1.082	-0.1906	-0.09	-1.511	0.55
1562	1	-0.3112	-1.178	-1.3	0.3494	-0.05812	0.2294	0	0.6294	0.63
1563	1	-2.26E-09	-1.517	-0.9788	0.2306	-0.9769	-0.09938	-0.06875	0.5106	0.1712
1564	1	0.1588	1.062	0.24	-1.141	-0.1981	2.749	-3.13	-2.431	1.82
1565	1	-0.4431	0	-0.2119	-1.303	0.46	2.657			1.718
1566	1	0.4488	1.452	0.74	-0.1006	-0.5281	3.389	-0.91	-1.111	2.34
1567	1	0.8734	-0.8734	-2.115	-1.476	1.647	2.784			1.585
1568	1	-1.661		-2.07	-1.691	0.6419	1.849			-3.34
1569	1	-0.6531	0.4	0.4081	0.0075	-2.79E-10	1.077	-5.112	-1.993	-0.05188
1570	1	-0.03875	0.9044	-0.1675	-0.7181	-0.3181	-0.5806	0.62	-0.2781	-0.3675
1571	1	-0.9612	-0.2481	-0.08	-0.5206	-0.9075	-0.53		0.4994	-0.45
1572	1	-0.8006		-1.009	-0.08				-0.05	
1573	1	-1.253	0	-0.4019	-0.01656	-0.62	-0.6525	2.008	2.697	-1.252
1574	1	-1.907	0.01594	-0.7959	-1.661				2.473	
1575	1	-0.4812	-0.2881	-0.84	-1.661	-0.4781	-0.1806	1.7	2.109	-1.27
1576	1	-0.57	-1.417	-0.7688	-0.5994	-0.1169	0.000625	0.3412	0.3206	0.00125
1577	1	-0.5312	1.512	-1.08	-1.221	-1.718	-1.561		2.399	1.02
1578	1	-0.5312		-0.62	-0.4606		-2.221	0.37	1.089	0.43
1579	1	-1.221		-1.26		-0.4181				
1580	1	-0.59	0.9931	-0.5788	0.06063	-0.9769	0.000625		-0.5894	-1.369
1581	1	-0.6012		-0.24	-1.211					0
1582	1	-0.4372	-0.2841	0.3641	-0.2766	-0.2741	-1.287		-2.797	-3.206
1583	1	-0.1331	0	-0.01188	-0.5625	-0.07	-0.1725		-2.433	0.9381
1584	1	-2.26E-09	-0.7369			0.2431	-0.1094			
1585	1	-0.005625	-0.6825	-0.3644	0.005	0.6175	0.375	-0.6744	-0.365	-1.454
1586	1	-0.2412	-1.278	-0.33	-0.1806	-0.8481	0.4694	-1.13	-0.6906	-1.13
1587	1	-0.7406	-0.6775	-0.4894	-0.63	-0.3675	0.27		-1.22	-1.259
1588	1	-1.276	-1.983	-2.024	-0.745	0.5175	0.265	-1.284	-0.535	
1589	1	-0.04438		-0.9331	-1.554	-0.4312	-1.414	-0.6131	-1.084	-0.08313
1590	1	-0.3912	-0.5581	-1.01	-1.801	-1.558	-2.401	-0.45	-1.331	0.05

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1591	1	-2.26E-09	-0.3269	-1.159	-1.949	-0.7069	-1.549	-1.599	-1.059	3.891
1592	1	-2.26E-09	-1.007	0.9212	0.4106	3.283	2.631	-0.4088	-0.9394	-0.4988
1593	1	-0.7044		0.1469	-1.124	0.4488	0.08625	-1.143	-0.9538	-1.423
1594	1	-1.103	0	-0.5719	-1.513	-0.33	0.1675	-0.08188	0.0775	1.068
1595	1	-0.54	-0.8069	-0.07875	0.3106	0.9631	0.000625	-2.319	0.9406	-0.7287
1596	1	-0.3556	-0.8625	0.09562	0.615	0.6975	-0.095		1.335	-0.1844
1597	1	-0.29	-0.4569	0.1612	0.7706	1.133	0.000625	-1.119	1.561	-0.1587
1598	1	-0.5112	-0.7681	-0.1	-0.000625	0.7819	0.1394	0.14	1.519	-0.17
1599	1	-0.08	-0.6869		-0.7994	-1.207	0.08062			-0.7088
1600	1	-0.3412	0.9019	0.01	-1.271	-0.8681	0.4894		-0.2106	
1601	1	-0.07875	-0.7556	-0.2475	-0.2081	0.6444	0.4219	-0.6275	-0.5081	-0.1975
1602	1	0.06438		-0.4644	-0.355	0.3275				
1603	1	0.4028	0.1459		-0.1466	0.7159	-0.8566			-1.256
1604	1	0.4188	-0.6581	0.28	-0.3706	-1.038	0.06938	-0.72	-0.1706	-0.15
1605	1	0.05875	-0.2681	-0.24	-0.2806	1.042	2.479		-1.581	-0.66
1606	1	0.1294	-0.5875	0.4606	1.75	-0.4075	1.06			-2.359
1607	1	-0.3912	-1.118	0.05	1.229	0.4719	0.3194	-3.17	-1.611	0
1608	1	-0.36	-0.8969	-0.4488	0.7006	-0.7469	0.000625	0.3612	0.1206	-0.07875
1609	1	-0.1156	0.5775	-1.204	-0.805	-2.042	-1.465	3.866	-0.495	-0.9344
1610	1	-0.1412	-0.3581	-2.91E-09	-0.5706	0.7019	-0.2306			
1611	1	-1.893	0	-2.702		-1.11			-1.773	-2.892
1612	1	-0.04125	-1.328	-0.68	0.03938	-0.01812	-0.3906	0.93	1.069	0
1613	1	-0.7862	0.8369	0.125	-0.1256		-0.4756		-1.986	-0.345
1614	1	0.009375		-0.8194	-1.34		-1.62		-3.13	
1615	1	-2.26E-09	-0.01687	0.7412	-1.199	-0.4169	-0.7394	0.2112	-1.409	-0.7888
1616	1	0.4388	-1.428	-0.81	-0.000625	-1.448	-1.411	0.96	1.019	-1.81
1617	1	-2.26E-09	-1.157	-0.5888	0.4706	-1.227	-1.319	1.291	1.921	-1.189
1618	1	-0.9912	-1.648	-1.11	0.2394		-2.781	1.67	2.309	-2.93
1619	1	1.108	0.1809	-0.5009	-1.562	-0.7291	-0.9316	4.649	3.818	-1.021
1620	1	1.809	0.9219	-2.91E-09	-1.871	-0.6081	-0.8406	5.31	4.369	-2.12
1621	1	-0.6812	-1.178	-0.49	0.1294	0.9619	1.209	3.15	3.119	-1.38
1622	1	-0.1912	-0.5681	-0.1	0.7494	2.042	1.569	3.29	3.349	-1.32
1623	1	0.4088	-0.5281	0.03	-0.5006	-1.468	-1.611	2.8	0.9194	-1.97
1624	1	0.2356	1.489	1.467	-0.3638				-1.104	-0.9931
1625	1	-0.4412	0.3619	1.55	-0.4506	-0.3569	-0.01063		-1.661	-2.63
1626	1	-0.09		1.791	0.4306		0.09062			-2.519
1627	1	-2.26E-09	-0.8069	-0.5988	-1.929	-1.327	-3.589	0.4812	1.261	-1.179

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1628	1	-0.4212		-0.21	-0.9506	-0.9081	-0.2406	-0.84	-1.131	-0.03
1629	1	-0.3462	-0.4431	-0.185	-0.8256	-1.703	-0.4856	-0.735	-0.9356	0.215
1630	1	0.8838		1.415	-1.356	-0.1531			-1.836	
1631	1	0.3887	0.7019	-0.09	1.169	0.05187	-0.2206			1.25
1632	1	-1.327	0.2459	-1.056	-1.637	1.566	1.133	-0.7859	-1.697	
1633	1	-0.6712	-1.808	-1.19	0.01938	0.2819	0.05938	0.83	0.5694	-1.63
1634	1	0.5188	0.05188	0.49	-0.000625		-3.271		-1.621	-2.62
1635	1	-0.05125	-0.8981	-2.91E-09	-0.000625	1.142		-0.24	-0.07063	
1636	1	-0.1712	-0.2081	-0.16	0.009375	-0.3981	0.2694		-0.000625	0.06
1637	1	0.07875	0.1419	-0.01	-0.2306	-1.168	-1.751		-1.681	-0.58
1638	1	-0.09125		-0.22	-1.461		0.01937			-0.37
1639	1	-0.2412	0.2219	-2.91E-09	0.08938	1.642	0.5906			-0.92
1640	1	0.08	-0.7269	-0.1688	0.4706	0.3331	-0.6781	-0.4488	0.000625	-0.6487
1641	1	1.231		0.6125	-0.4581	-0.7856	-0.4206		-0.4081	0.6625
1642	1	0.1288		1.07		-0.9981		-0.4	-1.191	-0.63
1643	1	-2.26E-09	-0.1169	1.441	-0.7194	1.063	2.441		-2.859	-1.689
1644	1	-0.5712	0.3019	1.04	-0.3306	-0.01812	0.4194	-1.86	-1.841	0.32
1645	1	-2.26E-09	0.9831	2.091	0.3106	0.01313	1.491	-2.419	-3.019	-1.329
1646	1	-0.6431	0	1.058	-0.5806	0.91	0.7075	-1.162	-0.8325	0.3681
1647	1	-0.2213	-0.5481	1.1	-0.285	0.9719	0.3094	-1.91	-1.591	1.64
1648	1	-0.1756		0.1456	-0.1694	0.1575	0.105	0.3456	-0.275	-0.1044
1649	1	-0.32	-0.5469	0.8712						
1650	1	1.243	-0.01406	0.04406	0.7534	-0.4241	-0.01656		-0.4666	0.3841
1651	1	0.02875			-0.000625	0.1619	-0.3506		-0.9906	
1652	1	-0.2612	-1.388	0.27	-0.5406	0.5419	0.5194		-0.2606	1.63E-11
1653	1	0.7512	-0.02563	0.8025	0.09187	-1.386	-2.278		-0.07813	-2.028
1654	1	0.1928	-0.02406	0.8241	0.1434	-1.294	-1.137	-2.326	-1.827	-0.8659
1655	1	-0.32		0.1112	-0.7694	-0.6269	-0.7294		0.000625	0.5412
1656	1	0.16	-0.4169	0.3412	-0.009375	0.1431	0.000625	-0.1288	0.000625	-0.7287
1657	1	0.05438	0.7975	0.2456	0.265	-0.1225				
1658	1	-0.1512	0.3719	0.8	-0.1606	0.3319	0.9694	0	-0.3306	
1659	1	-0.145	-0.4119	-0.3038	0.04563	0.5781	-0.2144		-0.4344	-0.6
1660	1	-0.5113	-1.158	-0.82	0.2094	0.1419	-0.4206	-0.41	0.02937	-0.4638
1661	1	-0.5906	1.203	-0.8694	-0.42	-0.0475	0.04		-0.38	0.32
1662	1	-0.3012	-1.048	-0.82	0.06938	-1.128	-0.2106	-0.83	0.7894	-1.259
1663	1	0.3769	-0.34	0.1081	0.3875	-2.79E-10	0.6675	0.2681	2.217	-0.32
1664	1	0.1612	0.2344	0.0825	1.032	-0.3756	0.8619	-1.958	-1.168	1.042

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1665	1	-0.4462	0.1869	0.135	-0.9456	-0.8031	-0.8456	-0.295	-1.016	0.125
1666	1	-0.07719	0.2359	-0.08594	-0.02656	0.02594			-0.9866	0.7641
1667	1	-0.8112			0.1194	0.1419	-0.2006		-0.9606	
1668	1	0.1	-0.1669	-0.5588	0.1306	-0.6069	0.3706	0.6312	0.000625	-1.679
1669	1	-0.07062	-0.6175	-1.159	-0.59	-0.7875	-0.27	0.07062	0.27	0.3906
1670	1	-0.6906	1.013	-0.2094	-1.07		-1.61		0.03	-0.1294
1671	1	1.749	1.202	2.32	1.599	-0.3781	1.179	-2.16	-2.421	-0.52
1672	1	0.2987	-0.2681	0.33	0.8394	0.09187	0.9194	-1.09	-3.381	-1.06
1673	1	-2.26E-09	0.2131	0.4712	1.191	1.273	1.581	-1.379	-4.959	-1.379
1674	1	-0.37	1.433	-0.5888	-1.289	0.3531	0.000625		-1.619	0.4413
1675	1	1.179	1.062	1.21	0.6994	0.6119	1.449	0.72	-0.8206	-0.89
1676	1	1.11	0.7831	0.8712	0.7206	0.1331	0.6506		-1.279	-0.4288
1677	1	-0.2512	-0.9881	-0.24	0.5794			0.14	0.9794	-0.23
1678	1	0.6188	-0.3181	0.01	-0.000625	0.5119	0.4594	-0.07	-0.8906	-0.6
1679	1	1.747	0.6	1.658	1.677	-2.79E-10	1.667	1.008	1.257	-1.942
1680	1	0.6712	0.7544	0.8125	0.7619	0.2744			2.022	0.6725
1681	1	0.2712	-0.6756	0.2825	0.1419	-0.4256	0.01187	0.0225	0.4019	-0.5175
1682	1	0.6988	-0.3281	0.5	0.5094	0.1419	0.5994	-0.78	-0.3806	-1.45
1683	1	-0.4131	-1.15	0.05812	-0.2325	-2.79E-10	0.4275	0.1081	0.2075	-1.792
1684	1	0.4069	0.03	0.5181	-0.3125	-2.79E-10	0.4775	-1.062	-0.0525	0.3881
1685	1	0.3088	-0.5081	0.94	-0.000625	0.6519	1.839	0.2	0.9594	-1.49
1686	1	0.6188	-0.4881	1.15	0.1794	-1.202	1.999	0	0.7594	-1.81
1687	1	0.6387		0.41	0.4694	-0.3181	0.07937	0.18	0.2794	
1688	1	0.6788	0.2219	1	-0.3306	-0.3181	0.4194	-0.46	0.1094	-1.52
1689	1	0.6987	0.2519	1.27	0.05937	-1.458	0.1594	-1.17	-1.211	0.61
1690	1	0.5878	0.4809	-0.2209	0.2684	-0.1591	-0.5116			
1691	1	-0.7912	-1.628	-2.91E-09	0.3794	0.2419	0.1194	-1.16	-0.3706	-2.54
1692	1	0.5788	-0.6481	-2.91E-09	-0.3606	1.012	0.3394	-1.6	-0.4806	-0.8
1693	1	0.1744	-0.7025	-0.1744	-0.525	0.6475	0.275	-1.874	-0.445	-0.7444
1694	1	-0.2412	-1.118	-0.49	0.3194	0.3819	-0.09062	0	0.1494	-0.05
1695	1	0.14	-1.487	-0.7388	-0.1294	0.07313	0.000625	-0.7288	0.09062	-0.00875
1696	1	-0.5612		-0.4	-0.3306	0.3219	0.6594		0.02938	0.31
1697	1	0.1412	0.2744	0.2225	-0.9381	0.6944	0.4019	-1.908	-2.308	-1.428
1698	1	0.1888	0.02188	1.22	-0.2406	1.182	2.559	-0.3	-0.3806	
1699	1	-0.8262	-1.143	0.915	0.9244	1.217	1.144	0.085	0.6744	-1.025
1700	1	-0.6612	-0.6081	-0.47	-1.101	-0.03812	0.06937	-0.45	0.5994	0.78
1701	1	0.18	-0.3969	-0.02875	-1.109	-0.8669	-0.2894	-0.1688	-0.8994	0.1212

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1702	1	-1.036	0.8169		-1.666		-1.176			-2.225
1703	1	-0.3113	0.02187	-0.99	1.879		1.449		-0.8806	0.73
1704	1	-0.5712		-0.1		-0.2781			-2.051	-1.95
1705	1	-0.2012	0.1919	-2.91E-09	-0.8006	0.8719	0.2894	-0.82	-0.3806	
1706	1	-0.1916	-1.198	-0.2403	0.1391	0.04156	1.719		-0.04094	-1.55
1707	1	-0.00125	0.05187	-0.47	-0.1206	0.9519	2.549	-0.37	-0.2006	-1.49
1708	1	-0.2912	0.7919	-2.91E-09	-2.141	-1.738	2.379	-2.63	-2.511	-1.49
1709	1	-2.26E-09	0.08313	0.5712	-0.02938	-0.3669		-0.4988	0.1106	
1710	1	-0.1512	-0.8381	-0.45	0.08938	1.082	-0.1406	0	0.3294	-0.45
1711	1	-0.2406	0.5025		-0.39		0.46	0.5106	-0.14	-0.3594
1712	1	-0.39	-0.2969	-0.2788	-0.2694	-0.6269	-0.2094	-0.3688	0.000625	0.2213
1713	1	0.1978		0.3891	0.06844	-0.06906	0.1884		-1.012	-0.8009
1714	1	0.2788	-0.2981	0.24	-0.000625	-0.5481	0.1094		-0.5106	
1715	1	0.3988	-0.5281	0.39	0.6894	0.03188	0.8894	-1.71	-0.3006	-0.06
1716	1	0.7288	-0.3081	0.61	0.4094	-0.7781	0.6194	-2.54	-0.4206	-0.06
1717	1	0.1888	0.2319	0.8	-0.000625	-0.6081	0.05937	-1.38	-1.461	-1.09
1718	1	-0.4612	-0.4181	-0.53	-0.09062	-0.6881	-0.2506		0.2894	0.08
1719	1	-0.2413	-0.2481	-0.54	-0.3006	-1.088	-0.3606	-0.17	0.1294	0.32
1720	1	-0.8012	-1.568	-1.07	0.08938	-0.2081	-0.4906		0.1094	0
1721	1	0.2512	0.4144	0.5225	0.2219	0.6744	0.2119		-1.838	-0.9375
1722	1	-0.3712		-0.11	-0.8306	-0.6481	0.5094			0
1723	1	0.8688	-0.09812	-2.91E-09	0.3194	-0.1819	-0.7306	-0.25	-0.7106	0.02
1724	1	1.337	-0.62	-0.7119	1.067	-2.79E-10	0.8675	-0.8819	-0.9125	-1.072
1725	1	0.7069	0	0.2381	0.6175	0.56	0.8675	-0.7419	-0.3825	-0.08188
1726	1	1.479	-0.1981	0.24	1.369	1.522	1.079	0.29	0.4694	1.47
1727	1	0.2888	-0.9281	-2.91E-09	1.039	1.612	1.319	0.31	0.4794	-1.36
1728	1	0.1428	-0.2741	-0.06594	-0.8466	-0.05406	-0.5766		0.07344	0.05406
1729	1	-0.5188	-1.026	-0.1875	0.2719	1.094	0.4819	-0.5875	-0.1381	-1.108
1730	1	0.1588		-1.15	0.4294	-0.8581	-0.09063	0.81	0.8394	-0.85
1731	1	-0.2512		0.49	-0.4806	0.7619	-0.1906		-0.2706	1.83
1732	1	0.9988	-0.1881	-2.91E-09	-0.2206			0.88	0.3794	-0.43
1733	1	0.7191	0.1122	0.5403	1.04	0.6722	1.45	-0.9597	-0.6603	-0.6097
1734	1	0.8178	-0.1391	-0.2309	0.1384	-1.339	-2.832	1.329	1.538	0.3591
1735	1	0.52	-0.3669	-0.8788	1.261	-0.5369	-0.5094	0.8512	1.071	2.621
1736	1	-1.37	-1.857	-1.019	-0.6194	-0.2069	0.4406		0.3806	-0.6687
1737	1	-0.08875	-0.3356	-0.4675	-1.018	-0.5656	-0.9281	3.262	1.662	0.0225
1738	1	-1.526	-1.363	-2.285	-0.07562	-0.9831	-2.966		1.344	1.055

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Table 2

	GWEIGHT	HMEC-C ARRY2X	HMEC+INFA ARRY4X	HMEC-C_CONFL2 ARRY3X	184AA ARRY5X	184A1-LATE ARRY1X	184B5 ARRY0X	HMVEC ARRY7X	HUVEC ARRY6X	MDA-MB-321 ARRY11X
1739	1	0.1688	-1.258	-0.43	-0.8106		-1.821	3.38	2.389	0
1740	1	-0.005625		-0.6844	-0.855	0.0275	-2.065	1.696	2.285	-0.4544
1741	1	-0.1256	-0.8425	-0.6844	-1.705	0.5375	-2.325	1.536	2.545	1.966
1742	1	-0.2313	-1.218	-0.78	-0.6006	-2.528	-1.221	2.17	2.799	0.38
1743	1	0.00875	-1.268	-0.93	-1.331	-2.198	-1.141	0.76	2.059	2.47
1744	1	-2.719	-2.416	-1.558	-3.448	-2.766	-3.988	0.5425	0.8419	0.3825
1745	1	-0.2388	-0.2956	-0.6775	-0.2681	-1.256	-2.338		0.8119	0.9525
1746	1	-1.66	-1.857	-1.219	-1.279	1.703	-0.9794	1.341	0.9806	1.671
1747	1	0.2738	0.1769	-0.035		-1.293	-5.716	0.725	0.8444	-2.965
1748	1	0.2578	0.01094	0.1091	-0.01156	1.131	-0.3716			0.7891
1749	1	-0.1812	0.4419	0.04	0.1794	-0.9381	0.03937	-0.75	-0.6706	0.26
1750	1	-0.1172	0.2959		-0.1866	-0.04406	-1.767			-1.126
1751	1	-2.26E-09	-1.097	-0.8288	-0.02938	-0.2769	-0.5894	-0.1388	0.1506	0.1112
1752	1	-2.446		-2.025						2.435
1753	1	1.251	1.044	0.9619	1.541	-1.106	-0.09875		-0.4388	1.842

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Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
1	1	1	1	1	1	1	1	1	1
1.675	-0.865	0.915			-4.347	0.735	-3.365	0.735	
1.646	0.2056	0.4156	-3.134	0.6544	-4.497	1.066	1.486	0.03563	-0.7744
1.361	-0.4894		-1.779	0.3694	0.9081	-0.5794	-0.1994	0.1206	-1.239
1.671	0.3112	1.132	-2.319	-1.62	1.629			0.6513	
0.2725	-0.0675	-1.65E-08	-0.5775	0.00125		0.1525	0.1025	-0.2475	
0.97	0.1	0.17	0.53	0.7287	1.348	-0.07	-0.15	0	-2.61
1.29	-0.2	0.49	0.57	0.8487	1.448	-0.35	-0.16	0	-2.31
0.55	-0.16	-0.405	0.47	0.1488	0.9275	-0.65	-0.54	-0.28	-1.71
0.565	-0.795	1.56	-0.075	0.6338	0.6425	0.445	-1.495	0.095	0.265
0.39	-1.47E-09	0.4456	0	-1.651		-0.87	-0.04	-0.01	-1.93
-0.7244	-0.2544	1.96	0.5656	-0.9256	-1.067		-1.674	-0.8844	-1.084
0.88	0.58	0.59		-1.191	-2.242		-0.47	-0.58	-0.32
0	-0.1	0.4325	-1.09	-1.451	-1.412	1.09	-0.34	0.08	-1.55
1.392	-0.3775	0.2962	0.0725	-1.829	0		2.082	-0.4875	-0.7375
0.7763	-0.09375	0.4512	-0.8438	0.095		1.622		-1.674	-0.09875
1.201	-0.2488	1.504	-1.799	0.05		0.3912	0.1913	-0.04875	-0.1259
0.4841	-0.01594	2.804	1.474	-0.8272	-0.6584	-0.7459	-0.1959	-0.3859	1.304
4.174	3.824	1.25	-0.2859	-4.087		-0.01594	-0.3759	1.614	-0.13
5.61	3.12	-0.11	0.89	-0.7512	-0.5125	0.13	0.4	0.59	-0.72
3.74	5.4	0.1306	1.1	-0.7613	0.1175	4.05		0.12	0.7006
4.501	6.461	0.22	0.3206	-1.291	-2.632	1.741	0	-0.7994	0.72
2.51	3.9	0.43	-0.02	-0.7512	-1.172	0.86	0.42	1.82	0.38
-0.94	0.18	0.84	-0.08	-2.041	2.318		-2.41	-0.01	-1.29
1.16	1.19	0.415	-1.73	-0.8413	2.108	1.83	-1.53	0	
1.135	1.225	0.8012	-2.805		2.412	1.575	-1.149	-0.415	-2.749
0.8512	-0.7388	1.024	-2.269	-0.47		-1.129	-0.4659	-1.469	0.2741
1.754	-0.2959	2.805	-0.8259		-1.978	-0.5959	-0.575	1.364	
1.945	1.435	0.27	-0.025	4.034	0.8425	-2.845	-1.16	0.025	-0.16
0.81	0.11	1.25	0.1	0.7088	0.1375	-1.51	0.34	-0.93	-1.15
5.23	0.53	2.275	-1.07	0.8288	-2.052	-1.19	0.1447	-0.32	-0.1053
5.725	0.8447	-0.14	-1.485	-0.2866	-2.048	-2.025	1.04	-0.07531	0.02
2.48	-0.15	0				-1.46	-1.725	-0.02	
4.145	1.285	0.57	0.075	-0.9212	-0.9675	-2.045	0.49	-0.075	-0.02
3.17	0.84		0.52	-1.621	-0.7525			0.78	-1.4
0.33	-1.14		-1.04		-2.022	0.24		-1.05	
0.7141	-0.2559	-0.03594	-2.096	-1.837	-0.4784	0.1641	-0.2459	-0.4959	0.05406

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.71	0.44	0	-2.19	0.9288	-0.2625		-1.05	-0.46	0.31
3.282	-1.008	0.9625	0.9125	4.421	0	-0.5575		0.7425	-0.0375
3.05	0	0.7	0.9	4.189	0.2575	-0.42	-0.59	0.56	-0.32
-0.225	1.625	1.745	-1.135			-2.755	0.335	0.225	-2.495
0	1.37	1.61	-2.44	3.049	0.0575	-2.56	0.81	0.73	-0.15
0.89	2.68	2.36	-1.06	3.179	-0.4825	-0.92	1.45	1.27	5.37E-10
2.51	0.6	2.31	0.13	2.879	-0.3025	-1.24	1.29	0.17	
1.364	1.064	2.244	3.694	2.103	-1.448		-0.05594	-0.5859	-0.1359
0.9725	0.1725	2.032	-1.778	-0.06875	0	-2.598	-1.068	-0.9475	-1.168
0.3456	1.186	1.136	-0.8144		-1.457	-1.504	-0.8144	-0.9744	-0.9744
3.331	3.771	2.051	-1.609	-0.1306		-2.529	2.211	0.1206	-1.909
1.506	0.8756	2.786	-2.614	-1.826	0.8831	-0.2344	-0.4144	0.7556	-1.954
0.1412	1.111	2.901		-1.4			-0.08875	-0.9187	
0	-0.37	2.61	-1.43	-0.19	0.4675	1.28	0.94	0.85	-1.1
1.031	-1.219		-1.269			-1.919	-0.6787	-1.319	-0.5888
-0.17	0	0.25	-0.85	1.529	1.148	-0.17	-0.75	-0.63	
0.1491	0.2691	1.049	-1.151	1.728	-2.513	-1.491	-0.6009	-0.03094	-1.951
0.3606	-1.089	-0.1594	-0.4194	-0.2206		1.361	1.411	-0.1494	-0.4994
-0.4875	-0.4275	0.0025	-0.0575	-0.8388	0	-0.9975	-0.9075	0.4125	0.4325
-0.5675	-0.4875	0.9325	0.1825		0	-0.2175	1.012	-0.0775	0.2325
-0.485	0.035	0.745	-0.545	3.154	3.233	-1.485	-0.405	-0.345	-0.035
-1.458	-0.8275	-0.0475	4.652	2.231	0			-1.008	
0		0.37	5.5	5.089	3.188		-0.42	0.46	-1.03
0.02906	-0.4809	0.3691	4.169	0.5578	0.1566	-0.9809	0.4691	-0.1809	0.2091
1.255	1.865	4.145	-0.025	-0.08625			0.805	-0.655	-2.105
0.97	0.74	0.5	-0.16	-0.6112	-1.762	-1.15	-0.73	0.07	-1.58
1.101	0.08125	2.291	-0.9888	-1.91			0.3413	-0.7187	-0.2288
1.541	0.4112	1.251	-0.6588	-0.32	-1.961	-1.929			-0.7388
0.75	0	0.36	-0.68					-0.77	0.43
0	-0.13	1.02	-0.42		1.688	0	-0.5	0.05	
0	1.42		-0.83	2.999				-0.6	
-0.495	0.335	0.635	-0.025	0.1738	0.0825	0.595	-0.195	-0.175	-0.76
0.44	0.23	0.92	0.39	-0.1612	-0.2425	1.17	-0.09	-0.34	0.34
-8.20E-09	-0.34	-0.06	-0.69		-1.542	-1.39	0	-0.73	0.82
1.9	0.07	0.84	-1.71		-0.3525	-0.98	-0.45	-0.5	
2.23	-0.08	2.19	-1.27	1.299		-0.73	4.02E-09	-0.54	-1.57
1.53	3.02	1.78	-0.23	-0.8813			0	-0.57	0.18

Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
2.12	2.92	2.87		-1.871		0.02	0	-0.04	0.31
-0.2788	0.4112	0.8712	4.161	0.2	-2.531	-0.4288	-1.199	-1.599	-0.1688
-0.7531	0.7369	0.4669	4.327	0.1256	-2.776	-0.5731	-2.123	-3.003	-2.153
-0.6	1.17	2.24	0.07				-1.88	-1.69	-1.94
1.79	-0.75	0.04	-0.69		-1.522	-1.42	-0.96	0.26	-1.3
4.242	-0.7075	-0.0175	-0.1975	0.00125	-4.34	-1.198	-1.947	-2.827	-3.858
3.58	0.16		-0.16	-0.7012	-1.362	-2.6	-3.39	-2.27	-0.88
2.869	-0.7209	1.059	-0.8109	1.818	-1.513	-1.311	-2.121	-1.081	-1.351
5.128	0.1481	4.838	0.2981	-0.8231	0.5356	-0.7219	0.9781	0.5181	-0.3619
5.171	0.3106	4.611	-0.1794	-0.7606	-1.002	-0.8794	0.8706	0.4306	0.3306
0.7	0.78	2.89	-0.19		1.538	-1	0.66	-0.05	-0.14
0.005	3.775	3.775	-0.205	0.7838	-1.147	-0.275	0.875	-0.005	
0	4.65	4.65	-0.69	0.2388	-0.4225			-0.33	-0.77
-2.03	2.88	2.631	-1.65	-1.451	-2.452	-0.66	-1.06	1.14	-0.33
3.491	3.651	4.001	0.2812				-0.5487	-0.4287	
2.971	3.131	3.389	-0.2394	-0.8006	-2.882	-3.351	0.03063	-1.199	-0.3994
1.869	1.339	1.451	-1.771				-0.2709	-2.281	
-0.01875	0.6712	1.831	-2.029	-1.83	-2.171	-2.659	-1.099	-1.309	-0.3587
-0.8487	0.1012	0.8941	-3.999	-1.6	-1.841	-3.119	-1.759	-1.949	-1.529
-0.9759	0.01406	0	0.9841	-2.937	-0.7784	-2.576	-1.546	-2.506	-1.536
-1	0.52	1.668		-4.821		-4.04		-1.72	
0.4481	1.008	2.74	-1.792	-1.113	-0.6644	-1.852	-0.9319	-1.842	-1.592
0.96	1.03	2.57	-2.09	0.2788	-1.872	-3.21	-0.85	-1.36	-1.97
1.14	1.1	3.614	-1.14	0.5388	-2.332	-3.26	-1.16	-1.82	-1.94
2.224	2.834	4.029	-0.8159	-2.467	-2.548	-2.786	-0.07594	-2.036	
2.499	1.909	3.78	-3.801	-1.602	-0.6634	-4.921	-0.4509	-2.851	
3.01	2.15	3.94		-1.111	-0.7325		0	-1.1	
2.68	2.5	4.719	-2.68	-1.901	-1.442		0.05	-1.93	
-0.2809	4.159	3.078	-2.561		-1.383	-0.2609	0.9291	-1.611	-1.91
-0.7319	2.488	4.385	-1.752	-1.183		-0.5919	0.4681	-1.282	-2.76
0.495	1.995	3.71	0.675	-0.8262	-1.847	-2.145	0.125	-1.485	-0.9009
0.23	1.41	3.608	-1.76	0.4788	-2.322	-2.56	0.15	-2.49	
3.498	4.578	2.38	-2.152	-1.583	-2.514	-2.272	-0.4219	-1.302	-1.26
2	1.14	3.482	-1.32	-2.001	-1.542	-2.2	0	0.36	-1.712
0.8625	3.692	2.315	-1.438	0.00125	-3.22	-0.8375	-0.2775	-1.967	-0.16
-0.015	0.735	4.64	-3.915		-0.5375	-2.615	-1.495	-3.375	-0.1875
-8.20E-09	2.04		-2.95	-2.751		-1.48	0	-2	-3.575

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
0	2.19	4.31	-1.61				-0.2	-2.83	
0.26	2.82	1.92	-1.8	0.1488	-1.462	-2.12	-0.76	-2.27	-1.3
2.15	-0.04	0.44	-2.41	-1.871	-2.632		-0.91	-0.28	-1.1
1.46	0	1.5	-0.29	-0.9812	-0.9825	-1.3	-0.92	1.02	-0.45
0.5681	3.798	3.658	-2.602	-1.233	-0.9944	0.02812	0.1781	-0.5719	-1.362
0.59	3.72	3.78	-0.68	-0.5812	-0.5625	0	0.25	-0.11	-0.42
0.1281	3.748	3.568	-1.552	-0.6531	-0.9444	0.1781	0.6981	-0.2119	-0.6319
3.551	2.331	2.391	-1.659	1.169	-1.082	-1.779	-0.8294	-1.709	
0.3413	1.941	2.461	-2.959		3.569		-0.7387	-1.549	
0.94	1.07	0.63	0	1.329	0.6175		-1.85	-2.85	-3.54
1.568	2.628	1.588	-1.302	4.707	1.026		-0.2919	-1.232	-1.965
0.015	0.055		0.305	0.05375				-1.145	-1.982
-1.622	0.9181	2.458	-1.162	-1.963	6.583	-2.432	-0.9519	-0.8319	-0.865
5.655	-0.035	-0.105	-0.785		4.928	-1.645	-0.955	-0.835	
1.04	-0.64	-0.09	-0.7	-0.7912	3.818	-0.46	0.26	-0.01	
2.89	-0.83	0.16	-0.16	0.00125	2.58		0.25	1	2
2.732	-0.4475	2.112	0.2425	-0.4722	3.567	-0.8175	-0.0575	1.393	1.962
0.7291	-0.0009375	0.8591	-0.01094	0.295	3.018	1.309	-0.3609	0.6491	1.089
1.226	1.04	1.226	-1.084	1.389	-2.032	0.5962	-0.2937	-0.4037	-0.7538
-0.37	0.8441	1.21	-1.77	1.079	-1.782	-1.65	1.21	-1.32	0.48
-1.116	3.35	0.82	-0.7659	-2.441	-1.272		0.8241	0.1841	-0.6359
-0.3	-0.08	3.32	-3.47	-0.7512	-2.296	-1.13	0	0.8	1.8
0.08	3.68	1.65	-0.46	-0.015			1.41	-0.95	1.12
1.86	2.666	1.356	0.01625	1.109	-2.692		1.1	-0.38	5.37E-10
2.356	2.29	2.49	0.32		0.0975	-1.054	0.1963	-0.4337	
-2.57	0.27	1.79	0.45	2.569			-0.84	-2.5	
-0.94	-0.25	0.8	0.12	0.6688	0.6375	-0.23	-0.32	-0.22	-0.01
3.61	0.76	2.93	-0.54	0.8988	1.948	-0.8	0	0.54	0.04
4.65	1.19	1.74	0	1.269	0.5775		0.56	0	-1.2
0.9	1.5	-0.03	-0.17	1.909	-0.7325	-0.04	-0.19	-0.37	0.25
1.94	0	1.74	-1.1	-0.2662		-1.44	-0.65	0.03	0.4
-0.42	0	1.46	0.11	-2.472		-0.64	0.15	-0.3	
-0.69	0.305	0.775	-0.355	-2.181			0.05	-0.32	
-0.145	2.059	1.049	-1.651	-1.711	-3.613	-0.525		0.945	-1.17
-1.201	0.1	0.73	-0.1		-5.332	2.359	0.6091	-2.571	-0.835
0.35	0.18	0.61	-0.59			1.04	-2.24	-2.92	-1.621
-0.61					-1.772	0.73		-0.18	-2.21

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
	0.3112	1.521	-0.00875			-0.4088	-0.7887	-2.469	-1.659
0.1206	2.621		-0.2794	-1.351	-1.052	-0.4794	1.001	-2.919	1.701
-0.85	0	1.34	-2.18				-0.88	-2.5	
-1.1	0	3.48					-0.86	-3.74	
0	1.18	4.41	-3.24	-2.461			-0.02	-2.29	-1.32
0	1.2		-1.3	-1.581				-1.35	-0.72
0	0.3	2.33	1.07	-2.421	-2.322		-1.35	-2.81	-4.16
0.36	0	2.36	1.39	-4.191	-5.532	-2.77	-0.75	-3.44	-3.73
0.46	0	2.26	1.34	-3.441	-5.522	-2.76	-0.89	-3.69	-3.72
0	-0.42	2.4	0.41	-2.581	-2.762			-2.83	-2.16
-1.229	1.211	5.191	-1.669	-3.271		-0.5094	0.4406	-2.199	-1.969
-0.09	0		1.54	-1.041	-1.462		0.28	-1	-0.43
-0.55	-0.78	2.83	1.97	-3.081	-3.262	-1.23	-0.13	-1.25	
0.1	-0.1	2.51	-0.85	1.149	-1.512	0		-0.55	-0.47
0.2612	1.231	0.1412	-0.1688	-0.14	-0.2912	0.3412	0.3813	-0.4187	-1.679
0.9	1.14	2.57	-2.07	-0.3512	-1.462	-0.44	-0.49	-1.54	-0.02
0.5191	0.8591	2.559	-2.041	-0.9322	-1.603	-0.5809	-0.5809	-1.801	-0.2909
0.52	0.31	1.68	-0.64	-0.1312	-0.3825	0.31	-0.01	0.06	$5.37E-10$
1.171	0.6706		-0.07938	-0.2606	-0.8219	-0.09938	-0.5594	-0.1594	-0.1594
0.05	1.06	0.3	-0.07	0.6387	0.1275	-0.9	-0.29	0	-0.68
-0.09	1.41		-0.34			0.09	0.24	0.49	
		0.1747		-1.017			-0.1553	0.1147	
-1.154	0.2062	0.9462	-0.4038			-0.5938		0.2663	
-0.4059	1.054	0.2241	-0.5259		0.3316			1.134	
0.04	0.46	0.03	-0.52	0.7387	-1.032		-0.05594	0.16	-0.91
-0.8688	0.08125	0.7612		0.12	0.3988	-1.389	0	-0.03875	-1.179
0.805	-2.255	1.255	-1.205					0.415	-2.985
0.38	-0.99	0.92	-0.94	0.2988		-0.64	-0.015	0.94	
3.475	3.055	3.675		0.2437			0.59	-0.185	-0.675
1.56	2.13	1.9	0	-0.8912	3.228	-1.12	-0.125	0.02	-0.67
1.106	4.726	3.826	-1.024				0.12	0.1456	-0.6944
0.11	2.49	4.02	0	-1.581	0.2375	-0.32	1.586	-0.2	0.69
0	5.52	5.64	-0.56	-0.3612	-1.342	-0.9	0.76	-0.24	0.36
-0.05	5.53	5.93	-0.73	-0.5313	-0.7725	-0.48	1.93	0	-0.15
1.246	-0.5438	6.926	-0.6138	-2.415			2.706	0.3363	0.3062
1.816	-0.7144	7.436	-0.04438			-0.5844	2.916	0.4856	1.196
1.451	0.8412	6.231	-0.3288	1.99	-0.1512	-1.029	2.311	0.3613	-1.409

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.2	2.75	7.92	0	1.419	-1.142	-0.7	3.6	0.37	-0.66
0.36	3.39	5.76	0	2.869	-0.2425	0.34	2.04	0.12	0.09
0.5012	3.051	5.271	0.04125		-0.04125	-0.3988	2.251	0.9113	0.8812
0.7891	4.979	6.139	0.3491	0.06781	-0.4334	-1.571	2.659	0.8191	0.04906
0.8381	3.768	6.668		-0.6231	0.03563	-1.522	2.598	0.5481	
0.66	4.18	7.14	0.4	-0.1412	0.5175	-1.04	3.19	1.03	5.37E-10
0.7156	2.676	4.226	-0.5344	-0.5756	1.243		1.636	-0.8244	
1.04	4.65	5.29	-0.28	-0.5412	-0.3025	-0.54	1.48	-0.09	-0.36
3.212	0.0225	4.542	-0.5775	-0.6988	0	-0.8475	0.6825	0.5125	-0.2775
3.121	0.5412	3.731	-1.209	-1.01	-0.3912	-1.329	0.8813	0.3713	0.4312
2.79	-0.16	3.09			0.4275	-2.35	1.08	0.14	
4.05	0.14	3.78	0	0.3688	-1.562	0.05	0.96	0.34	-0.08
1.351	1.221	2.491	1.151	0.46	1.529	-0.8787	-0.04875	-0.6587	0.5413
2.69	2.31	3.25	1.79	-0.1913			0	-0.44	
3	3.24		-0.97	0.8488	-1.612	-0.78	0.2	-0.93	5.37E-10
1.161	1.981	1.311	0.1312	-0.7	-0.09125	-0.1688	-0.3287	-0.09875	-0.7988
1.428		1.738					0.06813	-1.232	
1.226	1.446	1.296	-2.454		0.05375	2.226	0.6263	-0.6937	-0.2138
0.7312	1.281	1.011	-2.549	-0.57	-2.111	0.2113	0.4013	-0.7387	0.2112
1.879	1.879	1.919	-0.6609	-2.262	-1.853	0.6091	0.8591	0.1591	0.3391
1.095	3.835	3.925	-1.125		-2.167	-3.045	0.185	-1.175	-1.835
1.36	4.15	4.01					0	-2.47	-2.28
-1.299	3.091	3.161	-2.759	-0.3306			-0.4994	-2.959	
1.244	3.204	3.694	-2.036	-1.177	-2.818		0.07406	-1.886	-1.916
2.28	-0.91	2.23	-0.28	-2.401	-0.5025	-0.5	-0.22	0.01	-1.02
2.36	-0.22	2.38	-0.41	-0.5912	-1.262	-2.41	8.05E-09	-0.6	-0.87
-1		2.62	-1.46	-1.631	-3.192	1.55	-0.31	-1.44	-2.13
1.92	0.08	2.06	-1.16	1.739	1.648	0.26	-0.2	-0.08	-0.68
4.54	1.36	0.43	0.17	-2.801	-0.9825		4.71	1.75	
4.781	1.351	1.701	0.7812	1.177		-1.799		-0.1487	
-0.1419	-1.652	3.158	-1.722	1.177	-1.284	-2.262	0.3481	-1.602	-1.802
0.2406	2.311	4.521	0.000625	1.499	-1.342		0.6706	-1.169	-1.659
-0.33	-0.22	4.45	0.16	-0.6412		-1.13	1.57	-0.16	-1.09
2.051	3.791	5.151	2.321	2.84	-1.561	-0.3787	1.571	-0.4587	-2.079
1.84	1.68	1.5	0	2.739	-1.562	0.22	0.22	-0.25	-2.5
0.2681	0.3381		0.06812	-1.553	-2.454	-0.4819	-0.06187	-0.2219	1.148
-0.275	1.095	0.955	1.135	-1.036	-0.4575	-0.115	0.625	-0.505	-0.385

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Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
-1.03	1.25	-2.91E-09	1.3	-0.6812			-0.2	0.36	0.04
0	-0.45	0.33	2.53	0.6388	-1.832	-0.34	-0.26	-0.55	-0.58
	0	0.81	3.23	-0.7912	-3.102	0.39	-0.8	-0.89	-0.74
-0.12	0.3512	-0.4488	0.6312			-0.2488	-1.449	-0.07875	
0.6312	-0.8	-0.21	-0.55	-2.151	-2.912	0.23	0.06	-0.4	0.03
-0.77	-1.715	1.345	2.905	-3.686			0.865	-1.125	
-0.075	-0.3409	1.119	1.909			-0.1809	0.6991		
2.089	-0.1819	1.218	1.018	-1.313	-2.244	-1.102	-0.3919	-1.152	1.428
2.918	2.06	1.34	-0.26	-2.951	-2.712	0.85	6.89E-09	-0.44	-0.39
1.72	2	1.98	0.3		-2.112	0.54	-0.14	-0.11	-0.55
1.2	-1.17	0.25		-2.901	-4.432	0.42	-2.12	-2.49	0.47
-0.35	0	0.26	0.47	-4.251	-2.662		-1.38	-1.08	-0.81
0.63	1.26	2.09	-1.32	-3.381	-4.182	-0.78	-0.61	-1.63	-1.76
0.49	1.38	1.02	-1.12	-3.681	-6.171	-1.19	-0.52	-1.67	0.3112
0.21	0.8712		0.2612	-0.39	-0.9212	0.4912	0.4613	-0.02875	-0.4388
-0.04875	1.131	0.6612	-0.1288	-0.36	-0.3312		-0.4287	-0.6087	-0.1688
2.951	0.6612	0.9812	1.081	-2.89	-0.4425	1.31	-1.09	0.3213	2
0.01125	0		-0.73	-1.951	0.1175	0.15	-2.59	-0.61	0.26
2.04	-0.19	-0.11	-0.86		0.0675	0.23	-3.06	-1.54	0.08
1.29	0.12	-0.06	-0.87	-1.591	2.806	0.2981	-0.1919	-1.6	1.078
1.6	-0.2919	-1.212	-1.822	-2.723	1.108	0.63	-0.72	-0.3619	0.61
-0.4419	-0.58	-1.62	-2.73	-2.681	1.518	0	0.88	-0.71	1.4
0.7	-2.03	-1.59	-3.31	-3.701	3.463	-0.7244	-2.954	-2.21	-2.154
-0.1	-2.494	-0.2644	-2.544	0.006875	-0.4344	0.8881	0.2581	-1.904	0.3281
0.1456	-0.1819	0.1481	-3.312	0.1387	-0.2125	0.63	0	-1.362	-0.2
-0.1719	-0.18	-0.95	-1.01	1.109	-0.2725	-1.49	0.12	-0.11	-0.99
0.1	-0.01	1.1	-0.26	0.00125	-0.9	-0.2875	-0.5375	0.01	-0.2275
0.38	2.232	1.012	-1.108	-1.401			-0.59	-1.127	
0.3025	0.71		0.02		-0.8125	0.4	1.61	-0.53	0.85
-1.38	0.38	-0.09	-3.61	-0.5112		-0.26	0.77	-0.38	0.525
-0.22	0.52	0.46				0.005		-0.66	-0.105
	1.325	-0.305	-0.005	-0.9862		1.905	-1.975	-0.545	-0.06937
1.085	1.405	0.135	-2.365	-0.9272	-0.6319	0.2506		-0.485	-0.03594
1.455	0.02062	0.9641	0.3906	-0.59	0.6216			0.08063	
-1.019	0.5341	-1.589	-1.026	0.1591		0.2212		-0.2359	
-0.6959	-0.7188	0.7103	0.1712		-0.9722			-1.289	
0.7212	0.4003		-0.5197					0.6603	
-0.6697									

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.73	0.51	-0.25	0.94	0.5888	-1.432	-0.93		-0.36	0.21
0.57	0.38	0.99	-0.38	0.5588	0.8275		-0.64	-0.62	-0.38
0.3613	0.03125	1.181	-1.549		-0.2612	-0.5887	-1.639	-0.6487	-0.3887
-4.049		-3.149	1.061	-1.65	-5.891	-2.569	1.621	-1.769	
-1.052	1.188	-1.572	-1.312	-2.333	-3.434	-2.942	-1.992	-0.7719	1.628
-0.63	1.08	-1.15	-1.83	0.9188	-3.352	-0.54	-0.55	0.35	-0.2
0.2606	0.5506	-0.3594	-1.539	2.929		-2.069	-1.489	0.05063	-0.5594
0.2112	0.7512	-0.3288	-2.389	0.94	-3.471	-2.329	-0.2587	-0.1087	0.1012
-0.2119	0.07812	0.6581	1.788	2.367	-5.134			0.5081	
-0.18	0.11	0.06	0.58	1.539	-2.302	-0.47	-0.47	0.73	5.37E-10
3.18	0.07	1.79	-1.8	-0.1812	-1.942	-2.5	0.45	-1.43	0.5581
0.1281	-1.082	-0.5319	-0.6719	-0.9631	-1.574	-2.232	3.638	-1.722	-1.17
1.89	1.69	1.31	-0.09	-0.4113	-1.392	-2.53	-1.30E-09	1.30E-09	-0.9587
0.7513	1.111	0.9312	-0.2988	-0.51	0.01875	-1.419	-0.8787	-0.4687	-2.54
-0.65	-0.05	1.58	-0.52	0.8387		-1.41	0	-0.81	-1.944
-0.5038	-1.474	0.1562	0.6862	-0.155	-1.606	-1.344	-1.394	-1.234	-0.4988
-1.399	-0.3888	0.03125	0.4512	0.86	-2.031	-0.2387	-0.2687	-0.5187	0.2
-0.55	-1.12	0.07	-0.31	-0.1312	-0.1525	-0.17	-0.29	0.66	-1.368
-1.368	1.072	-1.468	-0.5275	-0.9488		-1.028	-0.1975	-0.1375	5.37E-10
-2.22	-2.34	-0.71	-2.04		-4.282	-2.12	-2.89	-0.01	-1.235
-0.545	-1.915		-1.815	-0.4662	0.2125	0.255	0.065	-0.715	4.822
-2.848	-1.318	-0.3275	-2.248	0.00125	-3.19	-1.348	-0.7975	-0.6075	0.9381
-1.862	-0.9319	-1.832	-1.812			-0.4419	1.008	-0.3119	-0.305
-0.655	0.115		-0.115		-0.9875	-1.605	-1.195	-0.645	-0.3519
0.4781	-1.102	-0.6119	0.8381	-0.4431	-0.2444	-0.9719	-0.4619	0.4281	-2.049
		-1.439	-1.629			-0.9887	-1.999	-0.4987	5.37E-10
-0.05	0.42	0.6	-0.98	0.3088	-0.8225	-0.54	-1.03	-1.47	-1.355
0.945		-1.625		-3.566	-5.328		-1.855	0.585	-0.2509
2.229	-2.601	-1.231	-3.261	-1.062		-0.7709	-1.431	0.7891	-2.228
-0.1381	0.5519	-0.2981	-1.898	-2.839	0.01938	-0.1881	-0.06812	-1.608	
0	0.08		-0.6				-1.36	-2.46	
1.978	-1.172	-4.292					-5.312	-5.192	
-0.3759	-0.2959	1.664	-1.426	-0.6672	-3.308	0.5741		-1.676	-0.2759
0.8956	-0.1044		-0.4244		-0.8369		-1.644	-2.004	
-0.285	0.085	-1.225	0.175	-0.09625	-2.407	0.245	-0.455	-1.625	-0.795
0.43	0.73	-0.37	-0.38	-0.01125	-1.942	-0.22	-0.22	-1.72	-3.53
-0.58	1.82	0.11	-1.65		-3.072	1.34	-0.75	-0.85	-1.84

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.5319	2.068	-0.01188	-1.502	0.05687	-3.244	0.9881	-0.3719	-0.8019	-1.442
0.15	1.67	0	-1.01	-1.361	-3.072	-0.06	-0.77	-1.01	-1.33
-0.6044	2.256	-0.2744	-0.5644	-1.276	-3.267		-0.7444	-2.244	-1.934
-0.215	3.695	-0.225	-2.435	-1.016	-2.307		-1.575	-2.075	-2.515
1.3	0	0.28	-2.11	-2.691			-1.1	0.1	
-0.775	-0.885	1.175	-4.265			-6.085	-2.715		
-0.4288	-0.9288				-2.411			-1.319	-2.929
-0.465	0.465	-1.225	-3.315	-3.016	-4.507	-1.885	-1.795	-2.815	
1.79	0.68	-0.11	-2.1	-4.331	0.1875	-4.65	-3.32	-2.1	-2.23
1.894	0.4841		-1.966	-4.347	0.1216	-4.406	-3.136	-2.016	-0.7359
-0.03	-1.35	0.03	-0.61	-1.411	0.1375	-2.38	-2.36	-1.09	-1.18
1.58	0.18	0	-3.29	-2.351	-0.0825	-4.19	-2.96	-3.12	-2.49
0.61	-1.22	0.01	-3.38	-3.601	0.4975	-2.22	-1.94	-2.53	-2.14
-0.8288	0.8012	-0.2788	-1.089	-1.72	-1.731	-1.139	-0.7987	-3.069	-1.909
-0.7809	0.4391	-1.571	-1.681	-2.442	-1.223	-0.7309	-2.121	-1.731	
-1.27	0	-1.89	-2.12	-3.221	-1.582	-1.83	-2.44	-2.71	-3.15
-1.29	0	-2.2	-1.74	-2.961	-1.202	-0.39	-2.68	-2.37	-2.88
-1.62	0	-2.12	-2.85	-3.991	-2.112	-1.88	-2.78	-2.75	-3.21
-0.9788	0.2112	-1.279	-2.349	-2.81	-1.011	-1.979	-2.339	-1.669	-3.199
-0.5688	0.2112	-1.049	-1.949	-3.11	-0.7612	-1.489	-2.449	-1.259	-2.679
-2.355	-0.9147		-3.995	-5.256	0.3928		-2.545	-4.505	
1.19	0.38	1.29	-2.25	-4.191	-1.372		-1.35	-2.96	-3.62
1.33	0.5		-0.64	-1.701	-0.2325	-2.74		-2.08	
-0.3087	0.7512	0.3312	-2.339	-0.79	-0.9612	-2.089	-1.369	-1.889	-2.679
0.3891	0.4091	-0.09094	-4.381	-4.772	-0.1734	-3.591	-3.261	-3.901	-4.311
0.7	0.26	-0.45	-0.59	-4.111	-3.412	-3.53	-2.96	-1.23	-0.87
0.48	0	-0.79	-1.03	-2.661	-1.512	-0.71	-2.97	-1.64	-0.51
0	0.29	-1.06	-1.07	-1.971	-1.792	-1.32	-2.28	-1.71	-0.73
-0.1319	-1.472	-0.7319	-5.482	0.5169	0.8256	-4.602	-4.652	-4.952	-5.562
-0.1619	-1.352	-0.9219	-5.132	0.6169	0.8856	-4.112	-4.622	-5.182	-5.952
0.715	-0.235	-0.025	-0.935	-1.616	-1.117	-3.425	-1.695	-2.115	-2.525
0	-1.36		-3.6	-1.601	-0.8425	-2.64	-2.19	-3.33	
-0.3194	-1.869			-2.171	-1.412		-2.589	-4.639	-3.169
0.08	-1.49	-3.74	-4.27	-1.541	-0.6625	-6.71	-2.52	-4.06	-3.09
-0.1	-1.51	-3.34		-1.441	-1.002		-2.43	-4.19	-3.8
-1.446	0.5941	0.6341	-2.226		-4.108	-2.276	-0.9159	-0.2259	-2.826
0.725	1.105	0.355	-2.665	-4.126	-4.147	-0.355	-1.375	-1.785	

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0	0.29	-0.36	-5.23	-5.831	-4.592	1.76	-1.88	-5.5	-1.08
0.09	-1.55	0	-1.12	-4.561	-4.322	0.04	-1.58	-3.22	-2.57
0.3741	-0.9659	-0.3359	-0.2559	-3.357		-3.676	-1.676	-2.086	-2.736
-3.032	0.3481	0.1981	-4.182	-3.563	-1.084	-4.422	-3.182	-3.912	-2.842
0.56	0	1.77	-0.88	-2.191	-5.652	-1.82	-1.51	-1.5	-1.42
1.274	1.124	-1.276	-3.106	-1.527	-3.198		-2.336	-3.056	-3.716
2.381	2.281	0.5306	-4.109	-1.361	-6.252	-4.809	-3.059	-4.159	
0.1841	0.5941	0.6141	-4.536	-4.757	-5.518		-3.006	-3.126	-3.446
-0.7088	-0.4088	0.06125	-3.859	-4.4	-6.061	-5.449	-3.539	-3.909	-4.999
-0.26	0.49	0.61	-1.4	-7.091	-6.272	-5.61	-3.66	-4.64	-6.79
-0.1675	0.5425	-0.1675	-3.638	0.00125	-1.2	-4.048	-3.367	-3.347	-4.008
-0.9175	0.4625	-0.8075	-5.918	0.00125	-1.64	-6.038	-4.347	-5.967	-5.578
0.3081	-3.302	-0.3019			-6.114	-5.672	-3.452	-4.182	-5.092
0.1181	-2.462	-1.889	-4.862			-7.519	-3.032	-4.772	
0.8412	-3.129	0.5997	-4.599		-6.961	-3	-5.399	-4.869	-2.96
0.2297	-0.6103	0.1806	-3.1		-3.323	-2.859	-2.51	-2.44	-3.499
0.07062	-0.6494	0.6806	-2.309	-3.771	-2.832	-1.399	-3.119	-2.839	-2.379
0.000625	-0.3194	0.5181	-2.679	-3.493	-3.532	-3.352		-2.239	-4.162
0.4997	-0.6619	2.44	-2.952		-2.944		-2.792	-4.332	
						-2.73		-5.36	
1.101	0.4712	1.241	-3.029	-3.05	-4.071	-1.529	-2.419	-2.799	-4.109
1.26	1.22	2.45	-3.59	-3.651	-4.732	-3.71	-1.76	-3.9	-4.25
1.08	0.13	0.61	-0.78	-0.8712	-1.162	-2.9	-2.27	-1.58	-2.13
-1.221	0.2491	0.3491	-2.461	-1.997	-4.603	-0.8109	-0.02094	-1.191	-3.121
	0.3741					-1.636	-0.04594	-1.066	
-5.294	1.026	0.3356	-1.706	-3.74	-6.217		-1.654	-1.624	-5.154
-2.099	0.9312	0.4812	-3.059			-3.319	-1.989	-1.359	
0.7606	-0.3094	2.531			-2.454	-1.799	-1.689	-2.639	-3.259
1.728	0.4581	1.148	-2.652	-1.763	-1.824	-2.672	-1.482	-1.942	-1.152
0.2781	0.9381	0.8781	-3.262	-2.063	-1.432	-1.762	-0.5219	-1.532	-1.122
-0.29	-0.85	-0.19	0	-1.581	-3.132	0.49	-1.38	-0.57	-1
-0.65	-1.19	-0.79	0		-2.212	0.49	-2.89	-1.19	-1.93
-1.3	-2.84		-2.77	-4.031	-2.692	0.23	-1.43	-1.22	-1.79
0.4	-2.08	-1.66	-2.44	-2.021	-2.994	-1.2	-2.33	-2.49	-0.79
0.2781	-2.482	0.1581	-1.052	0.1169	-4.872	-3.872	-2.462	-1.762	-2.662
0.39	1.05	1.63	-2.99	-2.791	-3.102	-1.66		-3.04	-1.51
0	0.24	-1.28	-2.06	-4.081			-6.03	-1.91	-2.14

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
-0.75	0	-0.88	-3	-1.581	-1.932		-2.17	-1.98	
1.818	-0.3419	0.3981	-1.492	-2.463	0.5356	-1.562	-1.202	-0.01187	-1.802
0.625	-1.055	-0.075	-3.355	-2.256	2.473	-3.155		-2.015	-2.435
1.164	-3.216	-0.04594		-4.647	2.382		-1.846	-2.236	
0.035	-1.495	-0.055	-2.165	-0.3662	-1.017	-2.395	-1.805	-4.385	
0.91	-1.56	0.31	0	-0.2412	-1.932	-2.25	-2.2	-1.64	-0.7
2.511	-0.9888	0.09125	-0.5088	-1.39	-0.1212	-1.399	-2.079	-0.6087	-0.2088
-0.29	1.97	-0.21	-2.91	-2.091	2.698		-2.7	-2.02	-2.37
1.18	-0.69	-1.13	-1.81	-2.681	4.048	-5.17	0	-4.1	-2.13
0	-0.29	1.44	-0.75	-1.781	1.698		-1.5	-3.55	-2.88
-0.12	0	-0.49	-2.27	0.3088	1.828	-1.39	-1.7	-1.46	-1.93
0.1741	-1.616	-0.8959	-1.666	-2.707	0.9416	-2.686	-1.816	-3.096	
-0.1	-0.84	0	-3.63	-2.191	-2.872	-3.95	-0.65	-1.88	0.84
0	0.73	0.34	-2.14	-1.541	-0.7425	-1.89	-2.52	-1.73	-3.19
0.5413	-0.3488	-0.5088	0.06125	-1.15	-0.8712	-0.2387	-1.699	-1.399	-0.6187
0.6813	-0.2788	0.08125	-0.2688	-1.64	-1.401	-0.5587	-2.119	-2.429	-0.6787
-0.9775	-0.5475	0.6025	-1.238	-1.479	0	-0.6675		-1.458	-3.518
-1.188	-1.978	-2.738	-2.898	0.00125	0.13	-2.428	-2.637	-2.837	-2.978
0	-2.4	-1.96	0.05	-0.8712	0.4075		-2.45	-2.75	-2.51
-2.375	-1.375	0.275	-0.275	0.8038	-1.667		-2.325	-2.405	-2.285
-1.562	-0.9119		-1.102	0.1369	1.016	-1.352	-2.632	-1.702	-2.112
-0.06	-4.26	0		-0.01125		-5.55	-3.72	-4.06	-1.21
-0.6353	-0.7953	0.3347	0.5347	0.7634	0.5722	-2.695	-2.535	-2.945	
0.5381	-3.422	-2.272	1.138	1.487	2.826	-3.292	-3.752	-3.482	-2.512
0.06	0.71	0.08	0	0.3788	1.078	-5.7	-3.43	-4.63	-4.92
-0.44	0.86	-0.41	0.25	1.079	1.318	-4	-3.17	-1.23	-4.22
-0.2019	-0.5519	0.02812	-0.7619		3.336		-3.852	-1.882	-1.622
0.08125	-0.8988	-0.4288	0.1712	-1.91	0.04875	-4.519	-0.2487	-3.299	-4.189
-1.69	0.85	0	-2.58		-2.462	-0.6	-3.15	-1.27	-0.08
0.12	0.68	-1.18	-3.12	-3.261	-3.162	-5.46	0.56	-2.22	0.7
-0.85	-1.17	0						0.29	-0.43
-0.1209	-2.571	0.8991	-2.381	-4.702	-0.2734	-0.8775	-0.3175	-2.561	-2.901
1.142	-1.258	1.622	-1.758		0	-0.81	-0.76	-1.288	-1.448
0.55	-1.14	-0.2	-1.21	-0.9312	1.008			-1.13	-0.88
-0.3075	-2.528	-1.628	-0.7275	0.00125		-0.2075	-1.627	0.4025	0.0625
0	-1.92	-1.46	-2.29	1.869	-2.032	-0.18	1.29	-1.87	-1.86
-0.33	-0.44	1.54	-2.99	1.369	-4.552	0.28	-0.23	-0.34	-5.07

Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.08		1.34	0.03	2.979	-2.882	-0.86	-0.03	-1.37	-0.32
-1.31	-1.47	-0.84	-1.09	0.01875	-1.412	2.54	-0.47	0.34	5.37E-10
-1.095	-0.955	-1.385	0.125		2.443	-0.125	-0.425	-0.285	-1.405
-1.3	-0.31	-0.84	-4.56E-09	-0.7512	-0.1925	-0.33		0.12	5.37E-10
-1.749	-0.6088	2.101	2.551	-1.01	-0.7712	-1.329	-0.6987	-0.7787	-1.609
-0.83	0.17	0	-0.76	0.4988	-0.0225	-3.77	-2.33	-0.84	1.32
-3.234	-2.744	-1.024	-2.494	-0.915	1.744	-3.414	-2.154	0.9163	
0.01062	-0.1894	-0.05938	0.4606	-0.6006	-0.01187	-0.4594	0.8406	0.2906	-0.6594
-0.225	-3.575					0.225	-1.595	-3.205	-2.945
-0.25	-1.17	2.62	0	-3.041	1.048	-1.78	-0.77	-1.29	-1.15
1.32	0	0.05	-2.51	-0.4012	-1.942	-0.7	-2.43	-2.63	-2.52
-0.62	-1.27	0	-0.19	0.3488		-0.38	-2.57	-2.57	-2.37
	-0.315	-1.155	1.725	-0.9262	0.5025	-1.275	-1.795	-0.675	-0.095
0.66	-0.46	-0.78	0	-3.411	-2.902	1.47	-1.26	-2.28	-1.07
-0.8288	0.7812	-1.689	-1.609	-2.77	-3.651	-3.989	-0.8987	0.3313	-2.169
-0.29	0	0	0.26	-0.6912		-0.52	-0.62	-0.87	
-1.28	-0.82		-0.14	-1.861	1.868	-0.18	0.59	-1.59	2.96
-0.36	-1.27	-0.87	-2.72	-3.721	0.8075	-4.26	-1.25	-3.19	-2.22
-1.255	-0.605	1.165	-0.635		-5.237	-2.795	-1.145	-1.925	-0.805
-1.928	-1.238	-0.4775		0.00125	-2.05	-1.208	-0.6075	-1.707	
-0.83	-0.93	-0.03	-0.97	-0.4813		1.78	-0.14	0	1.42
-0.835	-0.245	4.325	-0.895	-0.4963	-1.937	0.225	0.745	-0.225	0.395
-1.75	-0.73	3.3		-0.5713	-1.622	-0.71	0.15	0	-0.14
-0.8088	-0.2288	0.08125	-0.06875	-1.42	0.06875	0.1412	-0.6687	-0.4487	-0.1988
-1.119	-1.409	-0.9175	-0.2788	0.2	-1.351	-0.9988	-0.1987	0.3013	
-0.4875	-0.8975	0.255	0.2925	0.00125	-0.44	-0.2075	0.3425	0.6225	-0.1075
-0.855	0.015		-0.015			-1.375	-1.025	-0.615	
-0.58	1.49	-0.37	-1	0.1988	-0.9825	-1.5	-0.35	-0.92	-0.57
-0.79	-1.19	-2.305	-0.87	-0.1412	-1.152	0	-0.46	0.29	1.01
-1.595	-3.475	-0.915		-2.226	-2.207	-0.215	-0.645	0.215	1.245
-1.635	-2.615	-0.6	-1.66	-3.486		0.135	-1.195	0.405	
0.14	0	-0.2675	-0.1975	-0.7812	-1.592	-1.1	-1.76	-1.24	0.17
-0.4075	-0.0175	-0.5375	-1.688	0.00125	0.5	0.0125	-0.5375	-0.6575	-0.1175
	-1.098	0		0.00125		-1.938	-0.8475	-1.297	
-0.26	0.95	0.9125	-0.06	-2.621	-1.54	-0.13	-0.61	-0.06	0.38
-0.5375	-1.278	1.385		0.00125		-2.318	-0.3375	-0.9275	
0.365	-0.885		-1.145			-0.545	-0.835	-0.365	-2.375

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.39	0	0.54	-0.67	-0.1612	-1.622	-0.74	-0.77	-1.27	-1.3
2.32	0	-0.03	-0.93	-0.9712	-3.232	-2.67	-1.29	-1.6	-1.87
-0.75	0.7	0.6	-1.58	-0.6913	-1.142	-1.6	0	-0.43	
-0.7075	0.2025	0.2625	-0.2475	-0.08875	0	-1.658	-0.1775	-0.1275	
2.07	-0.46	-0.07	-2.43	-3.011	-2.912	-1.58	0	-1.14	-1.75
1.5	-0.1	-0.94	-1.96	-2.601	-2.522	-2.03	0	-1.42	-1.7
-0.09	-0.26	0.09	-0.91	-0.5112	-2.192	1.11	0.66	-0.22	-1.15
-0.5975	-1.498	-1.028	0.3525	0.00125	-0.52	1.402	-0.3075	0.0025	-0.0075
-0.7988	-0.1688	0.7012	-0.6588	-1.1	0.1688	1.631	-0.5787	-0.4687	-0.5888
-0.45	-0.8		-0.55	-0.3512	1.058	-1.09	0.74	-0.28	-0.31
0.145	1.585		-1.485	-1.386	-3.367	-1.855		-0.145	-1.415
-0.21	-0.02	1.5	-0.1	-0.2112	0.0075	0		-0.3	-0.4
-0.9744	-0.2244	0.4156	0.1756	-1.756	-0.5169	-0.5944	0.3756	0.4056	
0.8	0.86	-0.05	-0.22	-0.3812	0.8775	-0.21	-0.83	-0.86	5.37E-10
-0.6338	0.6462			-0.165	-0.6762	-1.624		-1.114	-1.314
-0.7488	0.5112	-0.08875	-0.4788	-1.29	2.989	-1.039	-0.9887	-0.3987	0.02125
1.51	-2.71	0.81	-0.05	-0.3612	-0.7425	3.12	-1.11	-1.76	-1.59
0.38	0	-0.35	-2.67	-2.301	-3.232	1.82	-1.59	-2.91	-1.2
2.66	0.07	0	-2.42	-1.531	-3.682	-0.07	-2.05	-2.27	
0.45	-1.42	-0.12	-2.95	-1.421	-0.4325	0	-1.79	-1.49	-0.39
-1.21	-1.56	-0.88	-1.1	1.069	0.6575	-2.18	-2.03	-1.95	-0.29
-1.15	0	0.8	-0.82	2.559	1.128	-0.87	-1.99	-2.18	-1.9
-2.63	-0.36		0.36	-1.911	-1.712			-4.04	
-0.3	-0.48	-0.73	-0.19	-0.1313	-1.402	-0.37	0	-0.94	-0.74
1.088	-0.9519	0.5281	-1.082		0.5756	-1.292	-2.052	-1.932	-1.162
1.066	-0.7444	2.716				-0.7644	-1.354	-2.474	
1.156	0.3656	2.416	-1.474	-0.1359	-1.657	-0.4544	-0.4144	-1.384	-1.484
2.545	1.715		-0.8347	-1.271	-0.02719	-2.075	-0.8847	-1.665	-1.915
1.87	0.62	0.25	-1.19	-2.619	-0.5725	-1.59	-1.3	-0.59	0.25
2.352	1.572	1.832	-1.968	-2.506	0		-0.1775	-0.1875	-1.138
0.595	2.665	1.205	-0.445	-1.041	0.6875	-2.065		0.795	-0.555
-0.35	-2.24	-2.08	0.36	-0.8012	0.0275		-2.04	-1.74	5.37E-10
-0.64	-5.12	-4.73	0.26		2.456	-2.57	-5.04	-1.38	0.31
-2.822	-2.412	-3.062	3.118	-3.283		-3.012		-2.792	-2.562
-0.8775	0.7525		0.8425	-0.08875	-2.742	0.3925	-0.3175	-3.488	-2.038
-2.65	0.06	-0.06	-2.01	-1.201		-1.63	-0.23	0.25	-1.77
-0.27	0	-1.69	-1.59	-2.571	-1.082	-1.82	-1.37	1.16	-1.53

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Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
-1.118	0.4325	0.2025	-4.878	0.00125	-1.96	-1.018	-1.907	0.8725	-2.428
0.2512	0.8812	0.1412	-0.3188	-1.71	-0.8112	-1.529	0.1713	-2.019	-1.439
	1.98	0.98	-1.58	-2.621	-2.762	-0.55	0.75	-3.49	-3.28
1.24	0.83	0.69	0.34	-0.5512	-2.722	-1.1	-0.4	-1.48	-1.41
0.5512	1.641	0.5712	-2.429	0.55	-1.231	-2.069	-1.679	-3.799	-2.249
1.721	2.111	1.871	0.4712	-0.79	-0.6112	-1.789	-0.1287	-1.299	-0.7488
-0.3387	0.8812	-0.06875	-0.8388	-1.03		-0.6287	-1.529	-2.459	0.7413
0.9541	0.9141	1.384	-3.376	-2.977	-4.158	-0.07594	-0.7359	-0.3259	
1.208	0.8381	1.498	-5.312	-3.313	-4.874	-0.2119	-0.8419	-0.3919	1.118
1.39	0.91	1.1	-0.06	-1.901	-1.662	0	-0.73	-1.81	-0.64
1.18	-0.03	0.9	-1.82	-1.921	-2.382	0.38	-0.67	-1.48	-0.82
1.32	0.5	0.75	-1.47	0.3388	-2.952	0.41	-0.39	-0.96	-0.33
0.92	1.34	1	-1.08	-1.661	-2.032	-0.18	-1.9	-1.78	5.37E-10
0.08	0.42	-0.17	-1.56	-2.091	-2.702	-3	-2.11	-1.27	5.37E-10
-0.6888	-0.02875	2.211	-1.389	-1.47	0.02875	-0.7888	-1.149	-2.659	-1.749
-0.2788	-1.379	0.4012	0.7212	-0.26		-0.9988	-1.529	-0.9287	-1.049
-0.3388	-2.219	0.5112	1.001	-0.02	-4.851	-4.189	-2.139	-3.339	-3.489
-0.08	-1.14	0.2	-2.98	-1.781	2.568	0	-2.21	-1.76	-1.43
0.1491	-1.491	-1.451	-1.911	-4.592	1.647	-3.321	-0.0009375	0.03906	
-0.7275	-0.6575	0.9325	0.3125	0.00125	2.52	-0.4975	-0.4575	-1.247	-0.6575
-1.24	1.04	-0.47	-2.34	-3.041	1.158	-1.9		-0.75	-1.26
-0.9019	0.2081	-0.3819	-3.682	0.8069	0.9156		-2.732	-1.092	
-2.959	1.481	1.801	-4.319			-1.119	-1.409	-1.789	
-0.29	1.44	0.11		1.499	0.1075	-3.77	-0.53	-1.22	-1.22
0.5241	1.534	0.6241	-2.686			-3.426	-0.7259	-2.176	0.9041
0.5112	-1.079	1.811	-2.269	2.949	2.759		-0.6887	-1.779	0.1612
-0.09	0.35	1.07	-1.83	0.2888	-0.0125	-2.37	-2	-1.56	0.41
0.48	0.32	1.1	-2.13	3.589	0.6675	-0.92	-0.09	0.08	
-1.1	-0.3219	-0.2	-2.6		-0.5325	0	1.08	0.93	-1.54
1.198	1.519	0.008125	-1.742	2.668	-1.994	0.2681	-0.8419	-0.8719	-2.152
0.7791	1.228	0.4491	-1.471	3.247	0.3566	-0.3509	-0.3509	-0.6609	
-1.202	1.815	-1.342	-1.802	4.204	-1.054		-0.8119	-3.172	-2.132
-0.025	0	-1.505	-2.905	0.5288	-0.7475	-2.505	-0.415	-2.585	
0.18	0.9525	-0.15	-2.13	1.691	-0.0825	0.42	-1.95	-1.71	-1.99
-1.688	-0.6175	-0.6175	0.5225	1.667	0	-2.808	-0.9775	-0.4675	-2.178
-2.482	-0.3219	-1.692	1.788	1.667	1.136	-0.3319	-1.662	0.1081	-2.392
-0.31	-0.23	-0.81	0.65	0.5687	0.6375	-0.99	0	0.04	-0.39

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.9238	-0.7138	0.1262	0.04625	0.175	-0.04625		-3.524	-1.554	-5.174
0.11	-0.31	-0.84	1.15	-0.9113	-0.0125	-0.23	0	0.21	0.98
0.3663	0.02625	1.466	0.04625	-0.025	-0.9762	-0.9237	-0.5137		-1.184
1.582	0.3925	2.702	-0.5375	0.00125	-0.54	-0.6575	0.0025	0.3425	0.3125
2.359	-0.1509	0.4691	1.089	-1.072	0.4566	-2.271	-1.151	-0.4609	-0.1109
-0.7275	1.342	2.222	-0.2875	0.00125	0.18	-1.378	-0.1175	-0.1675	-1.898
-0.96	1.42	-0.12	0.16	-0.7312	0.5775	-1.27		-0.46	0.49
-1.84	0.49	-1.25	0	-0.7112	0.5675	-2.09			0.24
-0.2419	0.5481	0.3781	-0.1419	-0.09313	0.08563	-1.852	-0.2419	0.2881	-0.9219
0	-0.13		-0.95	0.5388	0.8975	-1.68	-0.62	0.01	0.42
-2.219	-1.029	-1.859	-1.339		3.949	-2.779	-2.709	-0.4587	
2.688	-0.7119	-0.01188	-1.512	1.597	-0.07437	-1.532	-0.8019	-0.7419	-0.9719
0.17	-0.18	-0.25	0	2.299	1.388	-2.82	0.43	-1.05	-0.3
0.41	-0.96	-0.09	-1.83	2.539	-1.172	-1.53	-0.26	0	-0.69
0	0.19	0.74	-0.42	-0.2512	-1.782	-0.67	0.77	-0.55	-0.34
0.2469	0.5669	-2.353	0.8769		0.1444	-2.853	0.6669	-2.913	-1.703
0.065	0.275	-0.635		0.5938	0.9725	-1.685	0.155	-1.295	
0.7	1.65	1.51	-3.27	0.8487	-0.0025	-0.3	0	-0.6	-0.2
-0.3019	0.1281		-1.302		2.856	0.7681	4.458	-0.2319	0.4981
-0.06	-0.07	-0.25	0	0.4888	2.588	0.23	2.63	-0.14	0.05
0.62	-0.84	1.29	-1.45	1.549	3.958	3.79	1.26	-0.01	0.01
-0.075	-0.105	-0.335	-3.495		-0.6175	0.075	1.325	-1.445	1.495
-2.66	-1.26		-2.3			0.92	-0.51	2.75	2.35
-0.6075	-0.0175	-1.858	1.312	0.00125	-0.44	0.9225	0.1925	-0.3875	0.3125
-1.22	-1.33	-1.03	0	0.04875	1.208	0.18	0.87	0.33	-0.73
-0.7953	-0.2453		-0.6353		-0.8978	0.2247	0.1747	-0.2653	-1.585
-0.96	1.2	-0.67	0	0.9188	-0.3425	0.66	-0.88	0.02	-0.15
-1.389	0.6012	-1.659	0.2312	0.42	-0.7712	0.01125	0.08125	-0.6087	-0.4288
0	-1.33	-0.82	0.82	-0.8812	0.4575	-1.52	1.19	-0.58	-0.12
0.34	-1.12	-0.29	0.18		-0.2525	1.29	1.61	0.4	
-0.07	-1.67	-1.26	-1.09	-1.03	1.638	2	-1.7	-0.76	1.49
2.311	1.131		0.4112	-1.151			5.271	-0.1987	1.521
1.15	0.07	0.89	-1.62	-1.151		-2.74	3.82	1.21	2.25
-0.2494	0.06062	-0.1194	0.9506	-1.241	1.048	-2.469	1.451	0.7806	2.081
-0.7088	1.141	0.6512	0.05125			-1.859	3.981	-0.2787	0.09125
1.31	1.54	0.18	1.24	-1.301	-1.062	0	1.93	2.69	3.6
-0.5694	0.5606	0.5806	0.5306		-1.642	0.3506		0.4506	1.191

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
-1.839	-1.069	-1.889	-1.039			-1.129	2.191	1.581	
-0.8619	2.198	0.6581	-3.562	1.057	-0.7544	0.6081	-0.1819	0.9981	0.2081
0.3241	-1.196	-0.1259	-2.076	-0.6072	-2.808	-1.736	0.1341	2.124	-1.666
0.81	-1.36	1.43	-1.89			1.27	-1.06	0.84	0.07
0.13	-0.03	0.38	0.22	-0.4212	-0.6125	0.03	-0.62	0.3	5.37E-10
1.81	0.37	0.78	0.08	1.759	-2.497	-0.13	-0.05	-0.15	0.335
0.305	0.365	1.505	1.145	-1.566	-0.1725	-0.105	0.105	-0.905	-0.25
-0.16	0	0.95	0.83	-0.5512	0.07875	0.16	2.94	1.84	-0.1188
0.08125	0.2712		0.8112	2.61	-0.3925	-0.5988	0.6413	0.3313	
0.95	0.5	1.17	-0.83	1.689			1	0.12	-0.4944
-0.3144	1.136	0.9656	-0.4144		0.1275	-1.534	1.316	0.3356	0.29
1	0.76	2.37	-0.05	3.009			0	0.71	
0.5206	1.371	3.061	-1.259	1.159	-1.603	-0.6109	0.3106	-0.5694	-0.1509
2.159	2.339	1.539	-0.6209	-1.202	-2.182		-0.3109	0.1291	5.37E-10
0.06	0.13	0.96	0.08	-0.6212	-1.682	-0.21	0.53	0.57	-0.49
0	0.17	0.82	-0.34	2.469	-1.197	0.2056	-0.47	0.04	
0.5356	0.04562	1.336	0.07562	-0.1956	-2.126	0.7762	0.3756	-0.2944	-0.6938
-0.00375	0.6662	2.406	-0.08375	0.005	-2.512		0.1663	-1.954	
-0.17	0.38	2.66	0.22	-0.1713			0.78	0	
0.18	0.43	1.58	-0.11	0.5488	-1.577	-0.48	0.34	-0.06	-0.71
1.035	0.235	3.255	-0.135	1.734	-0.4825	-1.135	0.135	-0.645	0.325
0.66	0	1.31	-0.34	2.489		-1.24		0.11	
4.531	2.071	3.221	-0.03875	1.11	-0.9212	-1.059	0.4113	-0.1887	-0.01875
0.3312	-0.01875	0.9112	-1.769	0.01	-1.331	-1.889	0.06125	1.181	0.1512
-0.08875	-0.04875	1.521	0.1612	0.18	-2.171		1.381	0.1113	
-0.3	0	1.07	-0.37	0.2688	-0.3125	-0.05	1.8	-0.24	0.09
0.495	0.095	0.685	-0.135	0.06375	-0.4375	-0.995	0.695	0.495	0.045
0.225	-0.065	0.345	-0.135	-0.3562	-0.1175	0.065	1.015	0.395	
1.718	0.02812	2.078	0.2781	1.597	-0.8644	-1.422	0.5281	0.4481	0.6181
0.54	0.31	2.76	0.08	0.9588	-0.8025	-0.04	3.13	-0.14	5.37E-10
-0.59	0.92	2.99	-0.37	1.479	-0.7525				0.91
0.4881	0.09812	-0.2219	0.2481	0.09687	0.1956	-0.5119	-0.3119	0.04813	0.3581
0.7447		0.4847	-1.195	-1.567	0.7422		-0.2253	-1.135	
-0.135	0.295	1.165	0.645	-0.9563	-0.7175	1.045	0.135	-0.625	1.285
-0.025	1.355	1.705	1.025		-1.537	0.485	0.855	0.295	-0.475
-1.011	-0.1509		0.5091	-2.472	0.06656	-0.3009	4.549	-0.5209	-0.03094
1.335	-0.215	3.305	-0.295			2.085	-0.035	-2.065	-2.895

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.5238	0.3162	0.1662	0.6962		-0.3262	0.08625		-0.1037	-0.3838
0.1056	0.3456	-0.7944	3.536	-2.046	-1.067		0.2156	-0.8744	-0.9544
-1.854	0.4156	0.1156	1.146			-1.594	0.8356	-0.3944	-1.714
-0.185	-0.315	1.405	2.815	0.8938	-2.327		1.615	0.185	-0.385
0.42	-0.03	1.84	3.85	1.779	-1.662	-0.34	0	-0.83	
0.22	-0.27	0.51	0.99	4.419	-0.5825	0	-0.05	-2.54	-2.04
-0.06875	2.181	3.031	2.331	0.53	0.06875	0.5112	0.2113	-0.6187	
-0.36	-0.25	-0.46	6.58	6.099	0.1475	0	1.12	0.19	0.16
0.97	0.36	1.81	8.2		-0.3725	-0.93	0.9	0.36	-0.47
-0.5594	-0.5894	0.1706	6.971	-0.3106	-1.492	-2.049		-1.239	0.3106
0.055	-0.775	1.105	4.615	0.8337		-1.225	-1.015	-0.055	
	0.5712	1.191	6.511		-0.1212	1.171	0.1212	0.2412	
0.1903	-0.4597	2.3	4.04	-0.01094		-1.33	1.51	4.16	3.29
0.18	-0.41	0.17	5.05	-0.6812	0.7075	-0.41	-0.21	0.51	0.96
0.145	0.295	0.325	4.975	-0.4062	-0.7075	-0.445	0.335	0.495	0.115
-0.2459	0.1641	0.7841	3.244	-0.2072	0.5916	0.03406	0.1941	-0.2759	-0.6859
-0.09875	-0.6588	0.4912	6.441	1.9	-0.5612	-0.2387	1.001	1.011	-0.07875
0.42	-0.93	0	9.1	0.5188		-1.8	0.73	0.85	
0.2263	-0.2238		9.076	0.225		-1.674		1.396	
0.015	-0.015	2.085	9.095	0.7538		-0.885	1.065	0.505	0.475
0.5825		0.8025	8.722	0.00125			0.6325	0.7525	
-0.4175			8.042	0.00125	-0.76	0.0025	-0.0475	0.0725	0.02
-0.54	0.17	-0.22	8.88	-1.573	0.1175	-0.02	0.51	0.37	-0.6819
0.008125	-1.022	-0.7719	4.768				-0.2419	0.1781	-0.04094
-0.5509	-0.03094		0.2791		0.7766	0.3291	0.7991	0.4391	-1.171
0.6691	0.2691	-0.08094	-0.4209	0.8378	-0.3534	-0.3409	0.7691	-1.001	0.16
0.28	0.54	-0.51	2.55	-2.251	-2.352	-2.42	-0.59	0.27	-0.18
		1.46			-0.7225		-0.27	-0.39	
0.1006	-1.249	0.07062	-0.9494	1.029	-0.4319	-0.8194	-0.5294	0.1906	1.061
0	-0.06	-0.99	-1.58	0.01875	-1.622	-0.58	0.35	-0.28	0.15
-0.44	-0.29	0.01	-0.01	1.199	-1.262	-1.45	-0.54	-1.31	0.61
-0.16	0.62	0	0	-0.4412	-0.3825	-2.719	2.231	-0.13	1.38
1.151	0.5112	-1.039	-0.5688		-0.3912	-1.739	0.2706	1.541	
0.2306	-0.5194		-1.619		0.1681	-2.49	1.62	0.6706	0.1306
-1.08	0	0.49				-3.089	1.211	-1.42	
	0.3306	-0.09938			0.2681			-0.5494	0.08062
0.25	0	0.73	-0.63	0.2688	-1.492	-1.51	0.15	-1.44	-0.19

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.54	1.99	0.75	-0.51	-0.6512	-1.482	-0.21	-0.04	-0.39	
1.88	0	-0.32	-0.8	2.299	-3.262	-1.5	1.5	1.82	2.06
0.93	-1.38	-0.02	-1.65	2.139	-2.632	-1.97	1.78	-2.24	1.19
-0.065	0.455	-0.365	0.065	1.404	-1.107	-1.725	0.135	-0.265	
-0.275	0.005	0.085		-1.026			0.355	-0.225	
-1.48	3.23	0.77	-2.22	1.529			-0.95	-1.89	-1.065
1.045	1.655	1.885	0.215		-3.651		-1.735	0.595	
-0.06875	0.5412	1.541	-0.8788		-1.242	-0.22		-1.009	
1.12	0.03		-0.53	0.9988	-0.5325	-0.8594	0.22		0.12
3.14	0	1.62		1.359	-1.941	-1.499	-0.26	-0.8	-0.4994
0.5606	0.7106	1.981	-0.03938	1.47	-2.442	-0.24	0.4806	-0.7894	-1.029
0.5812	1.341	0.9412	-0.4888		-1.942	-1.95		-0.1387	-1.41
-1.13	-0.29	1.12	0.14			-0.83	0.66	-1.12	
-0.63	0.25	-1.28	-0.92	-0.9656	0.0375	-0.35	0.09	0.07	-0.52
0.32	0.7	0.05	0.73	0.9088	2.129	0.1112	-0.08	-0.05	
0.2156	0.5856			-0.38	1.708	-2.16	2.026	0.8856	0.95
0	0.05	-0.25	0.1	0.9688	0.2275	-0.33	0.8	0.33	
-0.2088	-0.08875	-0.3988	0.6412	0.05875	0.5738		0.1313	0.2513	
0.98	1.21	0.36	1.54	0.005	0.1225	0.41	-0.55	0.61	5.37E-10
-0.2	0.59	0	0.32	-0.4962	-0.5625	2.131	-0.03	0.47	
-0.4538	0.6262	0.2062	0.175	-0.8912	-3.231	0.08	-0.3637	-0.2337	0.06625
-0.635	1.195	0.495	-1	2.66	0.5875	0.285	-0.165	-0.795	-0.065
-0.12	0	-0.59	-0.08875	-1.081	0.4925	0.4925	-1.23	-0.67	0.62
0.6612	-0.1688	1.661	0.35	-1.056	0.74	-1.37	-0.03875	0.03125	4.331
-0.12	0.17	-0.02	0.105	0.00125	-0.7025	-1.359	-0.03	0.07	0.82
-0.505	-0.285	0.375	0.1225	0.01	0.7188	3.97E-10	1.195	-0.285	
-0.4175	-0.0775	0.0725	0	-0.8712	-2.082	-0.09875	0.0025	0.2125	0.6625
0.22	-0.08	-0.57	3.121	0.78	0.4788	0.34	-0.75	0.36	-0.05
	-0.9688	-0.00875	-0.07		-0.8325	-0.55	0.2113	-0.00875	-0.6588
0.03	-0.63	0.77	1.25	0.01	1.128		-0.16	-0.17	1.40E-10
-1.86		-1.39	0.01125	-0.8712			-0.6187	0.16	-1.43
-0.1488	-0.7888	-0.7588	-0.7075	0.00125	-0.1825	-0.76	-0.2175	-0.3887	-1.709
	-0.1775	0.3325	0.2	-0.5212	-1.152		0.21	-0.8675	
-0.16		0	0.83			0.34	0.21	0.3	0.45
-0.2	0	-0.89	0.3	1.339		-0.55	-0.38	-0.06	-0.21
-0.23	0.18	0.62	0	0.3488		-0.76	-0.21	-0.23	-0.18
-0.44	-0.67	0.85				2.19		1.39	2.7

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Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
2.908	0.3581	3.888	0.1181	0.3569	-1.444	-0.9219	0.6681	-0.6119	-0.3819
	0.165	1.395	-1.895	1.674	2.263	0.015	-0.505	-0.015	-1.235
-0.3988	1.051	-0.2588	0.1712	1.12	-1.151	0.1812	0.6013	-0.2087	-0.4688
-0.255	-0.015	0.535	0.915	-0.8262	0.3225	0.055	-0.135	0.015	
1.75	-0.64	1.73	3.48	-0.9212	2.538		0.62	-0.76	0.8906
-0.2894	-0.3894		2.611	0.1994		0.1006	-0.1894	0.2106	0.7781
-0.09188	1.098	1.638	-0.7219	-1.263	0.3956	-0.5819	0.8681	0.3681	0.6591
0.3491	-0.05094	0.06906	-0.1909	-0.2122	0.8866		-0.4309	0.3991	1.555
-1.105	-0.315	-0.175	0.415		-1.447	-0.645	-1.205	1.435	
-0.14	0.92	0.6		-0.5212	-0.3425		-0.55	-0.75	-1.562
0.2081	0.1481	0.03812	0.4281	1.267		0	0.5181	-0.3119	-0.04
-0.13	-0.31	0.11	0.76	0.4088	0.8275		0.13	0.56	5.37E-10
0.5	0.42		-0.49			-0.25		-0.33	-0.6819
3.298	2.068	1.818	-0.8819	-0.1631	1.388	1.768	1.148	-0.3419	-0.9044
1.426	1.396	0.2956	0.5256			-0.3644	-0.7044	0.8556	
-0.12	-0.68	0.44		-1.611	-0.4769		-0.09	0.12	0.58
-0.5	1.14	-0.55	0	1.139	-2.082	0.2	-1.15	-1.03	-0.11
-0.22	-0.18	0.94	1.51	-2.261	0.2275	2.6	0.52	1.47	
0.705	1.195	0.095	-1.475	-0.9062	-2.172	0.645	-2.695	0.885	-1.91
1.69	-0.41	0.81	-0.51	-0.8312	1.813	2.55	-0.65	2.13	
1.616	-2.084	0.01562			-0.3125	2.866		2.196	-1.5
1.64	-1.29	0.8097	-1.42	0.4984	-1.487	3.12	-0.9203	2.54	0.13
0.45	-0.83	-0.09	0	0.05875	-1.483	1.96	-0.35	0.3	0.09
-0.27	0		0.61		-0.7225	-0.44	-0.14	-0.28	-1.592
-1.232	0.4381	-1.172	-0.9919	-1.613	-1.642	0.5681	-0.4919	1.328	-2.53
0.81	0.07		-1.18	-0.7312	0.8156		0.31	0.7	
0.2912	2.051		1.781	-1.92	0.8475	-1.239		0.08125	1.041
-0.16	2.38	0.36		-1.291		-0.8	-0.72	0.4	
1.41	2.77	1.81	1.02	-1.111	-1.172		0	-0.41	
-0.765	-1.015		-1.885	-0.6363	-1.092	0.505		-0.055	
-1.175	0.375		-0.455	0.04375	-0.1975		0.585	0.125	0.055
0.7281	-0.6619	1.198	2.638		-2.727	-0.9919	1.208	-1.432	-0.025
0.55	0.42	0.8		1.019	-0.1525	0	-0.14	-0.27	
-0.01	2.36	-0.5	-0.12		0.4275	1.41	0.44	0.65	0.06
0	0.93	2.8	0.14	-1.341	-0.5225	1.06	0.94	-0.39	0.8
-0.05875	0.2912	3.761	0.2612	-0.5	0.4088	0.2112	0.5213	-0.4087	
-1.46	2.41	3.92			-3.972		0	-1.66	0.08125

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
0.7091	2.779	4.399	-1.441	1.028	-0.7834	-1.141	1.089	-0.4909	
-0.88	0.36		-0.66				0	-0.27	0.6
-0.42	1.25		0.88	0.9088	-1.022		-0.21	-0.62	5.37E-10
-1.77	0.34		-0.15		-0.7025	-0.2044	0.63	-0.74	
3.156	0.6656	1.896	-0.7044	4.234	-2.587			-0.5744	-1.49
-0.05	0.34	0.59	0.91			-0.53	0.42	-0.46	-0.06
0.06	0.06	0.85	0.13	4.209	2.198		-0.33	-0.12	-0.08875
0.2712	-0.1688	1.171	0.6612		0.5888	-0.7488	-1.939	0.3213	-0.05437
1.556	-0.4244	-0.2944	0.02562		0.4631	0.9056	-0.3444	0.2956	
0.6625	1.012	0.7025	0.0225		0	-0.3875	-0.2875	0.0925	-0.7175
0.42	-0.4	0.48	-0.2	4.959	2.338	0.01	-0.59	-0.01	0.38
0.785	1.125		-0.035	5.804	2.703	-0.745		0.645	0.035
-0.31	0	1.5		2.699		0.32		-0.84	
1.328	0.7681	3.078	0.1581	6.317	-0.8644	-0.6219	0.1081	-0.03187	0.4181
-0.215	-0.825	2.145	3.395	6.444	-1.557	-1.115	-0.165	-0.455	
-0.4094	-0.1194	2.291	-0.6094	7.199	-1.752	-2.309	0.4406	-0.6594	-1.689
3.01	-0.8		-0.73			0.57	0	-0.29	0.33
-0.025	0.525	1.645	-1.505	5.704			0.025	0.725	
-1.285	-1.635		-0.805	6.954	0.6325	-0.925	0.245	-1.115	0.335
-0.135	-0.015		0.015	2.744	-1.717	0.575		0.255	
-0.8044	-0.4944	1.446		1.184		0.9756	-1.084	2.086	
-0.66	1.01	1.05	0.27	-0.00125			0.16	0.51	-1.52
-1.09	0.91	1.61		1.459		0.04	-0.04	1.08	-1.88
0.21	-0.95	-0.61	-0.75	0.05875	0.8075	4.72	-0.2	0.11	5.37E-10
0.87					-1.642		-0.35	0	
-0.9188	0.5412	-0.08875	-0.1888	0.5588		3.041	-0.6787	-0.5587	0.3512
0.59	0	-0.77	0.06		3.538		-1.04	-1.04	-1.46
0.7506		0.5806			4.678			-0.3794	
0	1.05	0.4	0.53	2.499	2.008	1.26	1.08	-0.14	-0.92
0.365	0.725	0.775	0.895	1.364	1.773	0.045	-1.075	-0.545	-1.315
0.19	-0.28	0.84	0.84	1.599	1.708		-0.33	-0.3	-1.2
-0.3109	1.659	3.019	-0.1309	0.6178	-0.9634	-0.9009	0.2791	-1.631	
-0.65	0.71	0.31	-0.15	-0.8812	-1.362	-1.55	1	0.09	0.11
0.75	0.21	-0.45	0	-0.6712	-1.102	-1.49	0.23	0.34	-1.2
0	-0.11	-1.44	-0.37	1.019	0.5275	-1.52	0.3	-0.76	-0.08
0.5641	-1.136	-0.6859	-0.9459			1.354	-1.116	-1.176	-1.916
0.12	0	-1.16	-0.04	-0.3812	1.208	0.59	-0.05	0.04	-1.01

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-1.095	-1.025	-0.195	1.545	4.794	4.013	-0.215	0.765	1.355	0.195
-0.05	-0.59	-1.15	1.02	-0.1712	3.058	0	1.28	0.63	0.34
-1.49	-0.65	-0.96	3.04	1.639	4.358	-0.21	-1.81	-0.49	5.37E-10
0.16	-4.38	-3.37	1.07	-0.3013	0.8275	-0.83	-0.86	0	-2.41
0.26	-2.45	-1.02	1.3	-2.351	1.478	1.16	-0.22	-0.43	0.3
-1.322	-3.812	-3.462	3.098	-2.143	2.196	0.5681	-0.4819	0.2681	1.188
-1.639	0.09125		2.111	-1.04	0.7188	0.8913	1.411	-0.9187	0.3313
-0.09	-0.25	0	-0.78		0.0975	0.64	0.97	-1.18	0.79
-1.45	-1.14	-1.7	0.19	-1.391	1.488	0.42	2.61	-2	0.24
-1.1	-2.18	-0.02	4.17	-2.81	-0.2625	0.75	1.41	0	2.73
-1.429	-2.089	-1.689	3.721		0.09875	0.8313	0.3913	-0.4787	2.361
-1.84	-0.46	0.42	1.06	-0.6212			0.82	-0.85	
-0.1519	-1.172	-0.9519	-1.452	0.9369	-1.184	-0.1019	1.548	0.04813	0.01812
-2.436	-2.616	-1.336	1.904		-0.9284	-1.646	0.9841	-1.026	
-0.8288	-1.179	-1.319	1.521		-2.121	2.601	1.401	-0.7387	0.2812
-0.17	0	-1	-0.55	-0.4812	-0.8525	2.78	1.83	-0.79	-0.46
2.302		0.2425	2.562		0	1.322	1.022	-0.0675	2.922
3.835	-0.865	-0.935	3.775			2.065	2.765	0.135	3.975
1.83	-1.34	-0.79	1.2	-0.5513	0.0675	0.71	0	0.81	0.73
-0.03	-0.3	0.91	5		-0.7125		0.98	3.37	
-0.1894	0.4306	-0.2494	0.8306	-0.5806	0.9481	1.621	1.821	2.391	1.791
0.12	0.24	0.65	0.49	-0.6313	0.1875	-0.63	0	0.29	-2.91
0	0.72	0.71	0.52	-1.091	-0.1725	0.35	0.24	0.69	0.29
-0.7309	0.9591	0.9591	-0.02094			2.279	-0.2609	-0.7609	-0.04094
0.76	0	0.73	2.14	-0.4412	1.618	0.4	-0.21	2.28	-0.65
-1.18	0.1	-0.03	1	-3.151	1.558	-2.54	1.15	2.14	-1.04
0.1556	-1.244	-2.074	1.626	-3.676	4.323	1.726	1.806	2.056	1.696
0.775	0.085	-0.255	0.585	2.864	1.513	-0.175	0.255	0.575	0.655
0.62	0.07		0.67	-3.109	1.528	0	-0.03	0.87	1.05
0.105	-0.105	0.335		1.724	2.063	0.255	-2.025	1.345	-1.515
-0.81	-0.63	-0.67	-0.04	2.549	1.778	0.43	0	2.13	-0.43
-0.09	-0.1	0.36	0.69	1.949	1.098	0.17	0.19	-1.27	-0.69
-0.3	0.25	0.16	0.71	0.7687	1.328	0.53	0	-0.09	-0.05
2.201		-0.3888	-0.3088	4.27	3.889		2.291	-0.1787	
0.565	-0.065		-0.015	3.904	4.753		0.015	0.505	
0.09	0.31	-0.72	-1.27	3.449	1.678		0.74	0.86	
-0.5887	0.3712		-0.07875	2.89	2.599	1.181	0.2113	0.2613	5.37E-10

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.22	-0.67	-0.96	0	1.239	2.228	0.11	0.39	0.97	0.72
1.57	-1.91	-0.28	-1.49	-0.1612	1.498		1.92	1.28	5.37E-10
1.261	0.3412	-0.3688	-2.269	1.38	1.239		-0.8887	0.2713	0.04125
-0.01	0.47	0.46	2.34	0.6887		2.34	0	0.16	-0.91
0.01125	-0.8088	-0.3088	0.5012	2.21	1.269	-0.06875	-0.4187	1.971	-0.9988
0.29	0.03	-1.1	0.84		0.9775	-0.11	-0.48	0.57	-0.03
0	0.98	-0.74	0.75	0.4488	2.328		-1.39	1.67	0.08
-0.1138	0.4062		-0.6638	0.135	0.07375	1.056	-0.07375	1.676	1.046
0.09	-0.67		2.45	1.689	2.348	-2.98	-0.12	0	0.17
0.39	0	-0.14	1.79	0.8388	1.718	-5	-0.33	-0.01	0.61
-0.02	0	-1.09	1.69	1.079	-1.432		1.86	0.57	2.47
-0.08438	0.2056	-0.8244	0.5456		0.1831	-1.504	0.5256	0.08563	0.8756
1.57	2.64	2.34	1.76	2.909	-1.262	-1.82	0.52	1.77	5.37E-10
1.27	1.63	0.25	3.01	2.259	-0.9025	-1.14	-0.24	2.22	5.37E-10
-0.1319	0.3781	-0.2619	1.238	1.327	2.436	1.278			-0.7519
1.57	-0.14	-0.43	0.89	1.019	1.208	1.24	0.23	1.26	-0.14
1.27	1.63	-1.99	2.99	2.309	1.568	-4.18	2.67	-1.79	-1.56
5.70E-09	0.06	0	2	1.559	0.2275		0.59	-0.46	-1.12
0.11	-1.3	0.05	2.2	0.2588	1.088	0.23	-0.86	0.26	-0.5
1.39	-2.48	-0.16	2.58	0.9288	0.5975	0.23	0.22	0.91	
5.23E-09	-0.16	-0.56	0	0.5288	2.028	0.06	-0.17	0.7	0.46
0.9	0.3	-0.08	0.06	0.4687	1.058	1.48	-1.03	0	-0.16
0	0.95	0.54	1.68	-0.01125	1.758	0.58	-0.32	-0.2	-0.03
1.38	1.07		2.48	1.429	2.308	0	-0.5	-0.48	-0.51
0.9713	-0.4588	-0.5888	1.881	1.79	2.779	-0.1287	-0.7587	0.5613	-0.9887
-0.47	0.09	0.27	0.57	0.7788	1.738	0.4	-0.33	-0.56	-0.22
0.07	0	-0.78	1.23	1.349	1.028	0.94	0.4	0.77	0.92
0.48	-0.08	-0.66	1.37	1.319	0.8875	2.73	0	0.76	0.92
0.07	0.07	0	0.1	0.4488	-0.0325	0.67	-0.36	0.64	0.52
-0.005	0.625	0.085	0.425	1.324	1.973	0.005	-0.585	1.235	-0.415
0	-0.17	0.29	0.73	0.03875	1.378	0.14	-0.89	0.88	-0.54
0.05	-0.59	-0.13	1.33	0.5388	3.798	0.8	0.72		-0.05
-0.815	0.055	-1.015	1.655	0.9438	3.833	0.015	-0.405		-0.015
-0.56	0.33	-0.79	0.53	0.2688	1.398	-0.23	-0.16	1.31	0.18
-0.27	1.11	-5.02E-09	1.57	1.779	1.488	0.46	0.41	0.7	5.37E-10
0.7	1.63	0.29	0	-0.4012	0.6575	0.25	-0.29	0.12	0.65
0.06406	0.4741	0.1041	-0.3859	0.5228	0.8916	0.1041	-0.2459	-0.1459	-1.156

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCl	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.00125	0.6812	0.1912	1.101	0.2	1.419	-0.8988	-0.9987	0.4813	-0.1688
0.6769	0.7769	0.3869	0.7469	-0.004375	0.5044	-0.2731	-0.4531	0.4369	-0.1231
0.7706	0.7606	-0.5094	0.8806	0.2994	0.2881	-0.6794	-0.1594	0.9306	-0.1994
0.1212	-0.2588	-0.5788	0.6412	-0.04	0.08875	1.231	0.7013	1.211	0.7512
0.7	0	-0.68	0.08	0.8388	1.778	0.2	-0.7	-0.08	0.11
0.21	-0.04	0	0.01	0.8188	0.4775	0.17	-0.77	0.03	-0.43
-0.96	-0.32	-0.4	1.15	2.069	2.848		0	0.58	0.02
1.09	-0.01	-0.54	1.26	2.139	0.2475	3.89	0.61	2.57	1.33
0.57	0.06	-0.27	1.27	0.1388	1.258	0.83	0.19	1.48	0.47
0.1613	-0.5688	-0.9488	0.1312	0.59	0.3388	0.02125	-0.7087	0.4913	-0.2887
0.2912	0.4812	-1.809	0.7912	2.12	1.359	-1.239	-0.4387	1.051	-1.029
0.37	0.21	-1.01	0.88	1.069	1.488	1.1	-0.07	0	1.38
0.5241	0.6641		1.024	1.353	0.9616	-0.02594	-0.4159	0.8241	1.704
0.92	0.18	-0.38	0.57	0.7988	0.2375	-0.32	-1.18	0.11	-0.51
0	0.54	0.51	1.23	1.399	1.018	0.74	-0.72	0.19	-0.8
0.2	0.28	0	0.56	0.8288	1.348	-0.05	-0.32	0.84	0.02
0.79	-0.01	-1.3	0.13	1.009	0.1375	-1.21	-1.21	0	-0.52
0.22	0.36	-0.65	1.63	1.639	2.348	-0.03	-0.37	1.88	1.2
0.89	0.49	-0.19	2.14	2.099	2.848	-0.08	0	2.49	1.47
0.6081	0.3681	-0.1119	0.4681	1.187	1.066	-0.4119	-0.6619	0.1981	1.258
0.69	0	-0.7	0.48	0.5788	0.9475	1.11	-0.13	0.53	-0.42
0.49	1.43	-0.19	0	0.4388	0.9675	-0.88	-0.46	0.91	-0.24
-0.1	0.28	0	-0.08	1.499	2.158	0.08	-0.71	0.93	-1.16
0.08	0.33	0.06	0.14	1.269	0.2075	0.07	-0.23	0	-0.44
0.47	0.02	-0.58	0.67	0.5387	0.3575	0.8	0	0.4	-0.16
0.04	0.53	-0.05	0.99	0.7188	1.688	0	-0.4	-0.78	0.27
-0.00875	-0.1988	-0.9088	0.2312	2.2	2.339	0.7913	0.4713	1.541	1.401
0	0.43	-0.72	1.74	1.549	1.618	0.13	0.48	1.22	0.92
0.25	0	-0.23	2.25	0.9188	2.598	-1	0.53	1.1	1.4
0.44	0.96	-0.28	2.25	1.809	1.868	0	0.34	0.5	-0.1
-0.1788	-0.03875	-0.8588	2.391	1.98	1.919	0.2412	0.2413	1.321	0.5012
-0.5488	0.3012	-1.309	2.621	1.97	1.999	0.4312	0.3313	1.381	0.1312
0.17	-0.66	-0.38	1.81	1.999	2.488	0	0.39	1.44	0.2
0.25	0.2	-0.24	1.59	1.419	3.038	-0.12	0.62	0.84	5.37E-10
-0.46	0.39	-1.17	1.1	1.759	1.578	0.55	0	1.09	0.23
0.45	0.92	-1.13	0.83	2.039	1.698	0.3	0.27	1.52	5.37E-10
-0.245	0.245		1.435	1.494	1.583	0.865	0.335	0.925	1.885

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.01	0.6	0.1	0.99	1.179	1.208	1.27	-0.94	1.4	5.37E-10
0.81	0	0.61	0.41	0.8388	1.968	0.89	-1.11	0.77	-0.15
0.08125	1.351	-0.8088	0.6412	0.44	1.089	0.1013	-0.5987	0.5613	-0.03875
0.2512	1.231	-0.8488	0.5512	0.55	1.009		-0.6087	0.4413	-0.08875
1.192	0.8825	-0.5975	0.4125	-0.3288	0	-0.6675	-0.9375	0.5425	0.2325
0.62	0.44	0	0.05	0.9688	0.2775	-0.48	0.04	0.83	-1.29
0.6012	0.2612	-0.08875	0.5912	-0.44	0.4588	0.1212	-0.6187	0.8613	0.03125
0.06	0	-1.03	0.9	0.6988	1.038	0.6	-0.66	1.24	0.95
0.78	0.41	-0.22	0.44	0.07875	0.8375	0.3	-0.16	0	-0.55
	-0.3559	-0.4459	-0.08594	0.1728	0.7116	1.304	-0.6759	0.7941	0.4341
1	0.82	0.24	2.49	-0.4112	0.9975	-0.23	0.2	0.45	0.81
-0.36	0.56	0.03	1.05	0.1687	0.8475	0.51	0	-0.49	0.23
-0.19	1.6	0.33	0.34	-0.00125	1.558	-0.91	-0.31	0.87	0.3
-0.23	0.13	-0.38	0.7	1.209	1.298	0.22	-0.41	0.72	5.37E-10
-0.2	0.17	0	0.59	1.249	1.468	-0.02	-0.76	0.89	-0.29
-0.4488	0.2412	-0.8188	0.2312	0.84	1.129	0.7712	-0.1087	0.7013	0.7312
0.7925	0.0325	-0.2975	0.7425	0.00125	0.87	0.0425	-0.4075	1.113	-0.1875
1.27	0.24	-0.15	1.15	0.2488	1.478	-0.07	-0.61	1.37	5.37E-10
0.67	0	-0.02	1.17	1.069	2.398	0.3	0.02	1	-0.09
0.49	0.39	-0.27	2.63	1.079	1.628	-0.25	0	0.91	-0.91
0.11	1.01	-0.49	0.65	0.3088	0.8675	0	-0.73	0.48	0.04
0.09	0.13	0	1.63	0.8087	0.9875	0.46	-0.09	0.96	1.02
0.4112	0.5512	-0.2688	1.081	1.79	1.059	0.7812	-0.4987	1.411	1.911
0.45	0.73	-0.14	0.48	0.2588	0.5275	0.41	0.2	0.69	-0.36
0.59	1.08	-0.25	0	0.1688	1.628	1.44	2.02	1.04	-0.06
0.5212	-0.3588	-0.7088	0.6912	1.04	1.619	0.4812	-0.1687	0.2613	0.1412
0.58	-0.15	-1.01	1.35	2.079	1.378	0.59	-0.24	0.62	0.72
0.4981	-0.1719	-1.112	1.298	2.237	1.516	0.6381	-0.3219	0.5481	0.5581
-0.285	0.775	0.135	0.295	0.6338	0.2525	2.725	-0.135	1.565	0.565
0	0.07	-1.18	1.26	0.2488	0.3975	0.59	-0.15	0.64	0.7
0.7906	0.06062	-0.009375	-0.4194	0.1194	1.678	0.06063	0.1206	0.4006	
-0.6687	0.04125	-0.7688	1.401	0.42	1.259	0.6113		0.6213	0.7113
0.2212	-0.1788	-1.709	0.8612	1.83	1.379	0.5913	0.1913	2.481	1.431
0.13	-0.03	-0.79	0.94	1.459	1.188	0.53	-0.09	0.93	5.37E-10
0.15	0		1.65	-0.6912	1.288	2.09	0.89	1.53	1.83
-0.2075	0.0125	-0.8175	1.222	0.00125	0.71	1.022	0.3625	1.213	0.7525
0.04	0.64	0.31	1.02	0.4088	0.8575	0	-0.38	0.6	0.35

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Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
1.67	-0.33	-0.54	2.12	1.849	2.328	0.11	-0.19	1.23	1.44
1.61	0	-0.37	2.01	1.719	1.218	0.27	-0.1	1.24	0.94
0.65	0	0.27	1.37	1.249	2.788	-0.75	0.57	1.53	0.52
0.38	-0.37	-0.23	1.88	1.219	1.118	0	-0.14	0.5	-1.74
0.6156	0.6556	-0.7844	0.4156	0.4144	-0.4469	-0.2544	-0.1044	0.4156	
0.25	0.03	-0.73	0.73	1.529	1.558	-0.22	-0.07	0.32	-0.55
0.95	-0.94	0.29	1.9	2.279	2.248	-0.05	-0.82	1.08	0.23
0.6712	0.4112	-0.3088	0.2912	0.86	1.609	-0.3288	0.3813	1.341	-0.09875
-0.3844	0.1156	-0.5544	1.086	0.8544	1.203	0.2356	-0.004375	0.3156	0.5556
0.8413	0.1512	-0.8888	0.9012	0.29	1.199	-0.9687	-0.3287	0.6313	0.2613
1.521	0.3312	-0.9088	0.7812	0.1	1.489	-0.5887	-0.3687	1.021	0.1513
0.83	-6.03E-09	-0.33	1.65	0.9288	1.188	0.76	0.44	1.08	5.37E-10
0.5612	0.3512	-0.8488	0.9612	1.26	0.6188	0.8012	-0.3687	0.5913	-0.02875
-0.05	0.52	-0.35	0	0.9588	-1.242	1.55	0.29	0.83	0.55
-0.67	0.34	-0.17	1.23	-0.05125	0.9375	0.18	-0.82	0.4	5.37E-10
0.1281	0.2481	1.098	1.758	1.657	2.286	-0.01188	-0.9719	1.48	-0.5019
-0.32	-0.02	0.17	1.21	1.359	2.088	0.24	0.09	0.7706	
-0.1894	0.9406	-0.01938	2.791	1.839	2.398	0.7206	-0.2294	1.47	-0.3094
0.8	0.76	-0.03	1.37	1.689	1.938	0.35	-0.09	-0.02	-0.04
-0.52	0.04	0	1.9	0.9388	0.2475	1.83	-0.18	0.25	-0.2
0.27	0	-0.24	0.23	1.259	1.268	0.79	0.03	1.656	0.02
-0.3538	0.1262	-0.1938	1.626	1.215	0.7138	1.146	0.5063	1.575	-0.3738
-0.025	0.035	-1.205	1.455	1.034	0.4925	1.075	0.025	0	0.235
1.28	0.95	0.67	2.72	0.8687	0.8075	-1.6	0.55	1.136	0.48
1.136	-0.3344	1.786	3.446	2.414	1.403	-0.3144	-1.68	-1.41	
-0.08	0.85	0.78	1.73	1.439	1.758	-1.15	-0.9475	0.8225	0.64
1.302	-0.2675	0.5225	0.7225	1.011	0	0.8125	-0.195	0.465	-0.9475
0.525	0.195	-0.325	0.545	0.5138	-0.4875	0.675	-1.38	1.05	-1.165
0.2	-0.15	-1.08	1.32	0.6688	1.408	0	0.14	-0.34	0.5
0.98	0.12	0.68	-0.27	0.6288	1.588	0.19	0.67	1.47	-1.15
-0.99	0.55	0.06	0.47	-0.07125	-0.0325	2.13	-0.3575	0.3825	2.38
-0.2875	-0.5275	-0.3775	0.1925	0.00125	2.03	0.1425	0.39	0.37	0.5325
-0.41	0.16	0.04	0.75	-0.9412	1.018	0.21	0.38	-0.31	-0.25
-0.09	0	0.67	1.47E-09	0.2688	1.008	0.57	0.5813	0.2513	-0.34
0.6112	1.341	-1.78	-0.07875	1.75	0.3688	0.4212	-0.23	-0.05	-0.7788
-1.55	-0.47		-0.11	0.2087	3.438	1.02	0.39	0.37	-0.2175
-0.0175	-0.4175		0.0825	0.00125	0.97	-1.118	-0.4975	-0.0175	

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
1.298	-2.582	-1.162	-0.6419	-1.423	1.976	0.6581	-2.502	-0.7419	-1.122
0.16	0	-0.15	-0.17	-0.3712	0.1875	-1.26	-1.13	-0.62	0.28
-0.2859	-0.2159	0.4241	0.3141	0.1928	-0.5384	-0.4759	-0.7859		-0.7959
0.0225	0.2425	0.5825	0.4225	-1.409	0	-2.998	-1.708	-0.9275	-1.138
1	-0.47	-0.41	0.41	-2.561	-0.7925	-0.98	-0.2	-0.75	0.79
0.9	0	-0.01	1.44	-0.08125	-0.0025	-0.2	-0.88	0.43	-0.88
0.6019	-0.1581	-0.1981	0.9019		-0.05062	0.1119	-1.358	-0.8481	-0.2981
1.02	-3.08	0.42	-0.63	1.289	3.208	-1	-0.34	-0.19	-1.19
2.818	1.988	0.9581	-2.752	-2.693					
0.97	2.98	1	-2.97	1.259	0.9775	1.3	-0.7	0	0.09
2.85	2.62	-0.02	-1.24	1.499	2.108	-1.06	0.02	-0.29	0.91
2.12	1.8	1.29	-2.01	-0.1512	3.108	-0.76	-1.52	-0.84	-0.25
1.652	1.432	0.9625	-2.368	0.00125	2.67	-1.028	-1.657	-1.047	-0.3075
0.2356	-2.114	0.6656	2.986	-1.296	-1.207	2.026	1.126	1.346	-1.104
-0.1044	-0.6044	0.9056	2.166	-2.476		1.046	1.296	1.176	-1.374
-0.5494	0.2506		1.331	0.1194		0.6506	-0.3394	-0.7494	0.02062
-0.1994	-0.6994	-0.5694	0.7706	-0.8706		1.221	0.9906	0.7106	
-0.9319	0.6781	-0.08188	0.4881		0.3456	0.7381	-1.222	0.2881	0.5881
0.7991	-0.07094	-0.9509	0.1891	-0.6922	1.097	0.3291	-0.2109	0.8191	0.8791
-0.86	-0.1	-0.49	0.92	1.029	0.6175	0.04	0.07	0	0.44
0.3512	-0.3688	-0.2988	3.341	1.21	1.529	-1.269	-0.4087	-1.389	-1.109
0	-0.08	0.19	0.92	0.9588	1.518	-0.5	0.43	-0.51	0.11
	2.68	0.92	-0.51	1.849	-0.7525	-1.82		1.01	
0.3041	0.1841	-0.5659	0.9241	1.193	1.072	-0.06594	-0.09594	0.2541	0.6941
5.70E-09	0.07	0	0.12	-0.1612	0.3175		0.57	0.17	-0.2
0	0.39	0.22	0.54	-0.18	0.5375	-1.48	0.64	-0.59	0.56
0.6112	0.04125	0.6812	0.2812	-0.2512	0.8888	0.1012	-0.3287	-0.1087	0.2712
0	-0.15	-1.14	-0.25	-0.91	0.0075	-0.71	-1.47	-0.48	0.1
0.2612	-0.5388	1.101	0.8812		1.189	-0.1488	-0.7787	-0.6587	-0.5788
0.3581	-0.7919		0.6181	1.077	0.7856	-1.162	0.02813	-0.2919	
-0.87	0	-0.17			4.558			0.13	
0.57	0.31	-0.15	0.16		0.3675	-0.62	-1.11	-2.43	0.41
1.228	-2.102	0.6081	0.3181	1.387	-2.094	0.7781	-2.022	-0.3819	2.988
2.39	0.58	-0.78	0.61	-0.8512	-0.6125	-0.29			-0.01
0.75	-0.33	-0.2	0.12				-0.78	-0.03	-0.06
0.4	0.13	1.4	0	-0.8812		0.7	-0.35	-0.23	0.88
			-0.4219			0.5381		-0.08187	

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.045	-0.425	-0.885	0.045	-1.486	-0.7575	0.915	-0.165	-0.155	0.385
0.44	-0.78	0.51	-0.68	-0.02125	-1.482	-0.87	0.43	0.31	5.37E-10
0.21	0.18		-0.03	0.4987	-0.4125	-0.47	-0.55	0	-0.46
-1.045	0.805		0.325		-0.1575		-1.965	0.055	
2.5	-0.25	0.46		0.3988		-1.92	1.35	2.32	1.7
2.681			0.9312	-0.57	-0.7512		0.9613	1.641	0.6112
2.2	0.21	-4.66E-10	0	0.1988	-0.5625	-1.54	1	1.47	0.62
1.86	0.28	0.85	-0.01		0.7675	-0.79	-0.06	1.23	0.03
3.522	-0.05813	0.5019	1.722	0.9206	0.03938	-0.2981	0.9319		0.9419
3.08	-0.08	2.24	-0.32	0.7688	0.4575	-1.1	0.8	-0.13	-0.22
4.111	-0.03938	0.7706	-1.419	1.259					
3.48	0.38	1.86	-0.51	1.669		5.70E-09	0.21	-0.71	
-0.3831	0.1869	0.7469	-0.4531	0.2556	0.03438	-0.6231	0.3169	0.3869	-0.8131
0.7206	0.3206	0.3306	-0.4594	-0.7306	0.1481	0.6206	-0.1694	-0.6394	-0.6894
0	1.47	-0.12	0.51	0.3488	1.138			0.53	-1.40E-10
0.28	0	-0.05	1	0.3788	0.6175	0.26	-0.04	0.44	0.16
-0.405	0.425	0.005	-0.005	0.1438				-0.055	-0.955
0.4291	0.7891	0.6191	0.4691	-0.3722	-0.6734	-0.4109	1.649		-0.09094
-1	0	0.49		-0.6612	3.248			1.75E-08	
-0.2	0.1	-1.4	3.19	2.579	3.318	1.86	-0.1	3.67	2.08
-0.105	0.105	1.215	3.505	-0.1462	2.993		-0.615	2.025	0.895
-0.035	0.045	1.345	0.655		1.603	-0.905	-1.575	-1.405	-0.985
1.158	1.078	0.1981	-0.8219	2.757	1.766	1.158	-0.9919	-1.632	-0.2019
2.09	2.12	1.6	-1.37		2.518	1.85	-0.32	-0.76	
1.485	0.185	1.535	1.055	1.554	2.173		-0.715	-2.505	-1.535
1.5	-0.47		0.96	3.319	2.248	0.63	-1.11	-2.34	
1.14	0.11		0.44	1.729	1.688	0.58	-0.69	-0.68	-0.82
1.57	-0.08	1.83	1.04	2.869	3.368	-1.32	-1	-1.05	5.37E-10
1.091	0.6812	0.2612	-1.399	0.56	2.599	-0.1188	0.1113	-0.6187	0.5112
0.8212	0.6812	0.5912	-1.779	0.57	2.659	-0.6288	0.06125	-0.7787	0.3312
0	-0.17	0.51	-2.69	1.949	4.268	0.76	-0.2	0.1	0.17
-0.06938	0.4506		0.09062	2.049	3.998	0.1106	-1.079	-0.6894	0.07062
-0.85	2.44	-0.56	4.62	3.139	3.638	-0.04		-1.24	-1.59
-0.275	0.755		1.485	2.324	3.973	-0.975	0.515	0.025	
0.5081	0.2281	0.7981	4.458	1.527	3.536	-0.9519	0.5881	-1.462	0.8281
1.42	-0.83	1.27	0	2.719	3.948	0.21	-0.6	-0.29	-0.08
0.3891	1.999	-0.4309	0.5891	-0.1922		0.1991	-0.1609	-0.3609	0.5091

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
-0.17	0.68		0.88	0.3788	4.978	-1.02	-0.61	0.29	
0.89	0.82	0.11	-0.42	-0.4812	3.008	-1.09	-0.89	0.11	5.37E-10
3.694	0.2341	1.744	3.514	-0.5172	6.072	-2.056	0.1141	0.2341	
0.82	0.22	-0.58	-1.26	-0.9813	5.258	-1.29	0	-0.51	0.83
4.42	2.08	0.93	-0.43		8.358			0	
3.09	1.05	0.9	-0.78	1.699	6.798	0	-0.05	0.56	-1.54
-0.55	0.17	2.12	-0.26		4.308		0.03	0.15	-1.37
0.98	0.58	1.2	-1.04	-1.461	4.058		-0.65	0	
0.05062	-0.1994		0.6806		2.838		0.2606	-0.5894	
0.4063	-0.03375	-0.6738	-0.03375	0.035	5.054	0.6063	-0.5737	0.1363	-0.07375
-0.1744	0.2456	-0.1044	-0.1244		4.063	-1.294	0.3556	-0.1944	-1.884
0.265	0.585		0.065	-0.9662	4.553			-0.265	-0.065
0.84	0.92	1.42	-0.06	-0.3813	5.738	-0.9	0	-0.05	
0	0.06	0.14	0.08		1.638	0.08	-0.5	-0.15	
-0.2894	-0.07938	1.311	3.581	-2.151	3.558	-1.369	0.1006		-0.7694
0	-0.35	1.22	1.22	-0.9012	7.948	-0.05	0.19	0.02	-1.18
0.635	0.295	1.535	-0.955		7.393	-0.335	0.095	-0.415	0.905
0.625	1.335	1.775	-0.415	2.044	7.133	-1.055	0.615	0.015	-0.015
-0.33	0.02	-0.43		0.1888	5.558	0.72	-0.51	0.3	0.84
0.12	-0.07	0.11	0.4	-0.1912	5.318	0.16	0.17	-0.25	5.37E-10
0.2806	-0.009375	0.6006	0.9206	-0.3006	9.138	-0.6194	0.3306	0.6706	1.421
-0.04937	-0.07938	0.2706	1.391	0.1094	8.898	-1.529	-0.2594	0.1206	1.511
0.24	-0.01	-0.42	0	-0.00125	6.638	0.05	-0.17	0.03	-0.18
0.6981	-0.1519	1.248	-1.022	0.7669	7.246	0.07812	0.1281	-0.4819	1.808
0.45	0.05	1.08	2.74	0.4988	8.498	-2.62	0.79	0.45	5.37E-10
0.37	0.2	-0.02	-0.37	2.289	5.548	-1.25	0.18	-0.02	-0.45
1.96	-0.54	0.19	3.02	0.2487	2.578	-1.41	-0.41	0	-0.32
0.5825	-0.9375	0.5125	4.442	0.00125	4.77			-1.057	
0.8491	-1.241	0.2791	4.819	2.548	3.947		2.669	0.07906	-0.5709
0.27	-0.44	-0.69	4.26	4.009	1.538	-0.49	0	0.95	2.31
0	-0.45	1.07	3.75	6.229	3.258	-0.2	1	0.41	1.09
-0.6709	-0.6009	-0.0009375	1.409	0.9378	3.137	-0.7109		0.009063	-1.101
0.08	0.03	1.88	0.11	2.409	2.538	-0.54	-0.03	-0.13	0.2
	-1.029		2.301	5.56	3.229	-1.419	0.7513	-0.9587	
0.3041	-0.03594		4.004	2.573	5.152	0.6841	1.554	1.784	0.6541
-0.56	-0.87	-1	4.18	1.279	3.738	0.26	0.47	0.98	-0.22
0	-1.03		2.08	3.499	6.038		-1.36	1.54	-0.54

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-2.87		0	3.37	3.509	4.658	0.2	-1.6	-0.64	
-1.75	-2.2	0.9	5.36	4.859	6.348	2.3	0	1	-0.81
-1.42	-1.79	0.7797	3.19		3.847	0.5697	0.3197	0.1797	
-0.1188	0.8712	1.171	5.211	3.5			-5.069	-0.3087	
0.08125	0.4112	-0.4088	0.1512	3.91	5.659	-0.4088		-0.6787	-1.54
-0.44	0.32	-0.03	0.5	4.969	3.898	-0.96	-0.51	-0.12	-0.6009
0.3491		1.369	3.359	3.798	3.497	-1.021	-0.4509	-0.2809	-1.509
2.081	-0.4594	2.011	2.971	1.699	4.328	-1.019	-0.2494	-0.06937	
1.129	0.05906	0.6991	1.979	1.828	5.367	-2.181	-0.2309	-1.011	
1.707	-1.023	3.227	3.867	0.005625	8.014	-2.893	-0.3631	-1.243	
0	0.39	2.19	4.76	4.299	4.298	-0.31	-1.21	-1.61	0.14
-0.145	-0.665	0.035	4.345	2.754	3.823	-1.115	-1.535	-0.575	0.455
0.2756	-0.5844		5.486	4.134	6.733	-2.044	-1.094	-0.9744	-0.7844
1.57	0.23	2.74	3.3	4.129	5.378	-0.23	-0.38	-0.26	-0.99
2.661	-1.649	1.351	2.681	3.13	4.859	-0.6688	-0.4987	-0.1287	-0.2788
0.2491	0.2191	1.849			4.107	-0.07094	0.3891	-0.5509	
1.091	-0.4494	0.7906	3.941		4.248	-0.6394	-0.9294	-0.3094	0.2106
-0.1888	-1.339	0.4012	5.301	5.05	5.489		-0.1387	1.131	-0.9488
0	-0.08	1.87	3.78	3.119	4.468	-1.8	-0.15	-0.56	0.09
-0.9419	0.4181	1.818	2.948	5.027	3.596	-0.6019	1.318	-0.5319	-1.262
1.04	-0.93	-1.38	1.77	4.459	5.318	0.14	-0.85	-0.97	
0.23	0.15	0.15	3.1	4.019	5.428	-0.15	-0.2	-0.7	-1.63
-0.145	0.145	0.255	1.015		7.853	-0.455	0.645	-0.385	1.265
-0.5	0	0.75	0.01	5.599	6.928		0.08	0.08	
-0.33	0.02	1.57	0.89	3.989	7.618	-0.23	0.2	-0.02	-0.19
2.85E-09	-0.65	-2.85E-09	3.19		3.898	0.77		-1.41	
0.08563	-1.164	-0.5044	4.716	3.834	5.283	-0.03437	-0.6744	0.9956	0.2256
-0.545	-0.015	0.945	3.595	3.549	5.943	-0.445	-0.595	-0.375	0.015
0.4	-1.07	-1.36	5.35	5.459	6.528	2.68	0.01	0.41	5.37E-10
1.558	-0.7519	-0.3619	5.458	5.847	5.826		-0.2119	-0.09187	
0.165	-0.245	3.075	5.255	5.674	5.553			-0.285	
-0.055	0.005	1.115	5.465	2.804	5.673	-0.335	-0.005	-0.065	0.005
-0.11	-0.72	0.38	5.05	4.749	6.698		-0.06	0.06	
1.458	0.7081	1.028	4.198	4.547	4.896	0.2281	-0.2119	-0.6319	-0.9519
0.12	-0.66	1.61	3.28	3.549	5.668	-1.36	0.12	-0.88	1.03
0.945	-0.245	1.625	0.265	3.804	5.453	0.245	0.365	-0.365	0.455
-0.05	0.3	-0.06	0.55	4.769	6.008	0.05	0.09	-0.79	

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-1.13	0	-0.12	3.3	2.879	3.978	-0.21		-1.77	1.69
0.32	-6.03E-09	-0.37	3.82	4.199	5.198	1.38	0.23	-0.09	5.37E-10
0	0.01	-0.65	2.95	2.479	3.508	0.35	-1.12	0.32	-0.08
0.07	0.14		3.44	2.109	2.328		0.59	0	-0.79
1.336	0.3056	2.266	6.486	0.4144	5.453	-0.5644		-0.2944	-0.1544
0.88	-0.78	1.09	2.52	3.849	2.798	0.15	1.19	-0.52	5.37E-10
0.9212	-1.349	0.6112	1.361		4.499	-1.119	-0.2687	1.221	-1.079
	-0.065	0.295	2.945	1.754		-0.945		0.065	
0.605	0.805	0.625	4.805	-1.066	3.013	0.195	-1.195	-0.195	0.325
0.09	0.19	-0.01	3.39	0.6488	2.968	1.38	-0.14	-0.1	5.37E-10
1.7	0.63	0.33	3.15	1.279	2.978	-0.78	-0.31	0.6	0.32
1.78	-0.32	0.51	-0.97	4.649	5.858	-0.92	-0.82	0.88	1.92
0.75	0.21	0.62	2.7	2.499	4.448	-1.73	0	0.52	-1.06
1.84	-1.71	0.84	2.61	2.009	2.298	-0.58	-0.91	-1.51	
-1.08	0.4597		0.3697	1.788	2.757	-0.6003	0.1506	0.2897	-2.52
-0.2994	0.7906	0.4906	-0.3294			-1.169	0.2281	0.5706	-2.259
-1.152	0.3481	0.9881	-0.1119	0.9469	4.636	-2.232	-0.8487	0.3081	-1.482
-2.309	-0.2288	-1.079	0.6512	0.96		-0.4487	0.3113	0.3413	-1.639
-0.3788	-1.059	0.6812			0.9288		-0.4159	-0.1187	
-0.2159	0.7941	0.1441	2.044	3.633	0.6316		0.29	-0.7159	0.1441
-1.56	-0.46	1	-1.09	4.539	-2.292	-2.64	0.77	0	
0.58	-0.45	0.48	0.28	7.659	-1.082	-2.723	0.3969	0.6	
0.1769	-0.8531	1.157	0.1969	7.596	-0.1656	-0.305	0.495	0.3469	-0.3631
-0.145	-0.585	0.875	0.195	6.224	2.933	0.33	-0.82	0.145	
0.18	0.43	0.36	0.015	5.159	0.1575		0.845	-0.8	-0.95
0.675	-0.015	1.115	-0.105	7.274	-0.1275	-0.545	0.105	0.555	-0.065
0.675		2.035	-0.31	6.434	3.183	-0.665	0.99	0.105	0.195
0.69	0.07	2.26	0.305	5.889	-1.462	0.64	0.235	-0.07	-0.56
-0.215	0.135	0.525	1.26	4.094	-0.4075	0.3413	-0.67	-0.135	0.985
-0.45	-1.75	0		1.329	3.018	-0.8988	0.08125	-0.88	1.82
0.3113	-0.5088	3.291	0.1712			0.4291	1.221	-1.009	
-0.07875	0.2312	0.11			3.759	0	0.6591	0.05906	-3.771
-0.4509	-0.6209		0.009062		3.487		-0.66	0.36	-1.1
-0.15	-0.76		0.72	0.07875	1.888	-1.036	-1.376	2.354	-1.046
0.01406	-0.8359	-0.67	-0.4259	0.5928	0.9916	-0.01	-0.24	0.32	-0.08
0.01	0.18		0.91	2.689	1.788				
0	-0.64	-0.23	0.16	0.9288	0.1775	-0.02	2.05	-0.69	-0.9

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.2012	-0.7388	-0.5788	0.00125	0.69	2.069	-0.1788	-0.3787	0.6813	0.9212
-0.3788	-0.8188	0.5212	-0.2288	-0.31	1.399	-0.01875	-0.9087	0.3013	-0.9088
-0.625	0.615	-0.155	-0.105	1.544	1.553	-0.815	0.105	0.845	0.705
-0.12	-0.11		0.89	1.519	1.838	0.94	0.17	0.66	5.37E-10
-0.4	-0.15	-0.24	0.85	1.339	1.868	0.71	0	0.16	0.18
0.41	-0.12	-0.54	0.78	1.159	1.558	0.52	-0.75	0	-0.35
-0.38	0.42	-0.01	0.79	0.3187	1.118	0.59	-0.7	0	-0.66
-0.26	0.61	0	0.32	-1.611	0.6075	-0.26	-1.83	-0.62	0.14
0.54	-0.78	0	-0.5		1.358	0.84	-0.07	0.7	-1.96
0.5425	0.1425	-0.5375	-0.3975	0.00125	0.04	-1.638	-0.9075	-0.3175	-0.3575
-0.1319	-0.1919	-0.3019	-2.512	-0.3931	0.1456	-0.2119	-0.8319	-0.3919	-1.562
0.91	-0.17	-0.81	-0.36	-1.081	0.3175	-0.5	0.11	1.39E-17	-0.52
0	-0.49	0.12	0.07		0.0575		0.02	-1.01	-1.21
0.2106	0.1406	0.1006	-0.9694	0.3394	-0.2219	1.031	0.4006	0.1306	-0.4094
0.5225	-0.2975	-0.0475	-1.088	-2.019	0	0.2025	-0.5875	0.1225	0.4425
0	0.65		0.57	0.6288	0.9375	0.2		0.25	-0.15
-1.49E-10	-1.12	-0.52	0.06	1.229	1.018	-0.57	0.81	1.29	0.09
0.14	-0.85	-0.37	-0.4	1.209	1.218	-1.22	-1.66	-0.13	-0.07
0	-0.23	-0.4	-0.17	0.2888	0.5175	-0.39	-1	-0.76	0.34
0.8706	-0.04938	-0.08938	-0.1594	0.8594	1.608	-0.1894	-0.4594	0.9306	0.2406
0.3412	-1.389	-1.059	-0.02875	1.12	2.379	0.3613	0.09125	1.241	-0.3088
0	0.59	0.05	1.81	1.309	2.768	-0.7	-0.46	0.81	-0.55
-0.015	0.015	-0.815	0.265	0.1638	0.6925	0.105	-0.825	1.405	0.455
-0.285	-0.145	-0.735	0.865	0.2638	1.723	1.325	-0.745	0.965	0.875
-0.01875	-0.6088	-0.5588	0.7212	0.25	1.679	0.9813	-1.429	0.9513	0.5712
1.21	-0.17	-0.27	0.77	0.8488	0.3475	-0.22	-1	0.13	5.37E-10
-0.12	-0.12	0.51	0.86	0.8288	0.6175	0.69	0.93	0.6	0.24
8.33E-16	0.04	-0.33	0.9	0.5988	0.8075	0.73	-0.06	-0.26	0.59
0.25	0.41	0.18	0.05	-0.1412	0.7675	0.89	-0.64	-0.23	5.37E-10
0.81	-0.08	-0.19	0.71	1.449	1.398	-0.23	0	0.1	-0.02
-0.09	-0.25	-0.72	-0.12	1.259	0.9775	0.59	1.24	0	-0.44
0.08062	-0.8094	0.08812	1.151	0.5694	1.728	-0.03938	-0.1694	0.3806	-0.6094
-0.01188	-0.6219	-4.66E-10	0.9381	0.8269	1.606	0.2581	-0.5919	0.4281	-0.5519
-0.56	0.21		0	0.3688	1.608	0.02	0.38	0.41	-0.27
-0.6	0.28	-0.18	-0.07	0.1088	1.138	0.67	0.57	0.11	0.66
-0.4488	0.1012	-0.4388	0.2312	0.51	2.309	1.091	0.1713	1.141	0.3712
0.4906	-0.6294	-0.07938	0.08062	1.169	1.308	-0.4494	2.181	0.4606	

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.025	-0.475	0.765	0.275	1.354	1.603	1.195	0.595	0.165	-0.025
1.83	-0.38	-0.58	0.19	0.7988	0.8175	-0.73	-0.75	0.48	5.37E-10
-0.0875	0.1825	-0.4175	-0.3575	0.00125	0.37	0.9025	0.1425	0.1425	0.2525
-1.055	0.455	-0.095	-0.965	0.9738	0.8225	0.565	1.025	0.895	-0.115
-0.64	-0.22	0.67	0	-0.5712	-0.6425	0.05	-1.07	1.07	0.48
0.06	0.09	0.08	-0.86	-0.07125	0.2375	0	-0.37	0.64	-0.25
-0.89	0.74	0	-0.17	1.699	-1.482	1.18	0.28	0.81	-0.16
-0.3188	0.2112	0.4312	-0.06875	1.55	0.5888	-1.029	-0.2887	0.8413	-0.9888
0.27	0.24	0.85	1.05	2.509	0.6075	0.37	0	0.12	-0.49
-0.23	0.37	0.08	2.23	2.339	0.4875	-0.1	0.25	-0.3	0.36
0	-0.5	0.09	2.57	2.719	0.4375	-0.54	0.29	0.43	0.43
-0.68	-0.2	-0.85	2.17	2.519	0.2275	0.02	0.01	0	0.04
-0.1094	-2.629	0.2806				-2.789	0.5006	0.02063	
0.7	0	0.17	-0.04	-0.1412	0.9975	0.5	-1.33	1.03	-0.49
-0.6344	-1.024	-0.1944	0.5956	0.7744	-0.03687	1.206	-0.9644	0.2156	0.005625
1.218	-0.2419	0.4881	0.3381	1.277	1.996	0.5781	-0.6519	-0.4319	-1.142
-1.13	-0.08	-1.31	1.31	2.199	0.7275	-0.81	-1.35	0.08	-2.7
-0.57	0.23		0.4		2.068	-1.78		5.73E-09	-5.19E-09
0	1.19	0.26	0.46			-0.29	-0.34	0.87	
-0.9509	0.01906	0.2781	1.019	-0.1822	3.467	-0.8509	0.5291	-1.201	-0.7409
-0.9119	1.068	-0.1	0.7481	2.167	0.3356		0.6481	1.108	-0.2919
-0.83	1.16	-0.2688	0.53	1.859	0.4975	0.5	0.14	1.06	5.37E-10
-1.159	0.05125	-0.2	-0.2588	2.34	1.289		-1.299		
-0.66	0.67	-0.3388	1.19	1.149	0.9775	0.22	0.14	-0.38	1.96
0.3912	0.5412	1.35	-0.3288	0.31	0.8688	0.5913	-0.4287	0.2113	-0.4688
-1.85	3.01			3.449		0	-0.05	5.27	-0.54
-0.66	0.63	0.4312	1.05	2.779			-0.48	0.44	0.09
-0.2088	0.3112	0.2481	0.6412		-0.00125		-0.02875	1.461	0.8112
-0.74	0.18	-0.31	0.84	-0.05125	-0.3725	0.59		-0.27	1.22
0.08812	-0.2019	0.35	0.1281	3.117	0.9456	0.4781	-0.5519	0.3681	0.7981
0.65	1.03	0.61	2.32	1.289	-0.2425	-0.15	0.22	-0.04	1.63
-0.94	-0.73	0.28	1.64	3.379	2.628	0	0.72	-1.49	3.82
-0.5	-0.77	0.2212		4.119			3.59	0	
-2.17	0.59		-3.39	-0.09125	-0.1425	0.28	-1.84	-1.46	-0.16
	-0.00875		-0.9688		0.00875		0.1413	0.05125	-0.4888
-1.31	0.3		0.72	2.019	1.228	-0.28	-1.7	-0.56	0.19
1.892	-1.158		-0.0375	0.00125	-0.6		-0.1375	-2.927	1.272

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
1.181	-0.09875	-0.5488	0.9712	0.13	0.1288		-0.3087	-0.6087	-0.5988
0.1012	-1.589	-2.209	-1.469	0.57	-0.2612	1.941	0.09125	0.08125	-2.4
1.29	2.33	0.49	-1.24			-2.86	-2.17	-0.67	0.38
1.5	2.84	0	-1.19	-0.3712	-1.452	-0.77	-0.54	-0.55	1.504
3.614	-0.5159	-0.4159	-0.4559	2.263	1.972	1.634	-0.4359	-0.05594	5.37E-10
0.6	0.25	-0.4344	1.57	-1.426	0.1675	-4.02	-4.6	-2.65	-0.7444
1.176	-0.2244	0	1.706	-0.5912	0.9931	-0.9244	-1.284	-1.314	-0.6
1.35	-0.72	-0.005	2.12	-0.00625	0.3375	-3.52	-2.05	-2.28	-0.045
1.135	-0.625	-0.3088	1.885	-0.17	1.723	-2.125		-0.945	0.8613
1.561	0.4712	0.1056	1.961	-0.8856	2.819	-2.439	-0.02875	-1.529	0.6356
0.8256	0.2056	-0.86	1.686	0.1488	1.903	-1.784	-0.2944	-1.464	-0.72
0	0.77	-0.08	1.98	0.6188	1.818	-0.68	-1.99	-2.04	-0.39
0.09	-0.01		0		2.568	-0.69	0.26	-2.04	-0.1488
	3.491	1.741			2.379		-0.6687	-1.079	-0.6519
0.08812	1.658	-0.2719	0.03812	1.047	1.126	-2.112	-0.2619	-0.9619	-0.3644
-0.2144	1.056	-0.7344	0.4156	1.034			-0.1444	-1.504	-1.669
1.381	2.971	-0.9288	-0.7188	0.16	1.449	-1.209	-2.959	0.4313	-0.55
1.32	3.46		0	1.149	1.808	-1.5	-1.82	0.5	-0.4688
1.041	2.221	-0.2688	0.3512	0.89	1.749	-1.179	-0.1487	0.6113	-0.2188
-0.9288	1.831	-0.02875	-0.5188	0.3	-1.601		-2.029	-0.6187	
-1.105	3.235	0.945	-0.065	-1.436	-2.197		-0.245	-0.485	0.025
0.565	2.315	-0.135	-0.025	1.034	0.0825	-1.205	-0.395	-0.195	-1.159
0.08125	1.121	-1.179	0.02125	-0.02	0.05875	-0.4587	-0.1287	-0.09875	-0.4088
0.05125	1.711	-1.029	-0.5388	-0.64	1.359	-0.5088	0.1213	-0.5187	
-1.248	4.252	-0.4975	1.822	2.421	0			-0.8975	-2.44
-0.31	2.25	-0.79	0	0.03875	0.4675	-2.33	-2.21	-1.22	-0.895
-0.205	2.535	-0.845			0.4325	-1.905	-2.025	-1.145	-0.2694
0.4006	2.311	-0.4194	1.841	0.9394	2.228		-0.1694	-0.9094	-0.46
-0.15	2.01	-0.49	0.47	0.3688	1.078	-0.46	-0.07	-1.07	-1.808
0.0925	3.092		0.6325	0.00125	1.73	-2.208	-1.647	-1.377	-0.85
0.13	0.99	1.57	-0.44	-0.9012	1.698	-0.32	-0.28	-0.16	-1.06
-0.37	0.89	1.2	-0.37	-1.561	1.398	-0.78	-1.18	-0.61	-1.034
-0.4544	0.8056	1.056	-0.6944	-1.106	1.493	-0.6844	-0.7944	-0.5944	-0.37
-0.04	1.1	1.52	-0.5		1.378	-1.07	0	-0.14	-0.44
0.2	0	-0.78	0.58	-0.1512	0.0775	0.3	-1.97	-1.39	1.17
-0.32	0	-0.76	1.67	0.4688	-0.7225	0		-0.6	
-0.35	0.65		-0.61	3.239	1.688	0	0.27	-0.51	-1.43

Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
1.481	0.6912	0.1412	1.471	2.3	3.169	-0.1387	-1.769	-0.5287	-1.299
1.468	-0.05188	-1.612	1.478	1.637	2.876	-0.6619	-2.412	-3.292	0.01812
0.9	-1.18	0.94	3.6	1.659	2.108	-1.95	-1.1	-2.36	-0.91
1.191	-1.539	-1.029	1.571	2.26	1.559	-5.179	-3.349	-1.609	0.4313
-0.8775	0.1325		-0.4975	-0.7888	0	-1.628	-0.5875	-1.448	-1.128
-0.1194	-0.2594	-0.06938	0.3106	0.07938	0.7481	-0.4394	-0.02937	0.3206	0.3106
-0.03	0.33	1.51	-0.7	-0.9912	-0.5725	0	1.56	0.18	0.8
-1.834			0.1456			-0.8344	-0.1644	-0.9044	
-0.43	0	0.75	-0.97	0.8788	-1.332	-1.09		-0.55	-0.92
2.006	-2.194	-1.014	-3.114	0.9044	-1.097	3.246	-2.114	-0.9244	-1.294
2.501	-1.519	-0.3388	-1.979	1.22	-0.1512	3.661	-1.149	-0.3587	-0.3888
2.211	-1.339	-0.7188	-1.549	0.96	-0.4012	3.511	-1.319	-0.3787	-0.5888
-0.57	0.68	-0.06	0					0.4	-1.06
-0.045	0.055	0.045	-0.255	-1.716	1.113		-0.335	-0.675	0.335
-0.5194	0.6306	0.01062	0.3706		-0.4119		0.03063	-0.3594	0.9406
0.5425	-0.4275	0.1525	1.572	-0.04875	0	0.6925	-0.7575	-0.3075	-0.2775
	0.79	-0.12	0.54		0.0275	-1.37	0	-0.82	
-0.03094	-0.1509	0.4791	1.369	1.348	-0.2634	0.4191	-1.251	-0.6209	0.2891
-0.03875	-1.159	-0.7288	-2.109	-0.82	-1.671	0.4012	-0.9587	0.8213	1.291
0.58	0.55	0	0.55	-1.011	-2.092	2.47	-0.77	1.08	-0.21
0	0.02	0.9	0.87	-0.2612	-0.7425	0.52	0.36	0.11	-0.11
0.1925	0.2325	-0.4975	0.1425	0.2412	0	0.1225	-0.6075	0.7125	-0.0375
1.778	2.818	2.038	-0.9419	-1.843	-1.984	1.108	0.9281	-0.5519	-0.02188
2.425	0.275	0.055	-0.055	1.234	-1.057	0.785	0.915	1.765	-0.995
-0.815	-0.645	0.225	-1.595	-0.9262	-1.597	0.525	-0.115	-0.025	4.915
0.305	0.615	-0.255	-2.495				1.495	-1.175	1.705
0.425	2.145	-0.735	-3.785	-2.076		-1.885	0.135	-2.955	
0	-0.3	0.38	-0.28	-2.351		2.76	2.53	-0.94	
0.075	-0.285	-0.205			-1.177	5.055	0.345	-0.005	0.215
-1.17	-0.01	-1.01	-0.76	0.2488	-1.122	2.7	1.79	-0.13	3.92
-1.02	0.51	0.21	-0.55	-1.821		0.15	1.22	0	
-0.68	-0.27	0	-0.52	-1.201	-0.8625	-0.98	0.22	-0.2	1.21
-0.25	4.33	2.65	0	-3.831	-2.852		0.26	0.01	0.28
0.3913	0.6012	1.771	0.6712	-3.23	-1.991	-1.159	0.9813	0.07125	-0.04875
0.34	0.73	0.38	0.41	2.179	-2.902	0	0.88	0.51	-1.62
-0.31	0.29		0.32	-0.3613	-0.9125	0.23	0.51	0	0.47
-0.05	0.7	0.36	-0.17			0.05	-0.16	-0.29	0.09

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.48	0.31	1.06	0.72	0.7587	-1.202	0.59	0.32	0	0.29
0.4547	1.875	1.325	-1.725	-0.4966	2.142		-1.685	-0.7753	0.52
0	0.55	-0.42	1.48	0.4188	-1.082	-0.05	0.53	0.75	-0.06
-0.73		0.35	0	-0.6512		-0.41	0.31	-0.2	3.592
4.822	1.552	2.142	-1.048	0.00125	-1.93	-1.168	0.1625	1.793	3.592
-0.32	0	0.98	1.35	-0.8612		4.45	-0.2	1.05	
2.734	1.394	1.174	-1.276	1.163		1.414	0.8541	1.474	1.534
2.145	0.8847	0.8047	0.6047	-0.9966		3.345	2.585	1.465	2.565
0.34	0.02	-1.42	0	0.8088	-2.582	3.76	2.76	2.6	2.12
-0.345	-0.755	-0.445	0.075		-1.807	7.845	0.325	-0.075	0.845
0.2312	0.8612	-0.3488	3.001	-3.15	-1.591	5.461	2.751	3.131	-0.9688
1.166	1.186	1.066	4.676	-0.8456	-0.3469	6.606	4.906	4.516	0.01562
-0.6187	0.1412	-0.3388		-0.9	-1.011	2.541	0.2613	0.6513	0.04125
1.285	-2.205	-0.445	1.185	-1.676	-3.197	2.465	0.195	1.135	0.675
0.1725	0.1425	0.4625	1.092	-0.08875	0	0.4425	0.3025	-0.0775	-0.6875
0.39	0	1.02	0.47	0.7088	0.0775	1.13		-0.54	0.36
3.575	0.495	-0.095	0.035	-0.7662		1.125	-0.315	0.315	0.175
0.3181	2.098	4.168		-0.8431	-0.6044		1.428	-0.2919	2.928
-0.035	0.035	0.335	-0.055	-0.8862	-0.7675	0.275	1.135	-0.015	0.515
0.345	-0.645	0.475	-0.085	3.724	-0.2675	-0.325	0.125	1.765	1.895
0.42	0	1.63	0.12	3.719	0.4075	-0.42	0.08	1.29	1.17
0.3	1.85	1.51	0	1.889	3.818		-0.04		-0.72
0.1106	-0.5594	-0.2394	0.5406	1.819	1.168	0.7006	0.6506	0.8806	2.531
-0.2794	-0.4494	0.8506	-0.6594		-1.272		2.141	0.9606	2.761
-0.7244	-0.04438	0.8256		1.734	-1.537	-1.624	1.786	0.9856	2.106
-0.11	-0.14	-1.69	0.35		-0.5025	-0.11		-1.91	-0.49
0.1997	-0.2303	-0.8303	-0.2503	0.4484		-0.1703	-1.87	0.3197	-0.5903
-1.314	-0.1238	-1.044	-0.8938	0.125	-0.3762	-0.3637	-1.834	-2.124	1.156
-0.2519	1.028	0.02812	-1.022	-0.2031	-0.8744	-0.5619	-1.152	-1.972	-0.5519
-0.6575	0.1025	-0.0675	-0.2675	-0.9488	0	-0.5075	-0.6075	-0.0275	1.472
0.09062	-2.809	-0.8094	1.831	0.4594	1.048	-2.239	-0.6794	-0.6494	-0.6794
-1.59	-2.11	-1.76	1.89	0.9788	1.018	-1.18	-1.76	-2.35	-2.04
-1.052	1.868	-0.5219	0.8781		0.2756		0.1181	-0.07187	1.078
-2.22	1.33	-1.56	0.41			-1.35	-1.31	0.23	
-0.45	0	0.24	-0.1	0.7888	0.6175	-0.22	0.73	-0.1	0.38
-1.222	0.05812	-1.462	0.1481	0.8069	0.3156		-0.09187	-0.08187	-0.4819
-0.645	-0.575	-1.075	-0.845	-0.6262	-1.097	0.115	0.415	-0.145	-0.115

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.54	-0.18	-0.65	0.55	-0.1813		-0.68	0	-0.03	-1.15
-0.06875	1.011	-0.6488	1.291	-0.28	-0.5512	-0.2987	-0.2987	0.2813	-0.3488
-0.7775	2.562	-0.1675	0.3325	0.6812	0	0.4025	-0.3475	-0.4575	-0.5175
-0.9875	2.122	-0.6175	0.2925	0.1312	0	0.7725	-0.3175	-0.2075	-0.5675
-0.6919	1.518		0.8781	0.1769	-0.03437	-0.6619	-0.8919	-0.3019	0.3681
0.63	0.85	1.29	0.92	1.469	2.558	-0.62	-0.11		0.11
-0.9375	-0.9675	1.092	-1.258	3.731	0	0.0525	0.3325	-0.8375	1.242
-0.22	2.7	0.88	0	6.309	-1.782	0.72	0.03	-0.39	-1.3
-0.05	2.52	-0.08	-1.45			0.72	0.88	-1.29	
-0.4819	1.378	-0.3719	0.1181	3.187	1.666	-1.212	0.3781	-1.392	1.258
0.1947	-0.7053	-0.9453	-0.5453	2.663	3.862	-1.045	1.285	-0.7753	
-0.22	1.11	0.63	-0.25	1.169	-1.712	-2.27	-0.48	-1.15	-0.2
-0.34	1.75	-0.49	0	-0.00125	-1.242	0.6	-0.65	-0.17	1.51
-1.176	1.474	-1.116	0.4841	-1.107	-1.738	0.9941	-1.566	-0.5459	1.474
-0.2719	0.9281	0.5081	0.05812	1.437	-1.084		-0.2819	-0.03187	-0.9019
-0.01			0.72	0.2988	0.1375	-1.14	2.81	0.08	-0.17
	-0.79	-0.74			-0.7725	0.48	0	0.15	1.62
-2.539	1.251	-0.6588	-2.069	-1.41	-0.1712	0.1712	0.5112	0.4412	0.7212
0.095	-1.215	-0.095	-0.325		-1.277		1.535	1.545	
-3.378	-3.568	-3.478	-0.7475	0.00125		-3.498	0.5225	0.3525	-1.278
-2.1	0.06	-1.33	1.67	-2.051	-0.2925	0.55	0.67	0.07	-1.58
-0.1088	0.3412	-0.3688	0.3612	-1.39	0.1088	-0.6088	-1.369	0.2413	-0.6088
-0.7	-1.55	-1.08	-2	-2.481	5.698	3.5	-0.85	0.23	-0.23
-0.2038	-1.144		-0.3438	0.055	1.984		-0.4837	-0.8837	-0.7838
0.0225	-0.0075	1.162	-0.4375	-1.559	0	0.4425	0.0725	0.1925	
-1.74	-1	-1.31	-2.03			-1.22	0.94	0.36	-0.02
0.15	0.16	-0.61	-0.15	-0.2013	0.9975	-0.1	-0.52	0	0.21
-1.379	0.1612	-0.9188	-2.729	2.79E-11	2.048	0.01125	0.00125	-0.9887	-1.719
0.01	-0.72	0.86	-0.08	-1.571	2.728	0.41	0.06	0.43	
-1.042	-1.232		1.378	-2.063	-1.164	4.148	2.668	-1.112	-0.7519
0.7112	1.031	0.9912		-1.47	-0.6912		1.771	-0.4887	-1.809
3			1.82	-1.231		1.35	3.26	0.55	-0.27
-0.51	-0.08	-0.56	0.59		0.5875		0.68	-1.18	-0.11
1.67	-0.42	0.91	0.12	-0.6312	2.048	-0.29		-0.78	-1.91
0.6	-0.6		0.34	-0.1512	1.288			-0.53	-2.51
0.4006	0.06062	0.01062	-0.4094		1.048	0.2606	-1.159	0.3306	-0.5494
0.8	-1.03	0	1.17	-3.431	0.7575	0.71	-1.48	-1.81	0.58

Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
1.975	0.575	0.615	-1.505	-1.106		-1.425	1.045	-1.355	-0.065
0.28	0.85	-0.02	-1.12	-2.761	0.9275	0.02	0.16	-0.27	0.59
0.2691	0.02906		-1.971		0.7966		1.269	-0.7109	-1.291
0.2	0.95	-0.05	-0.88	0.3187	0.7475	0.01	0	0.81	-0.35
0.5	0.58	0	-0.51	0.08875	0.7075	0.12	0.08	1.02	-0.35
0.97	-0.84	-1.84	-3.08	-4.461	0.5475	0.6	0.12	0	0.84
1.33	-0.96	0.96	-0.25	0.9388	0.4175	-0.27	0.14	1.24	1
0.4	-1.25		-2.21	-0.8612	0.7275	-0.05		-2.4	5.37E-10
2.106		2.506		0.025	1.954		-0.02375	-1.604	
-0.92	-0.65	0.06	1.06	-2.941		0.9	-0.45	-0.53	-3.34
-0.5519	1.418	1.408	0.5781	-1.203		-2.112	0.7281	0.7681	-1.072
-1.645	-0.7053		1.655	-1.477		0.5147	2.245	1.485	-2.065
-3.4						0	0.48	0.12	
-0.76	0.53	-0.14	0.81	0.7188	-0.1825	-0.17	-0.51	0.26	-0.2
-1.034	-1.944		-0.4844	1.494	-1.677	1.686	-1.734	1.056	
1.91	0.27	2.43	0	-0.1512		0.75		-0.67	
1.109	-0.1709	1.589	-1.531			0.2791		-0.9709	3.089
0.51	0.45	-0.02		-1.191		0.78	0.11	0.52	5.37E-10
0.31	1.22	-0.03	0.63			0.03	-0.76	-0.05	-0.25
2.655	0.765	0.825	-1.305	-0.5962	-2.257	0.115	0.955		1.205
1.91	0	0.04	-3.61	-0.2412	-0.2625	1.53	2.11	2.05	1.95
-0.3831	0.1269	-0.6031	-0.6731	-0.1644	-0.04562		0.9269	1.757	-0.6531
0	0	-1.58	-1.73			0.12	0.78	0.99	0.44
0.54	0.24	-1.8	-0.1	-0.09125	-0.1425	0	0.48	1.3	0.19
0.56	0.27	-2.08	-0.32	-0.7312	-0.1125	0	0.64	1.08	0.31
-0.3397	-0.4897	1.68	-2.02	-3.041	0.007813	1.66	-0.4697	-4.46	2.73
-0.43	-0.43	0.3		-1.011		-0.63	0.01	1.75	
	0.2741	-0.3659	-1.476		-1.958	-0.4059	0.2241	0.5941	-0.3359
0.9525	0.4625	-1.188	-2.158	0.00125	-2.31	0.5525	-0.2175	0.9725	-1.018
0.2912	0.2012	-1.309	-2.769	0.15	-2.551	0.4112	-0.6087	0.8413	-1.009
-2.9	1.63	1.11	-3.42	-1.451	-0.1425	-1.22	0.13	-2.15	-0.89
-1.569	0.8112	-1.209	0.8712	-1.81	-1.831	1.291	1.341	0.1613	0.4112
-1.622	-2.022	-1.312	0.8481	-0.6731	-2.334	0.1881	1.038	0.1281	0.4281
0.2725	-4.358	-3.378	-3.488	0.00125	0.43	-3.178	-1.197	-0.8175	0.2425
0.81	-0.4	0.08	1.37	-2.691	-2.452	0.19	0.68	1.4	0.65
-0.43	-1.03	-0.1	0.01	-0.5313		1.51	0	1.38	-1.32
-0.4188	0.1412		0.9012		-3.271	-0.06875	0.8113	2.791	1.241

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-1.16			1.41		-5.302		3.14	1.39	
-0.73	-0.19	-2.59	0.34		-2.302	1.33	-0.2	0.47	-1.03
-1.649	-0.8394	-2.689	0.3006	0.00125	-4.992	1.511	-0.1294	0.3306	-0.7394
0.3525	-0.3275	-0.3775	-1.678	-2.677	-1.17	1.202	0.5125	-0.3375	-0.3675
-3.386	-0.6559	0.2241	-3.876	-2.311		2.344	-0.1659	2.554	-0.8459
0.3	-2.82	-0.61	-2.57	-3.083	-2.412	1.72	0.79	-0.05	0.4
0.4281	-2.532	-0.5019	-3.522	-1.02		1.848	0.6281	-0.3619	-0.1619
-1.359	-0.1688	-1.189	-0.8188		-1.061	0.2712	0.4413	-0.2887	1.621
-1.545	0.035	-0.995	-0.405	0.00125		-0.035	-0.325	0.125	
-2.798		0.3425	-1.818			1.742	1.513	0.7525	0.7125
-2.609	-1.439	-2.609	-0.7294	-3.327		2.151	2.321	1.101	1.571
-3.486	0.4541	-2.316	-2.846	0.00125	-2.828	2.334	2.534	0.2241	2.304
-1.368	0.1425	-1.498	-1.108	-4.971	-3.47			-2.177	0.8925
0	-1.59	-0.69	-3.59	-3.571	-5.152	0.4	0.11	1.78	1.06
-0.82	0.88	0.24	-2.49	-0.6331	-4.132	1.57	-0.14	-0.3	-0.8
-0.1219	-1.192	-2.442	-0.8919		-1.124	1.998	0.5381	0.7081	0.9981
-1.79	-0.91	-1.11	-1.46	-0.8313	-0.3525	1.56	1.68	0	-0.28
-2.73	-0.71	-1.09	1.24	-2.427	-2.652	0.12	-0.2	0	0.22
-2.206	-2.596		-0.5759	-5.591		1.414		-0.04594	
-2.51	-0.16	-1.59	0.13	-1.632		0	-0.13	0.4	
-2.131	-1.061	-0.8009		-1.941	-0.9934	0.2291	1.439	1.159	-0.05
-2.55	-0.27	-0.55	-0.33	-1.941	-1.322		1.25	0.12	
-0.86	0	-1.01	-0.54	-3.211	-0.3125	1.2	1.88	-1.12	-1.15
-1.03	-1.75	-0.61	0.94	-3.051	-1.882	2.36	0.72	0	5.37E-10
-2.38	-0.81	-3.76	-3.71	-1.991	-1.682	1.65	-0.1	0.89	0.1181
-0.4419	-1.032	-1.762	-3.292	-3.583	-6.244	1.988	0.1181	0.3981	
-0.5844	0.9756	-1.624	-3.404	-2.176	-5.497	0.3956	0.6556	-1.634	-0.21
-0.42	0.8	-1.61	-2.12	-1.251	-2.532	0.35	0.71	-1.27	0.71
-1.44	0	-1.24	-1.8	-1.021	-2.812	0.61	-0.26	1.75E-08	-0.8288
-4.529	-0.1388	-4.009	-2.559	-4.11	-4.751	2.601	1.311	-2.269	
-1.835	-2.405	-1.345		-4.476	-4.657	1.065	1.485	0.055	
0.5891	-2.391	-0.4809	-0.1109	-3.692	-5.333	1.499	-0.7409	-2.121	1.02
0.94	-1.29	-0.47	-0.64	-3.091	-2.552	1.65	-0.34	0.23	0.66
-0.31	0	0.23	-2.55	-1.641	-5.282	1.26	-1	0.79	0.49
1.09	0.03	-0.6	-5.22	-2.211	-6.362	-0.7	-0.5	1.09	5.37E-10
-0.12	-0.77	-0.57	-3.36	-1.181	-3.102	1.81	0.68	0.29	
-0.03094	-0.6909	-0.7209	-3.961	-1.252	-2.903	1.229	0.4591	0.1291	0.3591

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-3.38	-2.51	-3.02	-3.58	-4.381	-3.722	2	0.42	1.36	5.37E-10
-2.09	-1.5	-1.19	-2	-2.801	0.0175	0.48	0.69	0	-0.06
-1.962	-0.7519	-1.362	-0.3519	-1.743	-3.304		2.348	1.518	1.128
-3.21	-3.58	-2.06	-3.53	-3.861	-2.622	1.82	0	1.75	1.99
-3.01	-3.33	-3.99			-3.642	1.89	-0.08	1.78	2.04
	-4.184	-3.184			-3.347	2.296	-0.3444	2.176	2.006
-1.252			-3.692	-2.843		1.328	-0.5419	1.378	1.008
-0.72	-1.07	-1.11	-0.85	-1.021	-1.472	0.58	0.95	1.64E-08	-0.19
-0.78	-1.37	-2.01	-1.92	-0.3413	-1.152	1.67	0	0.73	1.15
-1.64	-2.79	0	-3.2	-2.051	-2.862	3.01	1.8	-0.68	0.61
-0.1	-2.46	-2.2	-0.65	-1.581	-1.652	2.03	1.4	-1.29	1.58
-1.364	-1.524	-1.974	-0.2538	0.055	-0.2262		-0.05375	-0.1537	1.456
-0.65	-1.55	-0.06	-0.92	-0.2812	-1.622	-1.26	3.57	4.16	3.26
-1.722	-2.012	-2.082	-0.2319	-1.273	0.1156	-0.2319	0.8881	2.408	2.178
-2.06	-2.4	-0.85	-1.71	-2.421	-1.832	2.03	1.87	1.75	2.6
-0.94	-3.13	-4.16	-0.25	-3.521	-1.602	1.25	0.38	0	1.65
-2.696	-3.666	-1.966	-0.5959	-4.217		1.804	0.01406	0.6641	-0.2259
-1.602	-2.202	-1.112	0.6081	-2.493	-2.024	0.6081	0.5081	0.7881	0.5481
-2.599	-1.989	-0.8394	0.2906	-1.151			0.9406	0.6306	0.7606
-3.261	-2.951		2.509	-4.422	-3.503	2.099	0.5691	0.4691	2.399
-5.674	-5.584	-5.654					0.1063	0.5763	0.1862
-4.089	-3.539	-1.869	0.4212	-1.06	-3.051	0.4513	0.8313	0.6213	0.5913
-5.119	-4.729	-4.799	0.1712	-1.26	-6.041	0.6013	0.6013	0.7713	0.4413
-4.599	-5.049	-5.119	0.3412	-1.03	-4.941	1.191	1.051	1.031	0.6213
-2.35	-2.14	-1.21	-2.2	-4.071			0.04	-0.04	1.25
-2.279	-2.159	-0.4888	-3.329	0.53	-1.621	1.911	1.761	1.851	1.221
-2.494	-3.214		-0.4744	-1.746	-0.7369	0.8156	0.1456	-0.06437	1.116
-1.72	-1.13	-0.19	-0.99	-1.021	-4.692	2.13	1.65	1.96	3.3
-2.03	-0.84	-0.97	-0.95	0.2388	-3.332	1.45	0.07	-0.35	1.46
	-1.549	-1.369	-1.509	-0.87	-1.711	0.8813		0.9113	0.7212
-0.06875	-2.299	-0.9988	-0.9688	-0.81	-0.4312	1.241	0.8413	0.04125	-0.2288
-0.06	-2.31	-1.89	-1.31	-0.8412	-0.7425	0	-0.08	1.01	1.09
0.5191	-3.491	-0.2509	-3.241	1.028	-3.803		0.2891	1.559	-0.1009
1.009	-0.5809	0.2391	-2.801	-0.4222	-3.483	-1.071	-2.431	0.1691	0.8491
-0.4159	-0.1059	0.2541	-3.346	-0.04719	-3.668	-1.106	-1.226	-0.5759	0.2341
-0.4809	-4.851	-3.071	-3.261		-3.163	-2.621	0.6491	-2.961	0.6591
0.9025	-1.798	-0.3775	-2.448	0.00125	-3.11	-2.338	1.823	-1.727	1.012

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-1.061	-2.191	-1.281	-2.311	0.6378		0.009062	-0.6809	0.9491	0.5991
0.255	-1.985	0.165	-1.885	1.304	-2.687	0.215	-0.165	-0.825	-0.275
-0.5331	-1.143	-1.343		-0.09438	-0.9756	0.6169	1.137	2.227	1.107
-0.31	-1.19	-1.06	-2.86		-1.352	0.6	1.28	2.46	2.21
0.5341	-0.1959	-1.166	-2.846	0.9728	0.1616	0.6841	0.9541	2.474	1.274
0.4025	-1.998	-1.438	-2.548	0.9812	0	0.5425	0.9725	2.302	1.412
0.005625	0.8356	-0.6444			-1.687	0.5556	-0.2144	0.04563	0.9756
-1.86	-2.09	0.18	-0.61	0.2988		0.73	2.09	0.93	-0.08
-3.352	-2.762		-2.072	-3.813	-0.2544	0.9181	1.888	0.8181	-0.6319
-0.45	-1.85	0	-0.89	-1.371	-1.342	1.6	-0.92	0.12	-2.32
-1.648	-0.9075	0.2125	-0.8075	0.7312	0	-0.6975	-1.398	0.2525	-0.6975
-0.94	-0.43	-0.04	-0.71	0.4088	0.4075	0.3	-1.24	-0.27	5.37E-10
-0.885	-0.185	-1.105	-1.295	-0.6563	-0.9075	0.855	-0.055	0.055	1.385
-0.9	-1.47E-09	-0.78	0	-1.121	-0.7925	0.91	-0.19	-0.43	1.56
-0.9787	0.3812	-0.9188	0.06125		-1.321	0.5513	-0.7587	-0.00875	0.6512
-1.42	-1.1	-1.48	0	-3.3	0.4875	1.16	-0.69	0.54	0.44
-0.515	-1.185	-0.535	0	-3.241		0.565	0.025	0.345	1.835
-1.364	-1.634	-1.994	1.406	-4.976	-0.09687	0.5856	-0.4544	-0.1644	0.4656
0	-3.22	-0.74	0.91	-4.161	-1.402	-0.66	1.01	-0.21	0.92
-0.9	-0.38	-1.46	-1.67	-2.471	-1.982	0.36	0.04	-0.35	-0.04
0.79	-0.45	-0.55	1.05	-4.581	-4.342	0.71	1.22	0.93	1.24
0	0.7	-0.53	2.64	-2.611	-4.252	1.58	1.04	0.52	
1.47	-1.17	1.09	4.21		-4.002	0.78	-1.71	-0.54	5.37E-10
-0.44		-1.08			-3.992	3.33	0.88	0	
0.085		0.375	-1.245		-2.547		-0.085	-0.315	
-0.1809	-2.591	-2.341	-2.021		-3.643	0.1791	-1.291	-2.251	2.649
-3.45	-3.59	-3.63	-4.12	-3.291	-5.832	1.26	1.39	-0.44	1.53
-2.079	-4.659	-2.579	-4.329				-3.679	-4.379	
0.3147	-0.5653		-2.315	-5.117	-2.468	0.9347	-2.185	-4.265	0.1047
-0.06031	-1.55	-1.82	-1.67	-3.422			-3.23	-2.67	1.72
-1.742	-2.102	-1.312	-5.112	-4.393		1.178	0.8181	-0.001875	0.2181
-2.05	-1.7	-0.69	-4.33		-2.722	0.92	0.94	0	-0.39
-0.43	-0.31	-1.04	-3.16	-3.691	-3.244	1.05	0.16	1.54	0.86
0.3281	-2.872	-0.8419	-3.092	-2.483	-0.9125	2.048	1.568	-0.07187	1.038
0.18	-2.57	-0.17	-2.02	-4.241	-0.8112	0.33	0.53	1.08	5.37E-10
0.1712	-0.4988	-0.6688	-1.569	-2.82		-1.039	0.7613	-0.08875	-0.4188
0.1212	-0.4788	-0.9288	-1.859	-3.17	-0.8312	-1.219	0.5313	-0.3387	-0.5488

Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.1987	0.1512	-0.6288	-2.559	-4.43	-1.021	-1.519	0.3613	0.6213	-0.05875
-0.145	0.265	0.605	-1.265	-5.086	-4.047	1.375	0.275	0.545	0.725
-0.55	-1.24	1.08	0.06	-5.371	-4.552	0.38	-0.19	0.03	5.37E-10
0.09	-0.21	1.14		-5.061	-5.402		0.86	-1.25	
-0.85	0	0.06	-3.72	-5.181	-3.282	-1.69	-1.16	0.17	0.45
-0.4103	1.82	1.14	-3.89			0.7297	-0.8403	0.4297	4.75
0	2.82	0.03	-4.07	-3.451	-4.632		0.4	-0.62	1.73
0.02	0.45	-3.06	-2.86		-1.922		0.88	-0.02	-1.44
0	0.19	-1.74	-2.08		-3.302		0.03	0.3	-2.5
-1.074	0.7956	-2.524		-2.146	-3.007	0.4156	0.3356	-0.06437	-3.744
-0.21	-0.37	-0.79	-1.36	-2.801	-2.182	-0.76	0.67	1.19	-0.62
-0.9719	-0.5619	-3.132	1.258	-2.563	-3.814	-0.02188	0.2081	0.8081	-1.732
-1.67	0.33	-0.12	-1.63	-1.291	-1.012	-0.52	3.32	0.05	-0.05
-0.8888	-3.719	-1.379	0.4712	-0.33	-2.281	0.2813	-0.4987	0.4113	-0.7988
	-0.1509	-0.4409	-0.5009		-2.893	1.999	1.109	-0.7809	0.2691
-1.349	0.1006	-0.02938	-0.9594	-0.5806		2.771	1.451	-0.7894	-0.9294
-0.9875	-0.7675	-0.4175	-1.128	-0.8188	0	1.082	0.2025	-0.6075	-0.0075
-1.288	-3.068	-2.008	-2.508	0.00125	1.95	1.522	-0.5975	-0.9775	0.8525
0	-0.14	-1.35	-0.37	-0.08125	-0.4525	0.75	-0.75	-0.2	-0.2
-0.66	-1.74	-0.47	0	0.78	-3.902	0.18	0.07	0.36	-1.29
0.08125	-0.7488	-1.559	-1.279		-0.06125	-0.5788	0.2013	0.7213	-0.3888
-0.695	-0.225	0.225	-1.545			-0.535	1.815	-2.795	2.525
-2.7	-1.68	-0.45	-2.82	1.379	0.5475	0.57	1.52	-1.33	3.02
-4.104	-2.994	-2.154	-4.614	2.305	-0.03625	-4.204		-3.754	
-2.44	0	-2.16	-2.22			-1.32	-2.86	-1.61	5.24
1.1	4.03	0		0.4891	-2.322		5.53	1.68	7.41
0.5103	3.45	1.39	-0.9997	-1.961	-1.732	-0.7097	5.03	1.17	7.03
0	2.1	-0.06	0.09	-0.6713	-2.162	3.97	1.3	2.16	3.82
0.34	1.18	-0.09	-0.16	-0.1244	1.428	2.16	0	1.1	2.31
2.487	1.147	-1.683	1.277	0.02563	-0.6856	1.257	-0.3231	2.447	2.967
-1.243	0.2069	-0.06313	0.6869		-0.6456	1.157	1.327	1.037	1.717
0.01	-0.73	-0.01	1.08	1.509	0.2175	-2.28	3.97	0.75	
0.23	-0.84	-1.25	0.71	0.36	1.078	-1	1.92	3.38	-0.36
0.3412	-1.499	-1.039	0.2812	1.469	-0.03125		2.301	3.211	0.07125
0	-0.03	-0.46	0.3	0.65	1.908	-0.95	2.29	3.17	0.74
0.1813	-0.7488	1.671	-0.2288		-0.7912	-0.5187	2.941	5.861	3.931
	-0.1688	2.541	-0.08875	-1.89	-1.071	-0.2088	4.171	7.141	5.661

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0	-0.57	-1.27	0.72	-1.271	0.6875	1.4	1.05	1.05	0.09
0.55	0.04	0.81	-0.04	-3.781	-0.1925	4.22	1.42	-1.86	1.41
-0.2819	0.6281	-0.6719	0.2881	-1.783	0.2756	2.298	-1.352	-1.002	1.398
-0.5987	0.5312	-1.729	-0.8988		0.1288	0.3113	0.8813	1.241	1.251
-0.4144	1.906	0.1456	0.8056	-0.2856		3.046	3.506	2.506	
-0.25	0.14	-2.44	1.92	0.9488	1.578	2.3	3.07	0.64	
-0.02	0.49	-0.02	1.59	-0.4212		3.35	-0.12	0.02	0.75
0	1.96	1.29	3.98	1.109	-0.1225	3.53	1.61	1.83	2.32
-0.14	0.14	0.74	2.45	1.899		3.53	1.02	1.87	
0.8806	2.361		2.001	-1.371	2.068	3.231	1.981	1.641	0.1006
-0.7038	0.7662	-1.494	-0.7738		-0.1062	1.446	3.166	2.806	0.7662
-0.92	0.38	-1.42	-0.26	-1.241		0.26	2.76	4.75	1.34
0.1241	0.004062	-0.2659	3.224		-0.1784	0.4441	2.834	1.664	0.2441
-0.41	0.34	-1.31	0.34	0.4388	0.6075	0.99	0.6	0.7	1.48
0	0.05	-0.34	-0.87	0.8488	-2.682	1.2	1.22	2.24	1.12
-0.2388	1.781		-0.6988	2.67	-1.461	1.211	3.051	1.541	1.461
0.65	0.54	0.05	-3.35	0.8188	-0.8825	-0.1	1.47	1.35	
0.42	0.5	-1.21		1.289	-0.9425	-0.17	1.18	1.24	0.93
0.3112	-0.1688	-0.1888	-0.9088	-0.59	-0.3612	0.6213	0.2513	0.9913	0.7412
-0.51	-0.64	1.09	-0.32	0.01875		0	1.54	1.15	1.98
-0.61	-0.1	0	-0.61		1.868	-2.54	2.61	0.74	2.7
-1.372	-1.642		0.5381	2.847	3.506	2.488	3.938	-1.202	6.178
-0.36		1.27	0	1.339	2.758	1.66	2.88	-0.31	4.93
-0.1887	-0.6488	-0.4288	0.7812	1.49	2.199	1.181	2.281	0.6113	3.791
-0.3488	-1.359	-0.5388	0.7212	0.25	0.8088	1.451	1.241	0.7913	
-0.18	0.19	-0.79	-0.65	-0.5812	-0.7325	2.36	2.28	3.05	1.95
-0.06	1.79	0	1.95	-1.941	-2.282	4.06	3.49	2.43	3.45
-0.51	1.78	0.82	1.67	1.03	-2.432	4.09	3.32	2.16	3.32
-0.1609	1.919	-0.02094	1.939	-2.062	-1.243	4.449	4.219	2.719	3.729
0.39	-1.42	-0.82	0.4	-2.051	-0.6225	1.55	-0.29	1.61	2.46
1.251	-1.479	0.5312	4.071	-1.45	-0.4712		2.381	4.591	3.671
-1.182	-0.6919	-1.312	-0.1719	-0.8231	-1.584	2.948	2.878	2.148	1.448
-1.58	-0.04	-1.26	2.8	2.129	0.8475	4.35	1.98	1.91	1.07
0.2113	-0.06875	-0.7688	1.011	1.03	-0.2512	2.351	1.731	2.021	2.241
-2.979	-3.009		2.291		0.3388	3.291	2.751	3.551	2.531
0.02625	0.09625	0.2762	2.116	0.445	-0.02625	2.686	3.046	2.206	2.296
0.69	-1.14	-0.57	0	-2.001	1.598	1.36	1.47	1.25	2.2

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-1.829	0.1106	-0.1994	-1.609	-2.651		3.161	2.861	2.401	1.936
-0.2738	-0.5238	-1.034	-0.04375		0.04375	2.456	1.476	0.7263	2.761
-1.009	-0.2488	-0.8288	-3.029	-1.83	-1.311	1.831	1.891	2.281	4.396
-1.454	-0.2644	-0.4044		-1.036	-1.387	3.546	3.636	3.966	2.31
0.91	-0.77	-0.02	0.2	-3.221	-2.612	2.98	2.08	2.69	2.29
1.12	-0.69	-0.36	0	-2.421	-1.712	2.91	1.53	2.56	3.899
-2.251	-2.061	-2.131	-2.611	-2.412	-2.593	3.979	2.259	5.329	4.22
-1.34	-0.93	0	-0.92	-0.9212	0.0375	3.83	1.87	4.2	3.31
1.58	-3.45	-0.1	-0.32	-4.581	-2.342	3.15	1.57	4.87	2.911
0.8212	-0.9988	-0.1888	-0.6988	-0.08	0.2588	2.631	1.181	3.091	4.45
-0.79	-1.31	0	-0.5	-0.8612	-1.352	4.9	3.3	3.47	4.338
-1.432				-1.693	-0.8744	4.958	3.478	4.158	4.61
-0.4	-1.72	-0.96	-0.9719	-0.2012	-0.3025	5.34	3.86	4.39	2.465
-1.695	-1.725	-2.535	0		-3.358	5.985	3.005	3.445	1.91
-2.39	-1.68		-1.215			5.01	1.8	2.48	4.018
	-3.872	-2.022	0		-4.504	4.508	2.458	4.028	3.902
0.6025	1.002	0.9825	-2.482		-1.54	4.892		1.783	2.71
0.02	0		-0.1475	0.00125	0.3975	4.04	2.97	0.87	3.851
-0.2394	0.5906	0.05062	0.2006	-0.06125	0.2881	3.951	2.561	0.3106	2.948
-1.082	-1.012	0.5581	2.558	-0.2606		2.478	3.708	2.878	2.574
-1.026	-0.3359	-0.9959	2.334	-0.1431	-0.5184	2.344	3.114	2.274	4.87
0.17	-5.03E-10	5.03E-10	3.36			5.3	2.94	3.6	2.161
-0.7287	-0.3488	-0.2788	1.451	-0.4412	-0.1712	2.871	1.621	1.321	4.72
3.48	-0.11	0	-0.3	0.37	-1.742	7.03	4.01	5.86	3.67
0	-1.77	0			-0.8625	4.97	4.14	5.11	6.65
-1.03	0.55	0		-1.101			4.1	3.68	
-0.7187	2.351	0.4212	0.1512	-1.26	-0.7612	3.191	4.951	3.691	6.77
-0.39	3.33		-0.17	-0.3112	0.2675	4.03	4.31	4.39	4.474
-1.576	1.544	0.2741	2.304			4.024	2.144	1.874	4.448
-1.552	1.708	0.4681	2.308	-2.983		3.868	2.178	2.098	
0.1812	-0.3688	-0.3588	1.921	-0.33			2.921	3.191	
-0.2944	-0.5644	-0.9644	1.416	0.1044	2.243	1.666	2.836	3.156	
0.9	-0.31	0	1.98	3.079	2.858	3.28	2.84	3.39	4.02
0.3906	-0.2694	-0.5194	1.481	2.969	2.368	3.071	2.131	3.081	3.751
-0.2644	-0.4544	-1.524	1.356	2.554	3.153	3.056	3.426	3.906	3.936
0.3369	-0.5431	1.457	5.437	0.04563	5.584	4.707	4.777	3.337	4.147
0	-0.41	0.4	5.23	2.009	5.258	4.36	4.37	3.14	4.33

Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
-0.05875	-0.5588	1.751	0.5112	0.09	3.699	3.911	5.451	5.591	3.501
-0.3088	-0.1388	0.05125	-0.1988	-1.31	-1.391	1.311	2.401	3.361	3.021
-0.8631	-1.223	0.1769	2.267	-0.08437	-0.7356	2.787	2.467	2.277	2.657
0.9781	-0.5019		-0.8719	-0.8531		4.098	4.978	4.548	4.458
-1.779	-0.7688	0.6012	-1.409	0.69	-1.831	0.5013	2.541	4.401	4.661
-2.414	-0.8644	-0.7844	-2.194	2.244	-1.927	0.9056	2.966	5.116	5.546
-2.489	-0.7188	-0.7388	-1.949	1.68	-1.831	1.001	3.101	5.041	5.091
-0.96	-0.62	-0.44	-0.91	-1.119	-0.8125	0.01	2.26	3.47	4.14
1.131		1.391		-0.09	0.08875	-0.2488	2.841	4.961	3.681
0	0.36	0.57	-0.59	-1.911	-2.152	-0.86	2.74	4.96	4.71
-0.1475	-0.5075	0.2525	1.902	0.00125	0.38	1.792	1.893	2.923	2.142
-0.4144	-1.644	-0.06438	1.876	-0.5756	-1.077	2.386	2.426	3.836	5.306
-0.2759	-1.036	-0.5759	-0.6659	-0.5672	0.1816	3.104	1.314	1.084	1.424
-0.92	0.04	0	-0.26	0.8988	-1.082	2.88	1.04	1.12	1.54
-0.5	0	-0.51	0.44		-0.1625	2.76	2.07	2.06	2.45
	-2.019	-0.6294	-0.1294	-1.571	-1.012	0.7806	2.791	5.071	6.081
0.63	-0.73	-1.8	-2.34	-1.521	-1.662	0.08	1.65	4.12	4.41
0.4413	0.6512	0.6212	-1.009	-0.87	-0.6312	0.1013			3.351
0.4756	-0.4244	-0.7644	1.206		2.283	0.1156	5.926	2.576	5.576
0.56	-1.08		-1.73			3.36	3.28	2.39	3.56
0.4881	-0.09188		0.7981			2.068	1.728	3.258	1.148
-0.17	0.79	-0.99	-0.62	-0.6412	0.8275	2.31	2.71	1.46	1.37
3.745	-0.335	3.345	-0.795	-3.056		4.215	6.145	3.375	4.715
4.981	-0.009375	4.561	-0.2794		-1.062	5.871	7.091	4.741	7.311
5.361	-0.3888	5.171	-0.3588	0.96	-1.501	6.341	7.321	4.571	7.201
0.29	0.58	-0.24	-1.77	-2.441	-1.092	-1.64	1.03	1.04	2.01
0.7712	0.8212	-0.05875	-0.6688	-0.42	-0.5412	2.541	1.561	1.511	2.551
0.86	0.83	-0.24	-1.82	-2.561	-1.942	2.73	1.98	1.57	3
-0.1809	-0.6209		1.639	-0.4222	-2.063	3.299	1.339	2.859	1.939
-0.9	-0.08	-1.17	1.89	-2.331	-2.242	4.09	2.11	3.22	2.41
-1.28	-1.21	-1.05	-0.13		-1.842	3.81	2.39	1.98	1.47
-0.73	-0.58	-0.65	0	-2.341	-1.482	4.09	2.86	2.19	2.05
-1.56	0	1.28	-1.02	-1.991	-3.432	2.71	2.21	1.24	0.61
-0.7531	-1.813		-0.4331	-0.2344		4.167	3.597	2.357	3.027
0	-0.37	0.65	-1.51	0.05875	-1.602	1.31	1.7	1.78	1.57
-2.269	-1.499		-1.299	-1.1		2.751	1.831	3.471	1.221
0.4312	-2.399	1.191	-0.9488	-1.32	0.7688	1.531	1.811	1.281	2.301

Table 2

| SW872 | BT-549 | HS578T | RPMI-8226 | MOLT4 | NB4+ATRA | SK-BR-3 | BT-474 | MCF7-NCI | T47D |
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.17	1.02	-0.34	0.44	1.319	0.6875	1.59	1.71	1.94	0.03
0.375	1.015	-0.065	0.605		0.8425	2.265	1.625	2.225	0.065
-0.665	-0.835	0.095	-0.095	-2.211	0.2325	-0.705	3.115	3.765	2.195
0.2	0.08	-0.15	-0.7	-1.277	-1.562	-1.04	-1.27	0	3
-0.6159	2.584	-0.2459	1.614		-2.208	0.9041	1.854	2.394	5.864
-1.32	0.69	-0.78	-0.02	-0.5412		-0.42	0.46	0.96	3.32
-2.05	1.34	-0.05	1.19	-0.2312	-0.5825	0.2	1.93	-0.62	1.15
0.21	1.17	0.94		-1.071	-0.7325		2.33	0.43	
0.02	-0.19	-0.53	0.66	0.8588	0.0175	0.12		-0.12	5.37E-10
0.78	0	0.89	0.74	-0.8412	0.3075		0.37	1.16	-0.59
-0.42	1	1.12	3.34					0	2.73
0.74	-0.11	0.21		-0.6212	-0.1525	-0.74	-0.48	1.04	1.48
-0.4988	-0.4488	-1.189	1.661	0.55	-1.871	0.6813	-0.7387	1.051	0.6012
-0.6175	0.9825	-0.3275	0.4625	-0.6188	0	1.652	2.002	-0.4175	0.5825
1.61	0.74	0	-0.48	-0.9012	-1.222	2.31	2.67	1.16	0.21
-1.249	-0.2788	0.6512				2.381	0.07125	2.791	-0.1788
0	-0.57	-1.17	0.87	0.3488	-0.8125	0.22	-0.02	1.36	1.86
0.08125	-0.9988	-0.7388	-0.4688	-2.33	-1.811	-0.4188	0.9613	1.181	1.671
0.3081	-0.8819	-0.8419	-0.2519	-0.5431	-0.8344		0.5881	0.5581	1.158
0.14	-1.13	-0.31	0.47	-0.5413	-1.012	0.18	0.09	0	1.27
-0.9844	0.5656	-0.1344	-0.3844	-1.116	-0.6569	0.4956	1.516	1.346	1.846
-1.069	1.181		-1.239	-1.85	0.1688		0.9412	0.8013	0.2712
1.184	-0.09594	1.194	-0.1059	-2.797	-0.7984	0.5241	1.944	-0.7859	0.01406
0.35	-0.16	1.18	-0.56		-3.082		1.52	0.6	-0.37
-1.14	-0.8	-0.1	-1.68	0.1188	0.1875	-1.63E-11	0.48	0.99	0.49
-0.0475	-0.6975	-1.138	0.2125	-0.9272	0	0.8225	0.3325	0.7825	0.1325
-0.2859	0.6141	0.02406	1.994	0.18	-0.6484	0.3341		0.4741	0.9841
-0.4588	0.5112		0.06125	0.44	-0.1212		1.561	0.1813	-0.1188
0.06125	-1.299	-0.04875	0.1912	-0.6056	-0.3712	-0.2087	0.00125	0.2013	0.8012
-0.6844	0.4556		-0.05438		-0.6969	-1.384	1.316	1.086	-0.06437
0.48	1.41	1.63	-0.57	0.4388	-0.4625	-0.63	-0.14	-0.81	0.29
-0.1638	-0.1238	0.8862	3.046	-0.005	3.764	0.3962	1.446	0.6563	0.00625
0.07	-0.75	-1	1.1	1.179	1.338	-1.1	0.14	0	-0.25
0.6906	1.221	1.961	-0.03938	2.189	-1.802	0.55	0.82	0.7506	2.341
0	0.43	-0.7	0.29	-0.1812	0.0275	-0.2019		0.08	0.77
-1.982	-0.5119	-1.262	-0.3219	-0.9731	0.1456			-1.192	0.01812
-0.6175	-1.328	-1.218	0.8625	0.2412	0	-0.0675	-1.468	-0.0875	1.082

Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
-0.375	0.195	0.155	-0.125	1.724	-1.867		0.165	1.915	1.825
-0.1159	0.2841		-0.1559	0.09281	-0.8184	-0.6759	0.8641	2.064	1.924
0		-0.08	-1.03		-1.822	0.33	0.2	0.81	2.09
0.9012		-0.3788	-0.7488		0.3588	-0.4288	0.8613	1.071	-0.2688
0.2706	-1.249		-0.4194	-1.351	0.9481	1.011		1.921	0.4006
1.211	0.09062		0.1506	-0.1912	-0.8919	-0.02937	2.181	2.091	3.201
-0.1	0	0.31	-0.08	-0.1912	-0.1625	-0.03	1.19	3.09	0.14
-0.7	0.28	-0.02	-0.4	-0.7213	-0.1325	1.83	0.64	0	1.01
0.5512	-1.389	-0.09875	-0.9988	-0.19	-2.881	0.5412	-1.809	0.6713	0.6112
-0.9687	1.231	-0.1988	3.531		0.3388	-1.929	2.011	3.611	-1.549
-2.42	-2.64	-2.92	-0.39	-1.191	1.308	-1.21	0	-1.16	0.69
-1.049	0.1712	-0.4288	-0.6788	-1.78	-0.02125	0.02125	-0.8187	-0.7487	0.7412
0	-0.97	-1.29	2.44	-1.571	-1.022	0.67	0.43	1.04	1.21
-0.58	-1.21	-1.16	0.37	-0.9812	-0.6525	1.29	0.21	0.23	1.78
	-2.752	-1.702	0.8381	-1.463		-2.782	-1.622	-0.6919	-2.382
-0.5875	-1.048	-0.8075	1.532	-1.019	0	-1.228	-1.748	-0.4175	-0.7875
-0.7775	-1.168	-0.6075	-0.1975	-0.01875	0	1.392	0.6025	-0.3275	0.2425
-0.71	-2.29	-0.52	-0.15	0.2688	-0.4325	0.57	0.8	0.58	5.37E-10
-1.012	-1.142	-1.212	1.478	0.1869	-0.05437	0.7281	-0.3319	1.248	1.308
-1.782	-0.4819			-2.033	-1.004	0.5581	-0.7819	0.5981	0.7781
-1.85	-0.8	-1.58	0.63	-2.291	-2.322	0.1	1.2	-1.24	-1.51
-1.45	-0.37	-1.33	0.63	-4.041	-1.952	0.86	0.71	-1.24	-0.7
-0.21	-0.72	-1.55	-0.01	-0.7913	1.248	-1.23	0.76	0	-0.77
0	-1.13	-0.98	0.19	-0.2212	0.6575	-0.05	-0.35	0.04	0.61
-0.84	-1.43	-1.61	2.27	-1.601	-1.322	1.28	0	-0.6	0.9
-0.7909	-0.2409	0.7191	0.1591	-0.3722	0.7766	-0.9609	-0.5609	0.8291	0.5691
-1.06	0.92	-0.66	1.48	1.159	-0.9025	2.99	1.23	0.99	-0.28
1.04	1.21	0.65	-1.63	-1.331	-2.242	-0.44	1.91	2.19	0.37
0.8056	1.046	0.3356	-1.654		-2.137	-0.5544	1.786	1.816	0.3656
-0.06	1.46	0.52	-0.98	-0.3612	-0.4725	0.93	0.52	0.51	0.46
-0.5087	-0.4988	-0.02875	0.6512	0.03	-0.7412	0.5513	0.8213	0.3613	1.231
-0.33	-0.23	-0.13	0	0.6988	-0.5125	0.57	0.99	-0.13	1.02
-1.198	-0.0675	-0.0875	-1.018	0.00125	-2.12	1.802	2.853	2.663	3.412
-0.05	-0.05	0	-0.31	-1.351	-1.812	0.66	0.48	0.69	1.405
-0.565	-0.835	-0.255	-0.015		-1.927	-0.115	0.015	1.155	5.37E-10
-0.32	-1.33	0.48	1.01	1.009	1.268	0.42	1.39	-0.66	0.2112
0.4112	0.2812		7.241	0.03	-0.1512	-1.289	1.181	0.5813	

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Table 2

SW872	BT-549	HS578T	RPMI-8226	MOLT4	NB4+ATRA	SK-BR-3	BT-474	MCF7-NCI	T47D
ARRY8X	ARRY10X	ARRY9X	ARRY16X	ARRY18X	ARRY17X	ARRY12X	ARRY13X	ARRY15X	ARRY14X
0.755	-1.145	1.395	0.435			-0.435	2.075	1.825	
-0.33	-1.59	0.88	2.35			-0.84	0	0.4	-0.39
0.1	-0.37	1.57	3.78	4.019	0.9875	4.32	1.66	-1.46	
-1.76	-0.46		0.6	1.149	1.148	2.6		-0.67	
-2.6	-2.31	-1.53	2.93	3.958	1.797	2.37	1.4	-0.4803	0.6197
-1.12	-1.35	-0.37	3.07	4.429	1.958	2.66	2.03	0	0.82
-0.45	-0.75	0.53	2.52	1.619	0.5375	-0.2	0.02	1.4	0.58
	-1.039	-0.2188	-2.549		1.249	2.231	3.261	-0.1287	0.06125
-0.22	-1.02	-1.55	0.46	0.4788	0.7975	1.85	2.71	-0.33	0.4
-0.5094	-1.259	-0.8194		-0.6806	0.3181	1.591	1.601	0.1406	0.8206
0.2212	-1.049	-1.029	0.3412	1.14	1.479	2.941	3.081	0.1613	0.7312
-0.9209		-0.7809	-3.161	-3.672	-2.573	4.959	4.029	0.2991	1.019
-0.54	-1.35	-1.22	-0.82	-0.8212	0.5175	3.93	3.19	0.7	1.37
-0.26	-0.75	-0.51	0	-0.3012	-1.372	4.52	3.72	0.99	1.33
0.06	-1.15	-0.65	-1.41	-1.491		5.16	4.32	1.31	1.6
-1.14	-1.2	-1.44	1.86	-0.2112	-0.5925	4.38	3.7	0.61	1.17
-0.04	0.04	-0.69	-0.2	1.329	1.608	3.72	3.9	0.06	0.63
0.11	-0.34		0.44	1.609	1.718	3.68	3.54	-0.11	0.74
0.27	-3.88	-1.34		1.329	0.9475	1.85	-0.78	0.45	0.83
-0.9475	-1.138	-0.3475			0		1.352	-0.0575	-0.0675
-0.86	0.47	-0.51		0.7988	0.1775	2.2	0.09	1.03	-0.2
-0.22	0.45	-0.95	1.27	0.8488	-1.372	-0.58	0.25	-0.02	0.82
-0.6919	0.4581	0.06812	0.02812	2.517	-1.244	-0.8319	1.128	-0.4919	0.1681
-0.2619	-1.042	-1.112	-1.352	1.467	0.04563	0.9881	-0.1919	-0.1219	0.06812
0	-0.01	-0.1	-0.61	-0.00125	-0.5225	2.01	-2.09	-0.44	-0.01
-0.35	-1.44	-1.89	-0.21	0.3288	-1.182	-1.66	-2.04	-0.56	0.43
-0.4959	-0.7059	-0.3659	0.7641	0.4728	1.022	-0.2259	0.3741	0.2741	2.114
0.6625	-0.9175	-0.6375	1.302	0.00125	0.09	-0.8775	0.8625	1.293	0.5425
0.72	-6.82E-09		0.56	-0.02125	0.2675	0	-1.11	0.63	-0.57
0	0.77		-0.63		-0.6825	0.5	0.33	-0.07	5.11
-0.4	1.35	0.23	-0.4	-0.6212	1.128	0.15	-1.43	-0.16	1.92
-0.2397	-0.8797		0.9503	-0.1109	0.6278	-0.6997	-0.3497	1.88	-0.6897
-0.3209	0.5891	0.4891	-1.541	0.9678		0.7891	-0.8009	-1.391	-3.061
1.141	1.331	-0.3388	0.6912	0.01	-0.2012	-1.459		-0.3687	-0.00875
0.2813	0.5212	-0.3488	1.441	0.14	-1.341	0.7013	3.141	0.1713	-0.1387
2.182	1.172	1.432	0.5425	-0.1288	0	-1.208	1.922	-0.6575	0.3325
1.725	0.975	0.075	0.075	-0.8362	-0.1375	0.285	4.025	-1.525	2.455

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Table 2

SW872 ARRY8X	BT-549 ARRY10X	HS578T ARRY9X	RPMI-8226 ARRY16X	MOLT4 ARRY18X	NB4+ATRA ARRY17X	SK-BR-3 ARRY12X	BT-474 ARRY13X	MCF7-NCI ARRY15X	T47D ARRY14X
0.52			2.35		-0.0625	2.1	2.03	-1.23	-0.68
0.005625	-0.3644	0.2056	3.306		0.1531		0.2956	-0.5544	-0.9844
2.146	-0.6144	-0.2144	0.1256		-2.547	1.246	-0.9144	0.5656	1.066
0.79	0.37	0.75	3.69	-1.111	0.2075	0.45	-0.32	0	-0.45
1.24	0.96	2.63	2.31	-0.6212	-0.8025	0.12	-0.44	-0.41	5.37E-10
0.8125	-0.6575	0.2925	1.732	0.8912	0	-1.138	2.332	0.7625	-0.6575
1.322	1.192	0.6725		-0.08875	0	-1.408	0.1225	1.212	1.072
0.9612	-0.3788	-0.4888	-0.2188	0.33	0.2188		1.361	-0.2987	2.231
-2.115	0.915	0.035	2.215	-2.226	-2.837	-0.225	2.135	1.845	-2.355
1.119	-1.091	-1.071	-1.331	-0.9222	-2.553	2.089	-1.261	0.5191	
0	0.22	-0.15	0.89	-0.1712	-0.0125		-0.18	0.68	
1.174	0.04406	0.1341	1.534	-1.147	-1.328	0.1441	1.384	-2.076	0.3241
0.3812	0.5412	-0.08875	1.701	0.45	1.309	0.1612	0.9213	-0.3587	-0.1688
-2.245	-0.055	0.435				0.055	1.505	-2.485	0.285
-1.138	0.1019		2.442	-2.369	0.09938		-0.4481	-1.568	-1.128

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Table 1

	YORF	NAME
	AID	
	EWEIGHT	
1	GF202:96(116F12):384(16L23)	ESTS, MODERATELY SIMILAR TO FK506-BINDING PROTEIN 65KD [M.MUSCULUS] AA496878
2	GF202:96(114E4):384(16I8)	CHONDROCYTE-DERIVED EZRIN-LIKE PROTEIN AA486435
3	GF200:96(3F2):384(1L4)	MATRIX METALLOPROTEINASE 9 (GELATINASE B, 92KD GELATINASE, 92KD TYPE IV COLLAGENASE) T72581
4	GF200:96(13B3):384(4C5)	DUFFY BLOOD GROUP T82477
5	GF200:96(23C5):384(6F10)	HEPARIN COFACTOR II T62086
6	GF201:96(68A8):384(24A16)	RIBOSOMAL PROTEIN S6 KINASE, 90KD, POLYPEPTIDE 3 R95841
7	GF200:96(7D1):384(2H2)	RIBOSOMAL PROTEIN S6 KINASE, 90KD, POLYPEPTIDE 3 H55921
8	GF200:96(31D11):384(8H22)	ESTS, WEAKLY SIMILAR TO RIBOSOMAL PROTEIN S6 KINASE 3 [H.SAPIENS] H67666
9	GF201:96(89C5):384(11F10)	LEUCYL/CYSTINYL AMINOPEPTIDASE H08816
10	GF201:96(93C9):384(12F18)	MEIS (MOUSE) HOMOLOG 2 R59167
11	GF201:96(70B12):384(24D23)	ESTS, WEAKLY SIMILAR TO HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I B FORM PRECURSOR [H.SAPIENS] N71796
12	GF201:96(70B4):384(24D7)	291290 N72228
13	GF200:96(8E10):384(2J19)	TIGHT JUNCTION PROTEIN 2 (ZONA OCCLUDENS 2) W31983
14	GF200:96(5H1):384(2O1)	HISTAMINE N-METHYLTRANSFERASE H53274
15	GF201:96(98A1):384(13B1)	ANTIGEN IDENTIFIED BY MONOCLONAL ANTIBODY MRC OX-2 H23979
16	GF201:96(97A4):384(13B8)	229901 H70866
17	GF200:96(19A7):384(5B14)	HOMO SAPIENS MYOSIN LIGHT CHAIN KINASE (MLCK) MRNA, COMPLETE CDS AA487215
18	GF200:96(4G3):384(1N5)	547247 AA085318
19	GF200:96(5D9):384(2G17)	NEURONAL PENTRAXIN I H22481
20	GF200:96(24F1):384(6L1)	HOMO SAPIENS MRNA; CDNA DKFZP586A1519 (FROM CLONE DKFZP586A1519) AA452981
21	GF200:96(13F3):384(4K5)	COLLAGEN, TYPE XV, ALPHA 1 AA464342
22	GF201:96(99H11):384(14O21)	79565 T62854
23	GF200:96(13C4):384(4E7)	DECAY ACCELERATING FACTOR FOR COMPLEMENT (CD55, CROMER BLOOD GROUP SYSTEM) R09561
24	GF200:96(7C3):384(2F6)	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE (CAM KINASE) II GAMMA T96083
25	PEROU:96(6D5):384(20G10)	ALPHA-1-ANTICHYMOTRYPSIN N72559
26	GF201:96(56E2):384(21I4)	HUMAN CHROMOSOME 16 BAC CLONE CIT987SK-A-362G6 N75498
27	GF201:96(96E4):384(13I8)	COMPLEMENT COMPONENT 1 INHIBITOR (ANGIOEDEMA, HEREDITARY) AA481438
28	GF201:96(85E6):384(10I12)	P311 PROTEIN H80685
29	GF202:96(110A7):384(15A14)	EXOSTOSES (MULTIPLE)-LIKE 2 AA490078
30	GF201:96(65D2):384(23H4)	503741 AA131466
31	GF201:96(102D12):384(14H23)	46694 H10192
32	GF201:96(57D6):384(21H12)	ENDOTHELIN RECEPTOR TYPE B N29914
33	GF201:96(55A1):384(21A1)	768344 AA424996

Table 1

34	GF201:96(66C7):384(23F13)	156322 R72618
35	GF201:96(98B4):384(13D7)	ENDOTHELIN CONVERTING ENZYME 1 H18427
36	GF201:96(62H12):384(22P23)	428485 AA004514
37	GF201:96(56H11):384(21O22)	HOMO SAPIENS MRNA FOR KIAA0467 PROTEIN, PARTIAL CDS N95780
38	GF200:96(18H11):384(5O22)	AE-BINDING PROTEIN 1 AA490684
39	GF200:96(7B11):384(2D22)	AE-BINDING PROTEIN 1 AA490462
40	PEROU:96(2F4):384(19K8)	FIBROBLAST GROWTH FACTOR RECEPTOR 1 AA281189
41	GF201:96(97B11):384(13D22)	FIBROBLAST GROWTH FACTOR RECEPTOR 1 (FMS-RELATED TYROSINE KINASE 2, PFEIFFER SYNDROME) R54846
42	GF200:96(30B2):384(8C4)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.SAPIENS] AA281189
43	GF201:96(98F9):384(13L17)	ESTS, WEAKLY SIMILAR TO KIAA0291 [H.SAPIENS] AA488178
44	GF200:96(3G8):384(1N16)	MADS BOX TRANSCRIPTION ENHANCER FACTOR 2, POLYPEPTIDE C (MYOCYTE ENHANCER FACTOR 2C) AA234897
45	GF200:96(3H6):384(1P12)	LAMININ, GAMMA 1 (FORMERLY LAMB2) H24650
46	GF200:96(31G2):384(8N4)	HOMO SAPIENS MRNA; CDNA DKFZP566B0846 (FROM CLONE DKFZP566B0846) R62780
47	GF200:96(3A4):384(1B8)	PERIPHERAL MYELIN PROTEIN 22 R26960
48	PEROU:96(10C2):384(18F3)	DIHYDROPYRIMIDINASE-LIKE 3 (DPYSL3) AI831083
49	GF201:96(65B7):384(23D14)	133864 R28660
50	GF200:96(29G2):384(8M3)	47043 H10721
51	GF201:96(82E8):384(9J15)	HOMO SAPIENS BAC CLONE RG041D11 FROM 7Q21 AA032221
52	GF201:96(89C7):384(11F14)	HUMAN OVARIAN CANCER DOWNREGULATED MYOSIN HEAVY CHAIN HOMOLOG (DOC1) MRNA, COMPLETE CDS W69790
53	GF200:96(15E10):384(4J20)	TISSUE FACTOR PATHWAY INHIBITOR (LIPOPROTEIN-ASSOCIATED COAGULATION INHIBITOR) T47454
54	GF201:96(97E5):384(13J10)	ALDEHYDE DEHYDROGENASE 1, SOLUBLE AA664101
55	GF201:96(64D9):384(23G18)	HOMO SAPIENS MRNA FOR KIAA0758 PROTEIN, PARTIAL CDS N95226
56	GF200:96(26A2):384(7A4)	VON WILLEBRAND FACTOR AA487787
57	GF200:96(2G11):384(1M22)	PLATELET/ENDOTHELIAL CELL ADHESION MOLECULE (CD31 ANTIGEN) R22412
58	GF201:96(89E9):384(11J18)	MANIC FRINGE (DROSOPHILA) HOMOLOG H22922
59	GF201:96(88D8):384(11G16)	INTERCELLULAR ADHESION MOLECULE 2 R21535
60	GF200:96(28H8):384(7P15)	245147 N76361
61	GF201:96(93A5):384(12B10)	REGULATOR OF G-PROTEIN SIGNALLING 5 AA668470
62	GF201:96(86D9):384(10H17)	TEK TYROSINE KINASE, ENDOTHELIAL (VENOUS MALFORMATIONS, MULTIPLE CUTANEOUS AND MUCOSAL) H02848
63	GF200:96(29F5):384(8K9)	LIM BINDING DOMAIN 2 H74106
64	GF200:96(24E2):384(6J3)	KINASE SCAFFOLD PROTEIN GRAVIN AA478542
65	GF201:96(82E1):384(9J1)	359722 AA011182
66	GF200:96(15E1):384(4J2)	TYROSINE KINASE WITH IMMUNOGLOBULIN AND EPIDERMAL GROWTH FACTOR HOMOLOGY DOMAINS AA432062

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Table 1

67	GF200:96(14B5):384(4C10)	CD34 ANTIGEN AA434483
68	GF200:96(12A12):384(3B23)	HUMAN DNA SEQUENCE FROM CLONE 1033B10 ON CHROMOSOME 6P21.2-21.31. CONTAINS THE BING5 GENE, EXONS 11 TO 15 OF THE BING4 GENE, THE GENE FOR GALT3 (BETA3-GALACTOSYLTRANSFERASE), THE RPS18 (40S RIBOSOMAL PROTEIN S18) GENE, THE SACM2 N78611
69	GF200:96(25F12):384(7K23)	69672 T53626
70	GF200:96(4A2):384(1B3)	HOMO SAPIENS KDR/FLK-1 PROTEIN MRNA, COMPLETE CDS AA026831
71	GF200:96(3H7):384(1P14)	LAMININ, ALPHA 4 R43734
72	GF202:96(109D2):384(15G3)	INTEGRIN BETA 3 (ALTERNATIVELY SPLICED, CLONE BETA 3C) [HUMAN, ERYTHROLEUKEMIA CELL HEL, MRNA PARTIAL, 409 NT] AA037229
73	GF201:96(91F10):384(12K19)	429349 AA007419
74	PEROU:96(7E6):384(20I12)	MITOGEN INDUCIBLE 2 H29253
75	GF201:96(91F4):384(12K7)	TRANSCRIPTION FACTOR 4 AA669136
76	GF201:96(83C5):384(10E9)	KIAA0476 GENE PRODUCT W81135
77	GF200:96(5E5):384(2I9)	DISABLED (DROSOPHILA) HOMOLOG 2 (MITOGEN-RESPONSIVE PHOSPHOPROTEIN) H54686
78	GF200:96(13E10):384(4119)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.SAPIENS] N73030
79	GF200:96(13F9):384(4K17)	COAGULATION FACTOR II (THROMBIN) RECEPTOR AA456375
80	GF200:96(13G9):384(4M17)	CATHEPSIN E H94487
81	GF201:96(55D7):384(21G13)	ESTS, WEAKLY SIMILAR TO EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.SAPIENS] H73479
82	GF200:96(31B1):384(8D2)	BIGLYCAN N51018
83	GF200:96(14C7):384(4E14)	BIGLYCAN R77226
84	GF201:96(95C12):384(13E23)	GLYCOPROTEIN A REPETITIONS PREDOMINANT AA122287
85	GF201:96(57H12):384(21P24)	CADHERIN 11 (OB-CADHERIN, OSTEOBLAST) AA136983
86	GF200:96(13H10):384(4O19)	CADHERIN 11 (OB-CADHERIN, OSTEOBLAST) H96738
87	GF201:96(87H8):384(11O15)	MICROFIBRILLAR-ASSOCIATED PROTEIN 2 N67487
88	GF200:96(29G5):384(8M9)	TUMOR SUSCEPTIBILITY GENE 101 R02529
89	GF200:96(11C2):384(3F4)	DISCOIDIN DOMAIN RECEPTOR FAMILY, MEMBER 2 AA243828
90	GF202:96(109C9):384(15E17)	MICROTUBULE-ASSOCIATED PROTEIN 1B AA219045
91	PEROU:96(2H9):384(19O18)	THROMBOSPONDIN 1 AA007557
92	GF200:96(1E8):384(1I15)	THROMBOSPONDIN 1 AA464630
93	GF201:96(58F3):384(21L5)	NEUROPILIN 2 N26125
94	PEROU:96(10B7):384(18D13)	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 2 W52204
95	GF202:96(109B8):384(15C15)	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 7 T53298
96	PEROU:96(3B6):384(19D12)	VIMENTIN AA147847
97	GF200:96(15A11):384(4B22)	VIMENTIN AA487812
98	PEROU:96(9D12):384(18H24)	SPARC/OSTEONECTIN AA031595
99	PEROU:96(7A6):384(20B12)	SPARC N95151
100	PEROU:96(9E7):384(18I14)	SPARC/OSTEONECTIN AA045463

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Table 1

#	Clone	Description
101	GF201:96(86G9):384(10N17)	SECRETED PROTEIN, ACIDIC, CYSTEINE-RICH (OSTEONECTIN) H95960
102	PEROU:96(8D9):384(20H17)	COLLAGEN, TYPE V, ALPHA 2 AA004204
103	PEROU:96(7F4):384(20L8)	CD46/TROPHOBLAST-LYMPHOCYTE CROSS-REACTIVE ANTIGEN AA678559
104	PEROU:96(8F11):384(20L21)	FIBRILLIN 1 (MARFAN SYNDROME) AA056415
105	GF200:96(12G8):384(3N15)	FIBRILLIN 1 (MARFAN SYNDROME) AA418811
106	GF201:96(90E8):384(11J15)	LYSYL OXIDASE-LIKE 2 AA676458
107	GF200:96(25D8):384(7G15)	COLLAGEN-BINDING PROTEIN 2 (COLLIGEN 2) R71440
108	PEROU:96(3B4):384(19D8)	937223 AA181288
109	GF201:96(96E7):384(13I14)	COLLAGEN, TYPE IV, ALPHA 2 AA430540
110	PEROU:96(8A5):384(20B9)	COLLAGEN, TYPE IV, ALPHA 1 R78226
111	GF201:96(96E8):384(13I16)	COLLAGEN, TYPE IV, ALPHA 1 AA150402
112	PEROU:96(2D6):384(19G12)	1126447 AA679959
113	GF200:96(17F11):384(5K21)	LAMININ, BETA 1 AA446251
114	GF200:96(13F2):384(4K3)	COLLAGEN, TYPE XVIII, ALPHA 1 W07798
115	PEROU:96(8F4):384(20L7)	CONNECTIVE TISSUE GROWTH FACTOR AA044993
116	GF200:96(15D3):384(4H6)	TRANSCRIPTION ELONGATION FACTOR B (SIII), POLYPEPTIDE 3 (110KD, ELONGIN A) AA133129
117	GF200:96(25C11):384(7E21)	CONNECTIVE TISSUE GROWTH FACTOR AA598794
118	GF200:96(23E2):384(6J4)	754358 AA436142
119	GF202:96(112C8):384(15F15)	KIAA0569 GENE PRODUCT N45100
120	GF200:96(5F6):384(2K11)	ESTS, HIGHLY SIMILAR TO NIL-2-A ZINC FINGER PROTEIN [H.SAPIENS] H46553
121	GF200:96(30F7):384(8K14)	ESTS, HIGHLY SIMILAR TO NEURITIN [R.NORVEGICUS] R66101
122	GF201:96(99B3):384(14C5)	FMS-RELATED TYROSINE KINASE 1 (VASCULAR ENDOTHELIAL GROWTH FACTOR/VASCULAR PERMEABILITY FACTOR RECEPTOR) T52674
123	GF200:96(29H1):384(8O1)	HOMO SAPIENS CLONE 23887 MRNA SEQUENCE R98695
124	GF200:96(4E9):384(1J17)	HUMAN TRANSGLUTAMINASE MRNA, 3' UNTRANSLATED REGION R97066
125	GF201:96(88G2):384(11M4)	590692 AA156324
126	GF201:96(98H5):384(13P9)	FC FRAGMENT OF IGG, RECEPTOR, TRANSPORTER, ALPHA T53509
127	GF201:96(91H6):384(12O11)	FC FRAGMENT OF IGG, RECEPTOR, TRANSPORTER, ALPHA AA430668
128	GF200:96(7B5):384(2D10)	KIAA0022 GENE PRODUCT H60460
129	GF200:96(11A9):384(3B18)	HOMEO BOX D3 AA411244
130	GF200:96(19H10):384(5P20)	GROWTH FACTOR RECEPTOR-BOUND PROTEIN 10 AA136336
131	GF200:96(31C4):384(8F8)	129610 R16604
132	GF201:96(97B6):384(13D12)	BONE MORPHOGENETIC PROTEIN 4 AA463225
133	GF201:96(65D3):384(23H6)	301995 N89738
134	GF201:96(94E8):384(12J15)	HUMAN HOX2.2 GENE FOR A HOMEOBOX PROTEIN AA610066
135	GF200:96(10H1):384(3O2)	HOMEO BOX B5 H02340
136	PEROU:96(10C4):384(18F7)	H FACTOR (COMPLEMENT)-LIKE 1 W88788
137	GF200:96(14A2):384(4A4)	84750 T74567
138	GF200:96(4F8):384(1L15)	RETINOIC ACID RECEPTOR RESPONDER (TAZAROTENE INDUCED) 2 AA481944

Table 1

139	GF201:96(101F10):384(14L20)	HOMO SAPIENS MRNA FROM CHROMOSOME 5Q31-33 REGION T57920
140	GF201:96(55A2):384(21A3)	PLATELET-DERIVED GROWTH FACTOR RECEPTOR, ALPHA POLYPEPTIDE H23235
141	GF200:96(26A11):384(7A22)	THROMBOSPONDIN 2 H38240
142	GF200:96(1F4):384(1K7)	HUMAN TUMOR NECROSIS FACTOR-INDUCIBLE (TSG-6) MRNA FRAGMENT, ADHESION RECEPTOR CD44 PUTATIVE CDS W93163
143	GF200:96(13F4):384(4K7)	134783 R31701
144	GF200:96(1A10):384(1A19)	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY MEMBER 2 T99653
145	GF200:96(21E11):384(6I21)	SOLUTE CARRIER FAMILY 16 (MONOCARBOXYLIC ACID TRANSPORTERS), MEMBER 2 (PUTATIVE TRANSPORTER) AA425612
146	GF201:96(70E8):384(24J15)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4589520) [H.SAPIENS] AA043878
147	GF201:96(89E3):384(11J6)	MICROFIBRIL-ASSOCIATED GLYCOPROTEIN-2 AA056013
148	GF200:96(29C1):384(8E1)	197474 H52098
149	GF202:96(159D2):384(17H4)	786609 AA478481
150	GF201:96(90G11):384(11N21)	FIBROBLAST ACTIVATION PROTEIN, ALPHA AA405569
151	PEROU:96(6E9):384(20I18)	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR AA056022
152	PEROU:96(10C3):384(18F5)	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR AA056022
153	PEROU:96(10B9):384(18D17)	CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN AA722599
154	PEROU:96(10B4):384(18D7)	PLASMINOGEN ACTIVATOR, UROKINASE RECEPTOR AA147962
155	GF200:96(24F2):384(6L3)	FIBRONECTIN 1 R62612
156	GF200:96(12G2):384(3N3)	FIBRONECTIN 1 R62612
157	GF200:96(25H1):384(7O1)	HUMAN ISOLATE JUSO MUC18 GLYCOPROTEIN MRNA (3' VARIANT), COMPLETE CDS AA497002
158	GF201:96(58A11):384(21B21)	H.SAPIENS MRNA FOR INHIBIN BETA(A) SUBUNIT N27159
159	GF201:96(57A2):384(21B4)	HUMAN MRNA FOR FIBRONECTIN (FN PRECURSOR) N26285
160	GF201:96(85D11):384(10H22)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] H77494
161	GF200:96(10A2):384(3A4)	244703 N52533
162	GF200:96(5D1):384(2G1)	HOMO SAPIENS MRNA FOR NIDOGEN-2 AA479199
163	GF201:96(88F8):384(11K16)	LIM DOMAIN ONLY 7 H22826
164	GF201:96(81A6):384(9B12)	LIM DOMAIN ONLY 7 AA005112
165	GF200:96(3G11):384(1N22)	LUMICAN AA453712
166	GF201:96(67C12):384(24E23)	782701 AA447610
167	GF201:96(88C1):384(11E2)	LAMININ, ALPHA 2 (MEROSIN, CONGENITAL MUSCULAR DYSTROPHY) AA034939
168	GF201:96(96C1):384(13E2)	DERMATOPONTIN R48303
169	GF200:96(23F9):384(6L18)	HEVIN AA490694
170	GF200:96(26G11):384(7M22)	SECRETED FRIZZLED-RELATED PROTEIN 4 AA486838
171	GF200:96(14B7):384(4C14)	CATHEPSIN K (PYCNODYSOSTOSIS) R01515
172	GF201:96(92H4):384(12O8)	OSTEOMODULIN N32201
173	GF201:96(101H5):384(14P10)	78921 T60482
174	PEROU:96(1F6):384(19K11)	PLATELET-DERIVED GROWTH FACTOR RECEPTOR-LIKE AA461197
175	GF200:96(6A2):384(2A4)	PLATELET-DERIVED GROWTH FACTOR RECEPTOR-LIKE AA455210

Table 1

176	GF202:96(116B12):384(16D23)	MUSCULIN (ACTIVATED B-CELL FACTOR-1) AA470081
177	GF200:96(13F5):384(4K9)	COLLAGEN, TYPE V, ALPHA 1 R75635
178	PEROU:96(8E6):384(20I1)	471748 AA035018
179	PEROU:96(8E9):384(20I17)	SMOOTH MUSCLE ACTIN, ALPHA2 AA040169
180	PEROU:96(8C12):384(20F23)	TRANSGELIN/SM22 AA010664
181	PEROU:96(9C9):384(18F18)	SMOOTH MUSCLE PROTEIN 22-ALPHA AA010664
182	PEROU:96(8E7):384(20I3)	LUMICAN AA035657
183	PEROU:96(10C11):384(18F21)	FIBULIN 1 AA614680
184	GF200:96(10G12):384(3M24)	COLLAGEN, TYPE VI, ALPHA 3 R62603
185	GF200:96(22G4):384(6M8)	HOMO SAPIENS OSF-2 MRNA FOR OSTEOBLAST SPECIFIC FACTOR 2 (OSF-2P1), COMPLETE CDS AA598653
186	GF200:96(14F10):384(4K20)	COLLAGEN, TYPE III, ALPHA 1 (EHLERS-DANLOS SYNDROME TYPE IV, AUTOSOMAL DOMINANT) T98612
187	PEROU:96(10C5):384(18F9)	COLLAGEN, TYPE I, ALPHA 1 W90360
188	GF200:96(25D11):384(7G21)	COLLAGEN, TYPE I, ALPHA 2 AA490172
189	PEROU:96(8F6):384(20L11)	COLLAGEN, TYPE III, ALPHA 1 (EHLERS-DANLOS SYNDROME TYPE IV, AUTOSOMAL DOMINANT) AA044829
190	GF200:96(24F7):384(6L13)	COLLAGEN, TYPE III, ALPHA 1 (EHLERS-DANLOS SYNDROME TYPE IV, AUTOSOMAL DOMINANT) T98612
191	GF201:96(63A6):384(23A11)	COLLAGEN, TYPE I, ALPHA 2 W93067
192	GF201:96(86E1):384(10J1)	THY-1 CELL SURFACE ANTIGEN AA496283
193	GF201:96(92D9):384(12G18)	HOMO SAPIENS, ALPHA-1 (VI) COLLAGEN AA046525
194	PEROU:96(8F9):384(20L17)	COLLAGEN, TYPE VI, ALPHA 1 AA047209
195	PEROU:96(10D9):384(18H17)	COLLAGEN, TYPE VI, ALPHA 1 AA047209
196	GF201:96(91D10):384(12G19)	HUMAN ALPHA-2 COLLAGEN TYPE VI MRNA, 3' END AA633747
197	GF201:96(55A6):384(21A11)	HUMAN METHIONINE SYNTHASE MRNA, COMPLETE CDS AA233650
198	GF201:96(55B6):384(21C11)	265694 N25353
199	GF201:96(96E1):384(13I2)	COMPLEMENT COMPONENT 1, R SUBCOMPONENT T69603
200	GF200:96(25D5):384(7G9)	COMPLEMENT COMPONENT 1, S SUBCOMPONENT T62048
201	PEROU:96(9D6):384(18H12)	COMPLEMENT COMPONENT 1 S SUBCOMPONENT AA055520
202	PEROU:96(10A4):384(18B7)	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR R56687
203	GF200:96(4C6):384(1F11)	810213 AA464525
204	GF201:96(64C1):384(23E2)	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA460304
205	GF201:96(57F10):384(21L20)	LYSYL OXIDASE W60414
206	PEROU:96(9D2):384(18H4)	HUMAN LYSYL OXIDASE (LOX) GENE EXON 7 AA037732
207	GF201:96(84A10):384(10A20)	137984 R63085
208	GF201:96(62F6):384(22L11)	120678 T95650
209	PEROU:96(2F2):384(19K4)	TISSUE INHIBITOR OF METALLOPROTEINASE 3 (SORSBY FUNDUS DYSTROPHY, PSEUDOINFLAMMATORY) AA445923

Table 1

210	GF201:96(86D1):384(10H1)	TISSUE INHIBITOR OF METALLOPROTEINASE 3 (SORSBY FUNDUS DYSTROPHY, PSEUDOINFLAMMATORY) AA099153
211	GF201:96(95H6):384(13O11)	FIBULIN 1 AA134871
212	GF200:96(2G12):384(1M24)	PLATELET-DERIVED GROWTH FACTOR RECEPTOR, BETA POLYPEPTIDE R56211
213	GF201:96(66F1):384(23L1)	ESTS, WEAKLY SIMILAR TO MACROPHAGE LECTIN 2 [H.SAPIENS] N53421
214	GF200:96(1A7):384(1A13)	DOWN SYNDROME CANDIDATE REGION 1-LIKE 1 H19439
215	GF200:96(7F8):384(2L16)	HUMAN EXTRACELLULAR MATRIX PROTEIN 1 MRNA, ALTERNATIVE SPLICE VARIANT, COMPLETE CDS N79484
216	GF201:96(101F8):384(14L16)	80643 T57803
217	GF201:96(86G3):384(10N5)	SECRETORY GRANULE, NEUROENDOCRINE PROTEIN 1 (7B2 PROTEIN) AA670429
218	GF201:96(96H4):384(13O8)	CADHERIN 2, N-CADHERIN (NEURONAL) W49619
219	GF201:96(64E10):384(23I20)	428048 AA002061
220	GF200:96(12B7):384(3D13)	GROWTH ASSOCIATED PROTEIN 43 H05445
221	GF200:96(5F1):384(2K1)	MELAN-A N26562
222	GF200:96(12A5):384(3B9)	MANNOSIDASE, ALPHA, CLASS 1A, MEMBER 1 T85698
223	GF200:96(3D12):384(1H24)	MYOSIN VA (HEAVY POLYPEPTIDE 12, MYOXIN) AA025850
224	GF201:96(79C10):384(9E19)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] N67810
225	GF200:96(1E7):384(1I13)	THYROXIN-BINDING GLOBULIN T64901
226	GF200:96(24C11):384(6F21)	GLUTATHIONE PEROXIDASE 2 (GASTROINTESTINAL) AA135289
227	GF201:96(87B5):384(11C9)	PROTEIN KINASE C, MU N53380
228	GF201:96(83F2):384(10K3)	HOMO SAPIENS MRNA; CDNA DKFZP434N103 (FROM CLONE DKFZP434N103) AA431753
229	GF201:96(101H1):384(14P2)	HOMO SAPIENS CLONE 24421 MRNA SEQUENCE T60063
230	GF200:96(26F3):384(7K6)	PHOSPHATIDIC ACID PHOSPHATASE TYPE 2B T72119
231	GF200:96(21C4):384(6E7)	PHOSPHATIDIC ACID PHOSPHATASE TYPE 2B T71976
232	GF201:96(94F4):384(12L7)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA130874
233	GF201:96(58E11):384(21I21)	AMYLOID BETA (A4) PRECURSOR PROTEIN (PROTEASE NEXIN-II, ALZHEIMER DISEASE) W42849
234	GF201:96(86H11):384(10P21)	RAS HOMOLOG GENE FAMILY, MEMBER E W86282
235	GF200:96(16B5):384(4D9)	784593 AA443302
236	GF201:96(63G6):384(23M11)	ESTS, WEAKLY SIMILAR TO IGE RECEPTOR BETA SUBUNIT [H.SAPIENS] AA128162
237	GF201:96(55G4):384(21M7)	C3H-TYPE ZINC FINGER PROTEIN; SIMILAR TO D. MELANOGASTER MUSCLEBLIND B PROTEIN W16832
238	GF201:96(58C7):384(21F13)	FIBRINOGEN, A ALPHA POLYPEPTIDE AA011414
239	GF201:96(70C5):384(24F9)	L1 CELL ADHESION MOLECULE (HYDROCEPHALUS, STENOSIS OF AQUEDUCT OF SYLVIUS 1, MASA (MENTAL RETARDATION, APHASIA, SHUFFLING GAIT AND ADDUCTED THUMBS) SYNDROME, SPASTIC PARAPLEGIA 1) N27145
240	GF200:96(16B12):384(4D23)	RADIXIN AA477165
241	GF201:96(97B4):384(13D8)	BRANCHED CHAIN KETO ACID DEHYDROGENASE E1, ALPHA POLYPEPTIDE (MAPLE SYRUP URINE DISEASE) AA477298
242	GF200:96(14F1):384(4K2)	HUMAN BINDING PROTEIN MRNA, 3'END H89664

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Table 1

243	GF201:96(85F7):384(10L14)	305809 N90051
244	GF200:96(12E9):384(3J17)	GELSOLIN (AMYLOIDOSIS, FINNISH TYPE) H72027
245	GF201:96(81E12):384(9J24)	259996 N32611
246	GF201:96(89A1):384(11B2)	SER-THR PROTEIN KINASE RELATED TO THE MYOTONIC DYSTROPHY PROTEIN KINASE N35241
247	GF202:96(112D8):384(15H15)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.SAPIENS] AA181868
248	GF200:96(16B2):384(4D3)	RIBONUCLEASE, RNASE A FAMILY, 1 (PANCREATIC) AA487797
249	GF200:96(7D12):384(2H24)	NEUREGULIN 1 R72075
250	GF201:96(87H1):384(11O1)	MONOAMINE OXIDASE B AA682423
251	GF200:96(18H9):384(5O18)	NUCLEAR FACTOR I/B W87611
252	GF200:96(15F8):384(4L16)	INTERLEUKIN 1 RECEPTOR-LIKE 1 AA128153
253	GF200:96(5C1):384(2E1)	SOLUTE CARRIER FAMILY 21 (PROSTAGLANDIN TRANSPORTER), MEMBER 2 AA037014
254	GF201:96(88E7):384(11I14)	INHIBITOR OF DNA BINDING 3, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN AA482119
255	GF200:96(2A9):384(1A18)	SELECTIN E (ENDOTHELIAL ADHESION MOLECULE 1) H39560
256	GF200:96(27B1):384(7D2)	FLAVIN CONTAINING MONOOXYGENASE 3 H71847
257	GF202:96(110B7):384(15C14)	ENDOTHELIAL CELL-SPECIFIC W46577
258	GF201:96(93G3):384(12N6)	ANGIOPOIETIN 2 AA125872
259	PEROU:96(2C4):384(19E8)	MAX-INTERACTING PROTEIN 1 AA179689
260	GF200:96(3F4):384(1L8)	MATRIX METALLOPROTEINASE 1 (INTERSTITIAL COLLAGENASE) AA143201
261	GF200:96(23G1):384(6N2)	H.SAPIENS MRNA FOR GLUTAMINE CYCLOTRANSFERASE AA282134
262	GF200:96(6C4):384(2E8)	NEURONAL CELL ADHESION MOLECULE R25521
263	GF201:96(69A10):384(24B20)	213850 H72368
264	GF200:96(6E1):384(2I2)	WASP FAMILY VERPROLIN-HOMOLOGOUS PROTEIN N59851
265	GF200:96(10A11):384(3A22)	THYMOSIN, BETA, IDENTIFIED IN NEUROBLASTOMA CELLS N91887
266	GF200:96(2E8):384(1I16)	PTK7 PROTEIN TYROSINE KINASE 7 AA453789
267	GF201:96(15G12):384(4N24)	SIALYLTRANSFERASE 8 (ALPHA-N-ACETYLNEURAMINATE: ALPHA-2,8-SIALYTRANSFERASE, GD3 SYNTHASE) A AA169311
268	GF200:96(26F2):384(7K4)	HUMAN CLONE 23826 MRNA SEQUENCE AA173746
269	GF200:96(10H9):384(3O18)	HEXABRACHION (TENASCIN C, CYTOTACTIN) T77595
270	GF201:96(89D9):384(11H18)	CANICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER AA429895
271	GF201:96(79B7):384(9C13)	CAG REPEAT CONTAINING (GLIA-DERIVED NEXIN I ALPHA) R95691
272	GF200:96(32D11):384(8H21)	CAG REPEAT CONTAINING (GLIA-DERIVED NEXIN I ALPHA) N59721
273	GF200:96(4G6):384(1N11)	SMALL PROLINE-RICH PROTEIN 2C AA399674
274	GF201:96(89A2):384(11B4)	RIBOSOMAL PROTEIN L5 AA027277
275	GF201:96(89E4):384(11J8)	ESTS, MODERATELY SIMILAR TO ALTERNATIVELY SPLICED PRODUCT USING EXON 13A [H.SAPIENS] AA157955
276	GF200:96(28H5):384(7P9)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4929675) [H.SAPIENS] R01796
277	GF201:96(57C4):384(21F8)	PROSTATE DIFFERENTIATION FACTOR N26311
278	PEROU:96(6C9):384(20E18)	CYCLIN-DEPENDENT KINASE INHIBITOR 1A (P21, CIP1) N23941
279	GF200:96(2F1):384(1K2)	PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 R06605

Table 1

280	GF200:96(26H4):384(7O8)	QUINONE OXIDOREDUCTASE HOMOLOG AA668595
281	GF201:96(100D10):384(14G20)	45629 H08730
282	GF200:96(21A3):384(6A5)	SULFOTRANSFERASE, ESTROGEN-PREFERRING AA449459
283	GF200:96(11E11):384(3J22)	PIRIN H69334
284	GF200:96(18G2):384(5M4)	HUMAN PROTEINASE ACTIVATED RECEPTOR-2 MRNA, 3'UTR AA454652
285	GF200:96(4A12):384(1B23)	INTEGRIN, BETA 8 W56709
286	PEROU:96(3B9):384(19D18)	INTEGRIN, ALPHA 2 (CD49B, ALPHA 2 SUBUNIT OF VLA-2 RECEPTOR) AA069096
287	GF200:96(4B4):384(1D7)	INTEGRIN, ALPHA 2 (CD49B, ALPHA 2 SUBUNIT OF VLA-2 RECEPTOR) AA463610
288	GF201:96(79B1):384(9C1)	271441 N34799
289	PEROU:96(1C11):384(19E21)	INTEGRIN, BETA 8 W56709
290	PEROU:96(6F2):384(20K4)	SECRETED FRIZZLED-RELATED PROTEIN 1 AA002243
291	GF200:96(25C8):384(7E15)	CRYSTALLIN, ALPHA B AA504943
292	GF201:96(55A3):384(21A5)	PROTEIN S (ALPHA) T74192
293	GF201:96(59C7):384(22E13)	METHYL-CPG BINDING DOMAIN PROTEIN 1 AA459922
294	GF200:96(5F8):384(2K15)	HOMO SAPIENS MRNA; CDNA DKFZP564L176 (FROM CLONE DKFZP564L176) N74741
295	PEROU:96(2E1):384(1912)	JUN ACTIVATION DOMAIN BINDING PROTEIN AA293362
296	GF200:96(26F6):384(7K12)	JUN ACTIVATION DOMAIN BINDING PROTEIN W96134
297	GF201:96(85F4):384(10L8)	HUMAN PROTO-ONCOGENE BCD ORF1 AND ORF2 MRNA, COMPLETE CDS AA013481
298	GF201:96(81C11):384(9F22)	502396 AA156946
299	GF201:96(95G6):384(13M11)	GRO1 ONCOGENE (MELANOMA GROWTH STIMULATING ACTIVITY, ALPHA) W42723
300	GF200:96(5B1):384(2C1)	PROTOCADHERIN 2 (CADHERIN-LIKE 2) R89615
301	GF201:96(79A3):384(9A5)	ESTS, WEAKLY SIMILAR TO ZINC FINGER PROTEIN 91 [H.SAPIENS] N64741
302	PEROU:96(8B7):384(20D13)	241097 H80335
303	GF201:96(15E11):384(4J22)	TISSUE FACTOR PATHWAY INHIBITOR 2 AA399473
304	PEROU:96(2G11):384(19M22)	TISSUE INHIBITOR OF METALLOPROTEINASE 1 (ERYTHROID POTENTIATING ACTIVITY, COLLAGENASE INHIBITOR) AA287220
305	PEROU:96(6G9):384(20M18)	CLAUDIN 4 AA506754
306	GF200:96(26H1):384(7O2)	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 10B AA453410
307	GF200:96(25H11):384(7O21)	CD44 ANTIGEN (HOMING FUNCTION AND INDIAN BLOOD GROUP SYSTEM) AA282906
308	GF201:96(89A7):384(11B14)	RAS INHIBITOR AA291556
309	GF200:96(31A2):384(8B4)	EST, MODERATELY SIMILAR TO CD-7 METALLOTHIONEIN-2 [H.SAPIENS] R16596
310	GF200:96(26C4):384(7E8)	METALLOTHIONEIN 1L N80129
311	GF200:96(27A1):384(7B2)	METALLOTHIONEIN 1H H77766
312	GF200:96(9G2):384(3M3)	METALLOTHIONEIN 1G H53340
313	GF200:96(14G3):384(4M6)	ALANINE-GLYOXYLATE AMINOTRANSFERASE (OXALOSIS I; HYPEROXALURIA I; GLYCOLICACIDURIA; SERINE-PYRUVATE AMINOTRANSFERASE) N57872
314	GF201:96(98A4):384(13B7)	HUMAN METALLOTHIONEIN (MT)1-F GENE N55459
315	GF201:96(89E5):384(11J10)	HUMAN METALLOTHIONEIN (MT)1-F GENE T56281
316	GF201:96(79F3):384(9K5)	487722 AA043551

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Table 1

317	PEROU:96(6A6):384(20A12)	FOS-RELATED ANTIGEN 2 AA101616
318	PEROU:96(6A7):384(20A14)	111437 T90760
319	GF200:96(2H3):384(1O6)	PLASMINOGEN ACTIVATOR, UROKINASE RECEPTOR AA455222
320	GF200:96(15B9):384(4D18)	PLASMINOGEN ACTIVATOR, UROKINASE AA284668
321	GF200:96(3A5):384(1B10)	PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE R66310
322	GF201:96(99B7):384(14C13)	SHC (SRC HOMOLOGY 2 DOMAIN-CONTAINING) TRANSFORMING PROTEIN 1 R52961
323	GF200:96(15B2):384(4D4)	SHC (SRC HOMOLOGY 2 DOMAIN-CONTAINING) TRANSFORMING PROTEIN 1 T50633
324	PEROU:96(7A5):384(20B10)	HEPARAN SULFATE PROTEOGLYCAN 1 AA122056
325	GF200:96(12C5):384(3F9)	GLUTATHIONE S-TRANSFERASE P1 R33755
326	GF200:96(12B5):384(3D9)	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA INHIBITING ACTIVITY POLYPEPTIDE 1 AA406420
327	PEROU:96(3G4):384(19N8)	INTEGRIN, ALPHA 6 H06635
328	PEROU:96(9B6):384(18D12)	INTEGRIN ALPHA 6 N22383
329	PEROU:96(3A6):384(19B12)	INTEGRIN ALPHA 6 T54750
330	PEROU:96(8B10):384(20D19)	254428 N22383
331	GF200:96(2E9):384(1I18)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, GAMMA POLYPEPTIDE R38343
332	GF201:96(66E7):384(23I13)	HOMO SAPIENS CLONE 24659 MRNA SEQUENCE AA454584
333	GF200:96(13H5):384(4O9)	CALPAIN, LARGE POLYPEPTIDE L2 AA102454
334	GF200:96(4H7):384(1P13)	HUMAN RAS INHIBITOR MRNA, 3' END R83224
335	GF201:96(91A6):384(12A11)	PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 AA417279
336	GF200:96(25F4):384(7K7)	GAP JUNCTION PROTEIN, ALPHA 1, 43KD (CONNEXIN 43) AA487623
337	GF200:96(6A8):384(2A16)	HOMO SAPIENS CLONE 23565 UNKNOWN MRNA, PARTIAL CDS AA464566
338	GF200:96(23E10):384(6J20)	SERUM/GLUCOCORTICOID REGULATED KINASE AA486082
339	GF200:96(26D6):384(7G12)	NICOTINAMIDE N-METHYLTRANSFERASE T72235
340	GF201:96(66F9):384(23L17)	HOMO SAPIENS MRNA; CDNA DKFZP586L2123 (FROM CLONE DKFZP586L2123) AA443119
341	GF200:96(8B12):384(2D23)	CAVEOLIN 2 T89391
342	GF201:96(96G3):384(13M6)	CAVEOLIN 1, CAVEOLAE PROTEIN, 22KD AA055835
343	GF200:96(14D11):384(4G22)	APOLIPOPROTEIN E AA478589
344	GF200:96(14E11):384(4I22)	ANNEXIN I (LIPOCORTIN I) H63077
345	PEROU:96(3D9):384(19H18)	CADHERIN 13, H-CADHERIN (HEART) AA160651
346	GF200:96(9B5):384(3C9)	CADHERIN 13, H-CADHERIN (HEART) R17717
347	GF200:96(21G5):384(6M9)	REGULATED IN GLIOMA AA425947
348	GF201:96(87G4):384(11M7)	SOLUTE CARRIER FAMILY 10 (SODIUM/BILE ACID COTRANSPORTER FAMILY), MEMBER 1 T68568
349	GF201:96(87C9):384(11E17)	PLACENTAL GROWTH FACTOR, VASCULAR ENDOTHELIAL GROWTH FACTOR-RELATED PROTEIN AA130714
350	GF200:96(4E3):384(1J5)	VASCULAR ENDOTHELIAL GROWTH FACTOR C H07991
351	GF200:96(2H5):384(1O10)	PLASMINOGEN ACTIVATOR INHIBITOR, TYPE I N75719
352	PEROU:96(6B9):384(20C18)	197450 H51958
353	GF200:96(3E9):384(1I18)	MET PROTO-ONCOGENE (HEPATOCYTE GROWTH FACTOR RECEPTOR) AA410591

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Table 1

354	GF201:96(86C10):384(10F19)	TRANSFORMING GROWTH FACTOR, BETA-INDUCED, 68KD AA633901
355	GF201:96(97B7):384(13D14)	BONE MORPHOGENETIC PROTEIN 1 R56774
356	PEROU:96(2F10):384(19K20)	EPHRIN-B2 AA292568
357	GF200:96(24G5):384(6N9)	796198 AA461424
358	PEROU:96(7F9):384(20L18)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1 AA088439
359	PEROU:96(6D1):384(20G2)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1 N47476
360	GF200:96(30F10):384(8K20)	ESTS, MODERATELY SIMILAR TO CALDESMON [H.SAPIENS] H48677
361	GF200:96(19B11):384(5D22)	HUMAN MRNA FOR UNKNOWN PRODUCT, PARTIAL CDS H99544
362	GF200:96(4B2):384(1D3)	HUMAN BETA-1D INTEGRIN MRNA, CYTOPLASMIC DOMAIN, PARTIAL CDS W67174
363	GF200:96(22F1):384(6K2)	FORKHEAD (DROSOPHILA) HOMOLOG 1 (RHABDOMYOSARCOMA) AA194765
364	GF201:96(60E2):384(22I4)	356835 W84612
365	GF201:96(90G1):384(11N1)	ESTS, WEAKLY SIMILAR TO N-WASP [H.SAPIENS] AA427561
366	GF200:96(22H2):384(6O4)	ENDOTHELIAL CELL PROTEIN C/ACTIVATED PROTEIN C RECEPTOR T47442
367	GF200:96(26F7):384(7K14)	MILK FAT GLOBULE-EGF FACTOR 8 PROTEIN AA448941
368	GF200:96(24F12):384(6L23)	EXOSTOSES (MULTIPLE) 1 AA487582
369	GF200:96(12G7):384(3N13)	FIBRILLIN 2(CONGENITAL CONTRACTURAL ARACHNODACTYLY) T98152
370	GF201:96(56F3):384(21K6)	ESTS, MODERATELY SIMILAR TO INITIATION FACTOR EIF-2B GAMMA SUBUNIT [R.NORVEGICUS] W58368
371	GF201:96(92G7):384(12M14)	345935 W72201
372	GF200:96(4B11):384(1D21)	INOSITOL POLYPHOSPHATE-1-PHOSPHATASE H52141
373	GF201:96(65D5):384(23H10)	809620 AA458491
374	GF200:96(15C10):384(4F20)	TRANSFORMING GROWTH FACTOR, BETA RECEPTOR II (70-80KD) AA487034
375	GF200:96(18D4):384(5G8)	SUSHI-REPEAT-CONTAINING PROTEIN, X CHROMOSOME AA448569
376	GF200:96(18A1):384(5A2)	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 6 AA478724
377	GF200:96(13B5):384(4C9)	DIPHTHERIA TOXIN RECEPTOR (HEPARIN-BINDING EPIDERMAL GROWTH FACTOR-LIKE GROWTH FACTOR) R14663
378	GF201:96(94G6):384(12N11)	DUAL SPECIFICITY PHOSPHATASE 6 AA630374
379	GF201:96(99H8):384(14O15)	76169 T59658
380	GF200:96(30H10):384(8O20)	66972 T69540
381	GF201:96(84D9):384(10G18)	ESTS, HIGHLY SIMILAR TO G PROTEIN-COUPLED RECEPTOR KINASE 6, SPLICE VARIANT B [H.SAPIENS] H97146
382	GF200:96(19B12):384(5D24)	NEUROBLASTOMA CANDIDATE REGION, SUPPRESSION OF TUMORIGENICITY 1 AA598830
383	GF201:96(97E12):384(13J24)	ADENOSINE A2B RECEPTOR AA055350
384	GF200:96(16A9):384(4B17)	CD59 ANTIGEN P18-20 (ANTIGEN IDENTIFIED BY MONOCLONAL ANTIBODIES 16.3A5, EJ16, EJ30, EL32 AND G344) H60549
385	GF200:96(14A10):384(4A20)	CD59 ANTIGEN P18-20 (ANTIGEN IDENTIFIED BY MONOCLONAL ANTIBODIES 16.3A5, EJ16, EJ30, EL32 AND G344) H60549
386	GF200:96(1G10):384(1M19)	SYNUCLEIN, ALPHA (NON A4 COMPONENT OF AMYLOID PRECURSOR) AA455067
387	GF200:96(11H2):384(3P4)	STIMULATED TRANS-ACTING FACTOR (50 KDA) AA083407

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Table 1

388	GF200:96(4C7):384(1F13)	CASPASE 1, APOPTOSIS-RELATED CYSTEINE PROTEASE (INTERLEUKIN 1, BETA, CONVERTASE) T95052
389	PEROU:96(8A6):384(20B11)	INTEGRIN ALPHA L (ANTIGEN CD11A (P180) LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 1; ALPHA POLYPEPTIDE) R48796
390	GF201:96(67A5):384(24A9)	810515 AA464542
391	GF202:96(111B6):384(15D12)	ESTS, WEAKLY SIMILAR TO (DEFINE NOT AVAILABLE 4336506) [H.SAPIENS] H96654
392	GF200:96(13B6):384(4C11)	DIHYDROPYRIMIDINE DEHYDROGENASE AA428170
393	GF200:96(16B11):384(4D21)	ESTS, HIGHLY SIMILAR TO (DEFINE NOT AVAILABLE 4679030) [H.SAPIENS] AA521232
394	GF200:96(3E6):384(1J12)	MOESIN R22977
395	GF200:96(27C4):384(7F8)	ESTS, WEAKLY SIMILAR TO (DEFINE NOT AVAILABLE 4502327) [H.SAPIENS] R65792
396	PEROU:96(3A8):384(19B16)	V-YES-1 YAMAGUCHI SARCOMA VIRAL RELATED ONCOGENE HOMOLOG T55472
397	GF201:96(95F3):384(13K5)	GLUTATHIONE PEROXIDASE 1 AA485362
398	GF201:96(79C7):384(9E13)	795757 AA460314
399	GF201:96(88B11):384(11C22)	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 3 (GALECTIN 3) AA630328
400	GF201:96(86D8):384(10H15)	TACHYKININ, PRECURSOR 1 (SUBSTANCE K, SUBSTANCE P, NEUROKININ 1, NEUROKININ 2, NEUROMEDIN L, NEUROKININ ALPHA, NEUROPEPTIDE K,NEUROPEPTIDE GAMMA) AA446659
401	GF202:96(109D1):384(15G1)	INTERLEUKIN 1, BETA W47101
402	GF201:96(88D6):384(11G12)	INTERLEUKIN 1, BETA AA150507
403	GF201:96(89A6):384(11B12)	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (RHO FAMILY, SMALL GTP BINDING PROTEIN RAC1) AA626787
404	GF201:96(89A5):384(11B10)	PROTEIN TYROSINE PHOSPHATASE J AA644448
405	GF201:96(56C11):384(21E22)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.SAPIENS] N21103
406	GF200:96(23F10):384(6L20)	FAT TUMOR SUPPRESSOR (DROSOPHILA) HOMOLOG AA159194
407	GF201:96(58H4):384(21P7)	271952 N35301
408	GF200:96(8C11):384(2F21)	179276 H50323
409	GF200:96(18E4):384(5I8)	INOSITOL POLYPHOSPHATE-5-PHOSPHATASE; 145KD AA521067
410	GF200:96(13G1):384(4M1)	CHOLINERGIC RECEPTOR, NICOTINIC, EPSILON POLYPEPTIDE R02058
411	GF200:96(13B9):384(4C17)	ALDO-KETO REDUCTASE FAMILY 1, MEMBER C1 (DIHYDRODIOL DEHYDROGENASE 1; 20-ALPHA (3-ALPHA)-HYDROXYSTEROID DEHYDROGENASE) R93124
412	GF201:96(97D4):384(13H8)	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 6 AA293571
413	GF201:96(96H6):384(13O12)	CYSTATIN A (STEFIN A) W72207
414	GF201:96(82C5):384(9F9)	347436 W81192
415	PEROU:96(10C1):384(18F1)	ANTILEUKOPROTEINASE AA026192
416	GF201:96(91H5):384(12O9)	JAGGED1 (ALAGILLE SYNDROME) R70685
417	GF200:96(2G8):384(1M16)	PRION PROTEIN (P27-30) (CREUTZFELD-JAKOB DISEASE, GERSTMANN-STRAUSLER-SCHEINKER SYNDROME, FATAL FAMILIAL INSOMNIA) AA455969
418	GF201:96(55C7):384(21E13)	ESTS, WEAKLY SIMILAR TO KIAA0639 PROTEIN [H.SAPIENS] AA284277
419	GF202:96(110H5):384(15O10)	843045 AA488420
420	GF201:96(97E3):384(13J6)	ALDEHYDE DEHYDROGENASE 6 AA455235

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Table 1

421	GF200:96(25G1):384(7M1)	CADHERIN 3, P-CADHERIN (PLACENTAL) AA425556
422	PEROU:96(1A3):384(19A5)	MDGI/FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART W04872
423	GF201:96(86C6):384(10F11)	TROPONIN I, SKELETAL, FAST AA181334
424	GF201:96(94H5):384(12P9)	MATRIX METALLOPROTEINASE 14 (MEMBRANE-INSERTED) N33214
425	GF201:96(94H6):384(12P11)	LAMININ, GAMMA 2 (NICEIN (100KD), KALININ (105KD), BM600 (100KD), HERLITZ JUNCTIONAL EPIDERMOLYSIS BULLOSA)) AA677534
426	GF200:96(14E8):384(4I16)	ANNEXIN VIII AA252968
427	GF201:96(93G2):384(12N4)	ESTS, HIGHLY SIMILAR TO PROBABLE ATAXIA-TELANGIECTASIA GROUP D PROTEIN [H.SAPIENS] AA055486
428	PEROU:96(8D6):384(20H11)	KERATIN 17 AA026642
429	PEROU:96(9D1):384(18H2)	KERATIN 17 aa026642
430	GF200:96(17G7):384(5M13)	ESTS, HIGHLY SIMILAR TO KERATIN K5, 58K TYPE II, EPIDERMAL [H.SAPIENS] AA160507
431	PEROU:96(9C6):384(18F12)	KERATIN 5 (EPIDERMOLYSIS BULLOSA SIMPLEX DOWLING-MEARA/KOBNER/WEBER-COCKAYNE TYPES) W72110
432	PEROU:96(8C11):384(20F21)	ESTS, HIGHLY SIMILAR TO KERATIN K5, 58K TYPE II, EPIDERMAL W72110
433	GF200:96(8C10):384(2F19)	BULLOUS PEMPHIGOID ANTIGEN 1 (230/240KD) H44784
434	GF200:96(11H4):384(3P8)	S100 CALCIUM-BINDING PROTEIN A2 AA458884
435	GF200:96(4B6):384(1D11)	INTEGRIN, BETA 4 AA485668
436	PEROU:96(3B12):384(19D24)	INTEGRIN, BETA 4 AA076514
437	PEROU:96(8A7):384(20B13)	2255577 AI679149
438	GF201:96(88B12):384(11C24)	LAMININ, ALPHA 3 (NICEIN (150KD), KALININ (165KD), BM600 (150KD), EPILEGRIN) AA001432
439	GF201:96(92B12):384(12C24)	COLLAGEN, TYPE XVII, ALPHA 1 H87536
440	GF200:96(14C12):384(4E24)	BASONUCLIN R26526
441	GF201:96(67B11):384(24C21)	504940 AA150619
442	GF201:96(87B6):384(11C11)	HUMAN DNA SEQUENCE FROM CLONE 973M2 ON CHROMOSOME 1Q24.3-31.1 CONTAINS PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2 (PROSTAGLANDIN G/H SYNTHASE AND CYCLOOXYGENASE) GENE, ESTS, STS, GSSS AA644211
443	GF201:96(80A8):384(9A16)	810904 AA459285
444	GF201:96(89D8):384(11H16)	MYOSIN IC AA029956
445	GF200:96(21F6):384(6K11)	EPHRIN-B1 AA428778
446	GF200:96(3F1):384(1L2)	MATRIX METALLOPROTEINASE 7 (MATRILYSIN, UTERINE) AA031513
447	GF200:96(28F3):384(7L5)	294682 W01603
448	PEROU:96(2E11):384(19I22)	INTEGRIN, ALPHA 3 (ANTIGEN CD49C, ALPHA 3 SUBUNIT OF VLA-3 RECEPTOR) AA293040
449	GF201:96(88E1):384(11I12)	INTEGRIN, ALPHA 3 (ANTIGEN CD49C, ALPHA 3 SUBUNIT OF VLA-3 RECEPTOR) AA424695
450	GF200:96(2B4):384(1C8)	SERUM AMYLOID A1 H25546
451	GF200:96(24E3):384(6J5)	GM2 GANGLIOSIDE ACTIVATOR PROTEIN AA453978
452	GF201:96(69B4):384(24D8)	ESTS, WEAKLY SIMILAR TO TRANSPOSON LRE2 REVERSE TRANSCRIPTASE HOMOLOG [H.SAPIENS] W48580
453	GF200:96(13H3):384(4O5)	CARBONIC ANHYDRASE II H23187

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Table 1

454	GF200:96(17F8):384(5K15)	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 2 AA424629
455	GF201:96(100F6):384(14K12)	SECRETED FRIZZLED-RELATED PROTEIN 1 T68892
456	GF201:96(58C4):384(21F7)	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 7 (GALECTIN 7) W72436
457	PEROU:96(4A6):384(19B11)	PLASMINOGEN ACTIVATOR, UROKINASE AA284668
458	GF200:96(27B4):384(7D8)	ENDOTHELIN RECEPTOR TYPE A AA452627
459	GF200:96(27H1):384(7P2)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 5231137) [H.SAPIENS] W30988
460	GF200:96(19E6):384(5J12)	N-MYC DOWNSTREAM REGULATED AA489261
461	PEROU:96(1H4):384(1907)	EPIDERMAL GROWTH FACTOR RECEPTOR (AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL (V-ERB-B) ONCOGENE HOMOLOG) AA234783
462	GF201:96(79B6):384(9C11)	359285 AA016234
463	GF200:96(17H4):384(5O7)	INTERLEUKIN 4 RECEPTOR AA292025
464	GF200:96(24H11):384(6P21)	DIACYLGLYCEROL KINASE, ALPHA (80KD) AA456900
465	GF200:96(3A11):384(1B22)	770670 AA476272
466	GF201:96(97E10):384(13J20)	ADRENERGIC, BETA-2-, RECEPTOR, SURFACE H90431
467	GF202:96(110E4):384(15I8)	592818 AA158252
468	GF201:96(79A11):384(9A21)	264166 N20482
469	PEROU:96(9B8):384(18D16)	TRANSFORMING GROWTH FACTOR, BETA 2 N48082
470	GF200:96(1D9):384(1G17)	TRANSFORMING GROWTH FACTOR, BETA 2 AA233809
471	GF200:96(27F10):384(7L20)	ESTS, WEAKLY SIMILAR TO SIMILAR TO S. CEREVISIAE HYPOTHETICAL PROTEIN YKL166 [C.ELEGANS] T82817
472	GF200:96(23H1):384(6P2)	667883 AA258396
473	GF201:96(79B9):384(9C17)	FRIZZLED (DROSOPHILA) HOMOLOG 7 N69049
474	GF200:96(8E7):384(2I13)	CHROMOSOME X OPEN READING FRAME 6 R08270
475	GF200:96(17H7):384(5O13)	INTERLEUKIN 15 RECEPTOR, ALPHA AA053285
476	GF200:96(22E2):384(6I4)	FK506-BINDING PROTEIN 5 W86653
477	GF200:96(13E3):384(4I5)	CYCLIN D2 H84153
478	GF202:96(113E8):384(16I15)	843283 AA488672
479	GF201:96(67D6):384(24G11)	810459 AA457138
480	PEROU:96(8E1):384(2011)	CYCLIN-DEPENDENT KINASE 7 (HOMOLOG OF XENOPUS MO15 CDK-ACTIVATING KINASE) AA031961
481	GF201:96(102B12):384(14D23	83297 T68333
482	GF201:96(88A3):384(11A6)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ BETA 1 AA669055
483	GF201:96(88A4):384(11A8)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DN ALPHA AA702254
484	GF201:96(88D4):384(11G8)	INTERLEUKIN 15 N59270
485	GF200:96(24C6):384(6F11)	GUANYLATE BINDING PROTEIN 1, INTERFERON-INDUCIBLE, 67KD AA486849
486	GF201:96(88D3):384(11G6)	INTERLEUKIN 6 (INTERFERON, BETA 2) N98591
487	GF200:96(30B3):384(8C6)	TUMOR NECROSIS FACTOR ALPHA-INDUCIBLE CELLULAR PROTEIN CONTAINING LEUCINE ZIPPER DOMAINS R70518
488	GF201:96(66C8):384(23F15)	490995 AA136707
489	GF201:96(93B9):384(12D18)	263013 H99816

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Table 1

490	GF200:96(3G9):384(1N18)	PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE 5-DIOXYGENASE (LYSINE HYDROXYLASE, EHLERS-DANLOS SYNDROME TYPE VI) AA476240
491	GF202:96(115C3):384(16F6)	ECTODERMAL-NEURAL CORTEX (WITH BTB-LIKE DOMAIN) AA102130
492	GF202:96(110D6):384(15G12)	ECTODERMAL-NEURAL CORTEX (WITH BTB-LIKE DOMAIN) H72122
493	GF201:96(89E6):384(11J12)	A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 9 (MELTRIN GAMMA) H59231
494	GF200:96(15H7):384(4P14)	SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY A, MEMBER 1 AA496809
495	GF201:96(63D10):384(23G19)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] W80619
496	GF201:96(87A11):384(11A21)	RAP1, GTPASE ACTIVATING PROTEIN 1 AA682897
497	GF201:96(87A12):384(11A23)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, M H26426
498	GF201:96(58C2):384(21F3)	PHOSPHORYLASE, GLYCOGEN; LIVER (HERS DISEASE, GLYCOGEN STORAGE DISEASE TYPE VI) AA147640
499	GF201:96(58F11):384(21L21)	HOMO SAPIENS MRNA FULL LENGTH INSERT CDNA CLONE EUROIMAGE 122439 T66902
500	GF201:96(94F10):384(12L19)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4704754) [H.SAPIENS] AA426053
501	GF201:96(81C1):384(9F2)	ESTS, WEAKLY SIMILAR TO ALTERNATIVELY SPLICED PRODUCT USING EXON 13A [H.SAPIENS] N80834
502	GF200:96(21H10):384(6O19)	PLEOMORPHIC ADENOMA GENE-LIKE 1 AA463297
503	GF201:96(65A12):384(23B24)	HOMO SAPIENS MRNA FOR KIAA0786 PROTEIN, PARTIAL CDS W74533
504	GF201:96(93D12):384(12H24)	HOMO SAPIENS CLONE L5 UNKNOWN MRNA, PARTIAL CDS N53385
505	GF201:96(69C2):384(24F4)	248849 H80749
506	PEROU-96(6E4):384(20I8)	1912786 AI304356
507	GF200:96(9G4):384(3M7)	TRANSMEMBRANE PROTEIN AA456008
508	GF201:96(89B8):384(11D16)	ESTS, MODERATELY SIMILAR TO PRO-A2(XI) [H.SAPIENS] N66396
509	GF201:96(80F9):384(9K18)	366815 AA029415
510	GF200:96(29C2):384(8E3)	241824 H93217
511	GF200:96(18C1):384(5E2)	781766 AA431678
512	GF201:96(99B9):384(14C17)	PURINERGIC RECEPTOR (FAMILY A GROUP 5) R91539
513	GF201:96(92E9):384(12I18)	PURINERGIC RECEPTOR (FAMILY A GROUP 5) N90783
514	GF200:96(12C4):384(3F7)	248261 N78083
515	GF200:96(24F11):384(6L21)	81331 T60111
516	GF200:96(1B7):384(1C13)	V-MYC AVIAN MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG AA464600
517	GF200:96(3E2):384(1I4)	CALCIUM CHANNEL, VOLTAGE-DEPENDENT, BETA 2 SUBUNIT R92452
518	GF201:96(86F9):384(10L17)	SOLUTE CARRIER FAMILY 16 (MONOCARBOXYLIC ACID TRANSPORTERS), MEMBER 1 AA043133
519	GF200:96(12D9):384(3H17)	823859 AA490688
520	GF200:96(27C6):384(7F12)	246035 N55540
521	GF200:96(11D3):384(3H6)	CHONDROITIN SULFATE PROTEOGLYCAN 4 (MELANOMA-ASSOCIATED) R53652
522	GF202:96(112E12):384(15J23)	HUMAN DNA SEQUENCE FROM CLONE 971N18 ON CHROMOSOME 20P12 CONTAINS PROCESSED PSEUDOGENE PHKBP1, NOVEL GENE, ESTS, CA REPEAT (D20S907), STSS AND GSSS AA457223
523	GF201:96(96H5):384(13O10)	CYTOCHROME P450, SUBFAMILY IVB, POLYPEPTIDE 1 AA291484

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Table 1

524	GF201:96(70C12):384(24F23)	ESTS, WEAKLY SIMILAR TO ORF2 [M.MUSCULUS] N73316
525	GF201:96(70B1):384(24D1)	267252 N24579
526	GF200:96(25D12):384(7G23)	COAGULATION FACTOR VIIIC, PROCOAGULANT COMPONENT (HEMOPHILIA A) AA437191
527	GF201:96(63G10):384(23M19)	307740 N92947
528	GF200:96(1E9):384(1I17)	THROMBOMODULIN H59861
529	GF200:96(2H4):384(1O8)	PLASMINOGEN ACTIVATOR, TISSUE AA453728
530	GF201:96(97H3):384(13P6)	PHORBOL-12-MYRISTATE-13-ACETATE-INDUCED PROTEIN 1 AA458838
531	GF200:96(2G4):384(1M8)	KIAA0159 GENE PRODUCT R00822
532	GF200:96(4A4):384(1B7)	50182 H17882
533	GF200:96(10A12):384(3A24)	PHOSPHOSERINE PHOSPHATASE-LIKE W05628
534	GF202:96(115D6):384(16H12)	PHOSPHOSERINE PHOSPHATASE AA488432
535	GF200:96(2G10):384(1M20)	PREGNANCY SPECIFIC BETA-1-GLYCOPROTEIN 11 R73909
536	GF200:96(3C7):384(1F14)	NON-SPECIFIC CROSS REACTING ANTIGEN AA054073
537	GF201:96(97A5):384(13B10)	CARCINOEMBRYONIC ANTIGEN AA130584
538	GF200:96(2B10):384(1C20)	S100 CALCIUM-BINDING PROTEIN P R32952
539	GF201:96(82B5):384(9D9)	HUMAN DNA SEQUENCE FROM CLONE 71L16 ON CHROMOSOME XP11. CONTAINS A PROBABLE ZINC FINGER PROTEIN (PSEUDO)GENE, AN UNKNOWN PUTATIVE GENE, A PSEUDOGENE WITH HIGH SIMILARITY TO PART OF ANTIGEN KI-67, A PUTATIVE CHONDROITIN 6-SULFOTRAN AA284109
540	GF201:96(99G5):384(14M9)	50114 H16743
541	PEROU:96(9C12):384(18F24)	HOMO SAPIENS MITOCHONDRIAL DNA D38112
542	PEROU:96(1H12):384(19O23)	236142 H61303
543	GF200:96(17G2):384(5M3)	LOW DENSITY LIPOPROTEIN RECEPTOR (FAMILIAL HYPERCHOLESTEROLEMIA) AA504461
544	GF200:96(9H12):384(3O23)	STEAROYL-COA DESATURASE (DELTA-9-DESATURASE) R00707
545	GF201:96(84H9):384(10O18)	CYTOCHROME B-561 AA457700
546	GF200:96(7C2):384(2F4)	LUNATIC FRINGE (DROSOPHILA) HOMOLOG R56562
547	GF200:96(14F11):384(4K22)	ALDEHYDE DEHYDROGENASE 8 AA443630
548	GF200:96(13G10):384(4M19)	CATHEPSIN D (LYSOSOMAL ASPARTYL PROTEASE) N20475
549	GF200:96(12G3):384(3N5)	FIBROMODULIN AA486471
550	GF201:96(100B1):384(14C2)	51344 H21040
551	GF201:96(58D5):384(21H9)	HOMO SAPIENS CHROMOSOME 19, COSMID F22329 T98002
552	GF200:96(7E8):384(2J16)	ESTS, HIGHLY SIMILAR TO GP330 PRECURSOR [H.SAPIENS] R76808
553	GF202:96(110A5):384(15A10)	HOMO SAPIENS CLONE 23876 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN MRNA, PARTIAL CDS H23124
554	GF201:96(81G6):384(9N12)	277463 N56872
555	GF200:96(10C3):384(3E6)	ESTS, HIGHLY SIMILAR TO INOSITOL POLYPHOSPHATE 4-PHOSPHATASE TYPE II-ALPHA [H.SAPIENS] R86721
556	GF201:96(81E4):384(9J8)	271989 N31935
557	GF201:96(88E5):384(11I10)	INSULIN RECEPTOR SUBSTRATE 1 AA460841
558	GF201:96(93A7):384(12B14)	KIAA0417 GENE PRODUCT H17950

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Table 1

559	GF201:96(89A4):384(11B8)	HUMAN RETINOID X RECEPTOR-GAMMA MRNA, COMPLETE CDS W96099
560	GF202:96(109C2):384(15E3)	NEURONAL PENTRAXIN II AA683041
561	GF200:96(15C7):384(4F14)	TYROSINASE (OCULOCUTANEOUS ALBINISM IA) N42770
562	GF201:96(99F12):384(14K23)	ZINC FINGER PROTEIN HOMOLOGOUS TO ZFP103 IN MOUSE R54105
563	GF200:96(9F1):384(3K1)	TRANSMEMBRANE GLYCOPROTEIN AA055862
564	GF201:96(97D10):384(13H20)	ALPHA-FETOPROTEIN T59043
565	GF200:96(4C11):384(1F21)	INTER-ALPHA (GLOBULIN) INHIBITOR, H2 POLYPEPTIDE R06634
566	GF201:96(90A4):384(11B7)	HUMAN MRNA FOR KIAA0282 GENE, PARTIAL CDS R44936
567	GF201:96(92H11):384(12O22)	CADHERIN 6, K-CADHERIN (FETAL KIDNEY) AA421819
568	GF201:96(88G7):384(11M14)	FORKHEAD (DROSOPHILA)-LIKE 8 AA069372
569	GF201:96(95H11):384(13O21)	FATTY ACID BINDING PROTEIN 1, LIVER T53220
570	GF200:96(10B4):384(3C8)	POTASSIUM VOLTAGE-GATED CHANNEL, KQT-LIKE SUBFAMILY, MEMBER 2 H51461
571	GF200:96(15A8):384(4B16)	VITRONECTIN (SERUM SPREADING FACTOR, SOMATOMEDIN B, COMPLEMENT S-PROTEIN) N58107
572	GF200:96(27A2):384(7B4)	PRE-ALPHA (GLOBULIN) INHIBITOR, H3 POLYPEPTIDE T68035
573	GF201:96(97C8):384(13F16)	ASIALOGLYCOPROTEIN RECEPTOR 2 R98050
574	GF201:96(97C12):384(13F24)	CARBOXYPEPTIDASE N, POLYPEPTIDE 1, 50KD AA679422
575	GF200:96(12H2):384(3P3)	FIBRINOGEN, B BETA POLYPEPTIDE H91815
576	GF200:96(16H8):384(4P15)	COAGULATION FACTOR II (THROMBIN) T62131
577	GF201:96(86G12):384(10N23)	SECRETOGRANIN II (CHROMOGRANIN C) H27864
578	GF201:96(97D5):384(13H10)	APOLIPOPROTEIN H (BETA-2-GLYCOPROTEIN I) H68848
579	GF201:96(92F7):384(12K14)	ESTS, HIGHLY SIMILAR TO PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA [H.SAPIENS] AA678335
580	GF200:96(27A4):384(7B8)	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER R91503
581	GF200:96(27B3):384(7D6)	ALKALINE PHOSPHATASE, LIVER/BONE/KIDNEY T94626
582	GF201:96(90G7):384(11N13)	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 4 (GALECTIN 4) AA130579
583	GF201:96(1D10):384(1G19)	TRANSFERRIN H69531
584	GF200:96(16G6):384(4N11)	PHOSPHOLIPASE A2, GROUP IIA (PLATELETS, SYNOVIAL FLUID) T61323
585	GF201:96(59H8):384(22O15)	144862 R78570
586	GF200:96(16H9):384(4P17)	DNA SEGMENT, SINGLE COPY, HOMOLOGOUS ON X AND Y, EXPRESSED PROBES AA496863
587	GF200:96(96F4):384(13K8)	CHROMOGRANIN B (SECRETOGRANIN 1) W37769
588	GF201:96(91H11):384(12O21)	FIBRINOGEN-LIKE 1 AA677287
589	GF200:96(1F3):384(1K5)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 3 AA045698
590	GF200:96(1G3):384(1M5)	TRANSCOBALAMIN I (VITAMIN B12 BINDING PROTEIN, R BINDER FAMILY) AA155695
591	GF200:96(1A9):384(1A17)	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY, MEMBER 5A W49672
592	GF201:96(58C9):384(21F17)	FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART (MAMMARY-DERIVED GROWTH INHIBITOR) AA148548
593	GF201:96(88C3):384(11E6)	LACTOTRANSFERRIN AA677706
594	GF200:96(9A4):384(3A7)	V-MYC AVIAN MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG 1, LUNG CARCINOMA DERIVED R62862

Table 1

595	PEROU:96(8H2):384(20P3)	N-MYC AA101678
596	GF202:96(109E8):384(15I15)	266146 N21576
597	GF200:96(13E2):384(4I3)	214572 H73724
598	GF201:96(97F8):384(13L16)	HUMAN AORTIC-TYPE SMOOTH MUSCLE ALPHA-ACTIN (SM-ALPHA-A) GENE, EXON 9 AA634006
599	GF200:96(3F8):384(1L16)	MAL, T-CELL DIFFERENTIATION PROTEIN AA227594
600	GF200:96(15F2):384(4L4)	CD8 ANTIGEN, BETA POLYPEPTIDE 1 (P37) AA293671
601	GF201:96(85H7):384(10P14)	V-MAF MUSCULOAPONEUROTIC FIBROSARCOMA (AVIAN) ONCOGENE HOMOLOG AA043501
602	GF202:96(116H2):384(16P3)	CHLORIDE INTRACELLULAR CHANNEL 2 T52201
603	GF200:96(13G3):384(4M5)	CHEMOKINE (C-X3-C) RECEPTOR 1 N51278
604	GF200:96(22H3):384(6O6)	ECHINODERM MICROTUBULE-ASSOCIATED PROTEIN-LIKE AA447196
605	GF201:96(91H7):384(12O13)	IMMUNOGLOBULIN GAMMA 3 (GM MARKER) AA663981
606	GF200:96(9F9):384(3K17)	COLONY STIMULATING FACTOR 1 (MACROPHAGE) N92646
607	GF200:96(26C3):384(7E6)	NEUTROPHIL CYTOSOLIC FACTOR 1 (47KD, CHRONIC GRANULOMATOUS DISEASE, AUTOSOMAL 1) AA489666
608	GF201:96(88F6):384(11K12)	IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 2 W73790
609	PEROU:96(6B12):384(20C24)	IMMUNOGLOBULIN LAMBDA LIGHT CHAIN R50297
610	PEROU:96(6D6):384(20G12)	HUMAN REARRANGED IMMUNOGLOBULIN LAMBDA LIGHT CHAIN MRNA N64851
611	GF200:96(26D3):384(7G6)	HUMAN REARRANGED IMMUNOGLOBULIN LAMBDA LIGHT CHAIN MRNA T67053
612	GF200:96(6B5):384(20C10)	HUMAN IG J CHAIN GENE H24896
613	PEROU:96(9A9):384(18B18)	IMMUNOGLOBULIN J CHAIN H24896
614	GF200:96(18A10):384(5A20)	HUMAN IG J CHAIN GENE T70057
615	PEROU:96(6B4):384(20C8)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ BETA 1 R73128
616	GF200:96(18A7):384(5A14)	IMMUNOGLOBULIN MU H73590
617	GF200:96(18G11):384(5M22)	EARLY DEVELOPMENT REGULATOR 2 (HOMOLOG OF POLYHOMEOTIC 2) AA598840
618	PEROU:96(2D10):384(19G20)	MAX-INTERACTING PROTEIN 1 AI087032
619	GF201:96(62D10):384(22H19)	HOMO SAPIENS MRNA FOR KIAA0640 PROTEIN, PARTIAL CDS N23996
620	GF201:96(83D3):384(10G5)	GLUTATHIONE S-TRANSFERASE M5 AA056232
621	GF201:96(80F6):384(9K12)	325583 AA284243
622	GF201:96(81G4):384(9N8)	244796 N52554
623	GF201:96(67E2):384(24I3)	346321 W74079
624	GF202:96(111H12):384(15P24)	ESTS, HIGHLY SIMILAR TO SCK [H.SAPIENS] H10072
625	GF201:96(81C6):384(9F12)	364865 AA035745
626	GF201:96(89H4):384(11P8)	HOMO SAPIENS MRNA FOR KIAA0640 PROTEIN, PARTIAL CDS N23996
627	GF201:96(62D12):384(22H23)	201440 R99105
628	GF201:96(16B4):384(4D7)	RIBONUCLEASE L (2',5'-OLIGOISOADENYLATE SYNTHETASE-DEPENDENT) T60223
629	GF201:96(86C7):384(10F13)	TROPOMYOSIN 2 (BETA) AA477400
630	GF200:96(6B11):384(2C22)	SAL (DROSOPHILA)-LIKE 2 H23365
631	GF200:96(10F4):384(3K8)	IMPRINTED IN PRADER-WILLI SYNDROME H93815
632	GF201:96(96G12):384(13M24)	CANNABINOID RECEPTOR 1 (BRAIN) R20626

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Table 1

633	GF200:96(19B5):384(5D10)	CBP/P300-INTERACTING TRANSACTIVATOR, WITH GLU/ASP-RICH CARBOXY-TERMINAL DOMAIN, 1 AA432143
634	GF201:96(100B6):384(14C12)	52684 H29574
635	GF200:96(14C11):384(4E22)	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:(N-ACETYLNEURAMINYL)-GALACTOSYLGLUCOSYLCERAMIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (GALNAC-T) R05336
636	GF201:96(100A4):384(14A8)	51644 H20570
637	GF200:96(26D9):384(7G18)	NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3 AA463251
638	GF200:96(4D6):384(1H11)	I FACTOR (COMPLEMENT) N62462
639	GF200:96(21G10):384(6M19)	PATERNALLY EXPRESSED GENE 3 AA459941
640	GF200:96(7F2):384(2L4)	FRIZZLED-RELATED PROTEIN W58032
641	GF201:96(65A6):384(23B12)	416855 W87281
642	GF201:96(100G12):384(14M24)	60540 T40531
643	GF201:96(67C1):384(24E1)	503819 AA131664
644	GF200:96(16F2):384(4L3)	PROLINE ARGININE-RICH END LEUCINE-RICH REPEAT PROTEIN AA434342
645	GF201:96(100B8):384(14C16)	69935 T48692
646	GF200:96(16A3):384(4B5)	S100 CALCIUM-BINDING PROTEIN, BETA (NEURAL) AA424045
647	GF200:96(27H11):384(7P22)	ESTS, WEAKLY SIMILAR TO W01A11.2 GENE PRODUCT [C.ELEGANS] H25606
648	GF200:96(27E11):384(7J22)	240945 H91000
649	GF200:96(32D10):384(8H19)	GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1 (SOLUBLE) AA192547
650	GF200:96(32F10):384(8L19)	ESTS, HIGHLY SIMILAR TO CARBONIC ANHYDRASE III [H.SAPIENS] AA464880
651	PEROU:96(1C10):384(4G24)	APOLIPOPROTEIN D AA457084
652	GF200:96(14D12):384(4G24)	APOLIPOPROTEIN D H15842
653	GF200:96(7F11):384(2L22)	ELASTIN (SUPRAVALVULAR AORTIC STENOSIS, WILLIAMS-BEUREN SYNDROME) AA459308
654	GF200:96(27A3):384(7B6)	COLLAGEN, TYPE XIV, ALPHA 1: UNDULIN AA167222
655	GF200:96(8H9):384(2P17)	MESENCHYME HOMEO BOX 1 AA426311
656	GF200:96(4B9):384(1D17)	INSULIN-LIKE GROWTH FACTOR 1 (SOMATOMEDIN C) AA456321
657	PEROU:96(6B1):384(20C2)	CYCLIN-DEPENDENT KINASE INHIBITOR 1C (P57, KIP2) R81336
658	GF201:96(100H7):384(14O14)	78946 T61792
659	PEROU:96(6E7):384(20I14)	FATTY ACID BINDING PROTEIN 4, ADIPOCYTE AA046090
660	PEROU:96(7A10):384(20B20)	FATTY ACID BINDING PROTEIN 4, ADIPOCYTE AI652163
661	GF201:96(95H10):384(13O19)	FATTY ACID BINDING PROTEIN 4, ADIPOCYTE N92901
662	PEROU:96(8H6):384(20P11)	MDGI/FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART AA128926
663	PEROU:96(3E4):384(19J8)	CD36 ANTIGEN (COLLAGEN TYPE I RECEPTOR, THROMBOSPONDIN RECEPTOR) R09416
664	GF200:96(14B4):384(4C8)	CD36 ANTIGEN (COLLAGEN TYPE I RECEPTOR, THROMBOSPONDIN RECEPTOR) N39161
665	GF202:96(110B10):384(15C20)	GLUTATHIONE PEROXIDASE 3 (PLASMA) AA664180
666	GF200:96(18E1):384(5I2)	FOUR AND A HALF LIM DOMAINS 1 AA456394
667	GF200:96(14G2):384(4M4)	ALCOHOL DEHYDROGENASE 2 (CLASS I), BETA POLYPEPTIDE N93428
668	GF201:96(92H12):384(12O24)	AQUAPORIN 7 H27752
669	GF200:96(18H1):384(5O2)	484535 AA036974

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Table 1

670	GF201:96(88B9):384(11C18)	LIPOPROTEIN LIPASE AA633835
671	GF200:96(23A7):384(6B14)	GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1 (SOLUBLE) AA192547
672	GF200:96(26C1):384(7E2)	RETINOL-BINDING PROTEIN 4, INTERSTITIAL T72220
673	GF201:96(88D12):384(11G24)	INTEGRIN, ALPHA 7 AA055979
674	GF201:96(102A5):384(14B9)	85660 T62068
675	GF201:96(89B11):384(11D22)	PHOSPHOLEMMAN H57136
676	GF201:96(97H6):384(13P12)	AQUAPORIN 1 (CHANNEL-FORMING INTEGRAL PROTEIN, 28KD) H24316
677	GF201:96(97H7):384(13P14)	APOLIPOPROTEIN A-I R97710
678	GF200:96(11D12):384(3H24)	SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 14 R96668
679	GF200:96(5C8):384(2E15)	PEROXISOME PROLIFERATIVE ACTIVATED RECEPTOR, GAMMA AA088517
680	GF200:96(13A3):384(4A5)	ENDOTHELIN RECEPTOR TYPE B H28710
681	GF201:96(101F5):384(14L10)	79412 T57691
682	GF200:96(14H2):384(4O4)	ACTIVATING TRANSCRIPTION FACTOR 3 H21041
683	GF201:96(92D8):384(12G16)	HORMONE RECEPTOR (GROWTH FACTOR-INDUCIBLE NUCLEAR PROTEIN N10) N94487
684	GF200:96(13B4):384(4C7)	DOPACHROME TAUTOMERASE (DOPACHROME DELTA-ISOMERASE, TYROSINE-RELATED PROTEIN 2) AA478553
685	PEROU:96(7C3):384(20F6)	P55-C-FOS N36944
686	PEROU:96(7D10):384(20H20)	V-FOS FBJ MURINE OSTEOSARCOMA VIRAL ONCOGENE HOMOLOG AA040944
687	GF201:96(87F1):384(11K1)	V-FOS FBJ MURINE OSTEOSARCOMA VIRAL ONCOGENE HOMOLOG AA485377
688	GF200:96(22B11):384(6C22)	FBJ MURINE OSTEOSARCOMA VIRAL ONCOGENE HOMOLOG B T62179
689	GF201:96(96D8):384(13G16)	CYCLIN-DEPENDENT KINASE 5, REGULATORY SUBUNIT 1 (P35) AA442853
690	GF200:96(4A5):384(1B9)	HUMAN TRANSCRIPTION FACTOR JUNB (JUNB) GENE, 5' REGION AND COMPLETE CDS T99236
691	GF201:96(86D5):384(10H9)	TETRANECTIN (PLASMINOGEN-BINDING PROTEIN) W73889
692	GF200:96(9B7):384(3C13)	GTP-BINDING PROTEIN OVEREXPRESSED IN SKELETAL MUSCLE AA418077
693	GF201:96(63B5):384(23C9)	502155 AA126676
694	GF201:96(98F11):384(13L21)	ESTS, WEAKLY SIMILAR TO P126 [H.SAPIENS] T51630
695	PEROU:96(10A8):384(18B15)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] H42682
696	GF201:96(67C6):384(24E11)	300038 N78909
697	GF202:96(114G11):384(16M22)	595078 AA164819
698	GF200:96(1B8):384(1C15)	V-KIT HARDY-ZUCKERMAN 4 FELINE SARCOMA VIRAL ONCOGENE HOMOLOG N20798
699	GF200:96(18A6):384(5A12)	INHIBITOR OF DNA BINDING 4, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN AA464856
700	GF200:96(5H7):384(2Q13)	CALPONIN 1, BASIC, SMOOTH MUSCLE AA399519
701	PEROU:96(8F5):384(20L9)	ACTIN, GAMMA 2, SMOOTH MUSCLE, ENTERIC AA053297
702	PEROU:96(7B5):384(20D10)	PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1) AA001449
703	GF200:96(16F12):384(4L23)	PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1) AA001449
704	GF200:96(13D12):384(4G23)	CYSTEINE DIOXYGENASE, TYPE I AA497111
705	GF200:96(9H11):384(3Q21)	27787 R40400

Table 1

706	GF201:96(69C6):384(24F12)	220078 H82527
707	GF201:96(79B4):384(9C7)	272038 N31948
708	GF201:96(100F2):384(14K4)	SPONDIN 1, (F-SPONDIN) EXTRACELLULAR MATRIX PROTEIN H09099
709	GF201:96(58E2):384(21J3)	CATHEPSIN G W92603
710	GF200:96(18A3):384(5A6)	HUMAN KRUEPPEL-RELATED ZINC FINGER PROTEIN (H-PLK) MRNA, COMPLETE CDS N54596
711	GF201:96(88E4):384(11J8)	INSULIN-LIKE GROWTH FACTOR 2 (SOMATOMEDIN A) N74623
712	GF200:96(9A5):384(3A9)	HUMAN KRUEPPEL-RELATED ZINC FINGER PROTEIN (H-PLK) MRNA, COMPLETE CDS N54596
713	GF201:96(95G9):384(13M17)	PHOSPHORYLASE, GLYCOGEN; MUSCLE (MCARDLE SYNDROME, GLYCOGEN STORAGE DISEASE TYPE V) AA496032
714	GF201:96(87H7):384(11O13)	MICROFIBRILLAR-ASSOCIATED PROTEIN 4 AA496022
715	GF201:96(97E6):384(13J12)	ALCOHOL DEHYDROGENASE 4 (CLASS II), PI POLYPEPTIDE H63124
716	GF200:96(1D12):384(1G23)	HUMAN TCF-1 MRNA FOR T CELL FACTOR 1 (SPLICE FORM B) AA480071
717	GF201:96(96H9):384(13O18)	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 2 N93505
718	GF201:96(79E10):384(9I19)	782730 AA447978
719	GF201:96(63E2):384(23I3)	212489 H68404
720	GF201:96(97A1):384(13B2)	CD1C ANTIGEN, C POLYPEPTIDE AA002086
721	GF201:96(84B4):384(10C8)	INTEGRAL MEMBRANE PROTEIN 2C N53447
722	GF201:96(9688):384(13C16)	DIPEPTIDYLPEPTIDASE IV (CD26, ADENOSINE DEAMINASE COMPLEXING PROTEIN 2) W70234
723	GF201:96(95F8):384(13K15)	GLUTAMYL AMINOPEPTIDASE (AMINOPEPTIDASE A) AA102107
724	GF200:96(1B5):384(1C9)	ARGININE VASOPRESSIN RECEPTOR 1A AA448190
725	GF200:96(26F4):384(7K8)	MATRIX METALLOPROTEINASE 16 (MEMBRANE-INSERTED) H09997
726	PEROU:96(7A1):384(20B2)	KIAA0735 AI669959
727	GF201:96(83A3):384(10A5)	CATHEPSIN B AA004638
728	GF200:96(10C5):384(3E10)	HOMO SAPIENS HYALURONOGLUCOSAMINIDASE 1 (HYAL1) MRNA, COMPLETE CDS AA464791
729	PEROU:96(9E2):384(18J4)	SPARC/OSTEONECTIN AA031596
730	GF202:96(11D5):384(15H10)	ESTS, WEAKLY SIMILAR TO AORTIC CARBOXYPEPTIDASE-LIKE PROTEIN ACLP [H.SAPIENS] AA598945
731	GF201:96(90B11):384(11D21)	KIAA0161 GENE PRODUCT W95118
732	GF201:96(81H8):384(9P16)	307645 N93582
733	GF201:96(99G3):384(14M5)	52865 H29620
734	PEROU:96(6F7):384(20K14)	ESTS, MODERATELY SIMILAR TO SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS [M.MUSCULUS] AA057170
735	GF200:96(12G11):384(3N21)	FOLATE RECEPTOR 2 (FETAL) AA453816
736	GF201:96(95H7):384(13O13)	FIBROBLAST GROWTH FACTOR 7 (KERATINOCYTE GROWTH FACTOR) AA009609
737	GF200:96(21G12):384(6M23)	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT, POLYPEPTIDE 1 (P85 ALPHA) R54050
738	GF201:96(87G3):384(11M5)	NERVE GROWTH FACTOR RECEPTOR (TNFR SUPERFAMILY, MEMBER 16) R55303
739	GF201:96(92C9):384(12E18)	PROLINE-RICH PROTEIN WITH NUCLEAR TARGETING SIGNAL AA669637
740	GF200:96(3F11):384(1L22)	V-MYB AVIAN MYELOBLASTOSIS VIRAL ONCOGENE HOMOLOG N49526
741	GF202:96(116B11):384(16D21)	HUMAN LIVER CARBOXYLESTERASE MRNA, 3' END T68878
742	GF200:96(21D5):384(6G9)	PROTEIN TYROSINE KINASE 2 BETA R85257

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Table 1

743	PEROU:96(6G3):384(20M6)	HHCPA78 HOMOLOG AA044633
744	GF200:96(26H3):384(7O6)	LPS-INDUCED TNF-ALPHA FACTOR AA625666
745	GF201:96(99H5):384(14O9)	CELLULAR REPRESSOR OF E1A-STIMULATED GENES T71991
746	GF201:96(84A4):384(10A8)	272262 N35592
747	GF200:96(10E2):384(3I4)	KIAA0914 GENE PRODUCT N51424
748	GF200:96(17F4):384(5K7)	FATTY-ACID-COENZYME A LIGASE, LONG-CHAIN 1 T73556
749	GF201:96(101B6):384(14D12)	HOMO SAPIENS MRNA; CDNA DKFZP586A0522 (FROM CLONE DKFZP586A0522) T50041
750	GF201:96(83B7):384(10C13)	HOMO SAPIENS MRNA; CDNA DKFZP586A0522 (FROM CLONE DKFZP586A0522) N70948
751	PEROU:96(8B4):384(20D7)	MEMBRANE METALLO-ENDOPEPTIDASE (NEUTRAL ENDOPEPTIDASE, ENKEPHALINASE, CALLA, CD10) H65598
752	GF200:96(10D2):384(3G4)	CYCLIN G2 AA489752
753	GF200:96(9E4):384(3I7)	B-CELL TRANSLOCATION GENE 2 (PHEOCHROMACYTOMA CELL-3) H69582
754	GF201:96(91G4):384(12M7)	769796 AA429034
755	GF201:96(100H6):384(14O12)	77911 T61269
756	GF200:96(23E7):384(6J14)	SELENOPROTEIN P, PLASMA, 1 AA070226
757	PEROU:96(10C7):384(18F13)	428431 AA004415
758	GF200:96(12F7):384(3L13)	FUCOSIDASE, ALPHA-L- 1, TISSUE N95761
759	PEROU:96(8D10):384(20H19)	HEMOGLOBIN, ALPHA 1 AA027875
760	GF201:96(102A3):384(14B5)	ESTS, WEAKLY SIMILAR TO F56A11.5 [C.ELEGANS] T61938
761	GF200:96(16D5):384(4H9)	PROTEOLIPID PROTEIN (PELIZAEUS-MERZBACHER DISEASE, SPASTIC PARAPLEGIA 2, UNCOMPLICATED) T75041
762	GF201:96(96A10):384(13A20)	EARLY GROWTH RESPONSE 2 (KROX-20 (DROSOPHILA) HOMOLOG) AA446027
763	GF201:96(65A8):384(23B16)	357396 W93847
764	GF201:96(89F10):384(11L20)	MITOCHONDRIAL 3-OXOACYL-COA THIOLASE H07926
765	PEROU:96(6E6):384(20I12)	MESODERM SPECIFIC TRANSCRIPT (MOUSE) HOMOLOG AI369005
766	GF201:96(95G7):384(13M13)	HUMAN GRANCALCIN MRNA, COMPLETE CDS R44739
767	GF200:96(22E10):384(6I20)	ESTS, MODERATELY SIMILAR TO CADHERIN 12 [H.SAPIENS] AA418564
768	GF200:96(9G1):384(3M1)	ESTS, MODERATELY SIMILAR TO CADHERIN 12 [H.SAPIENS] W02256
769	GF200:96(17B1):384(5C1)	ORNITHINE DECARBOXYLASE 1 AA460115
770	GF201:96(57D5):384(21H10)	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H1 (H) R11019
771	GF201:96(87B4):384(11C7)	PROTEIN KINASE, CAMP-DEPENDENT, CATALYTIC, BETA AA018980
772	GF201:96(95G1):384(13M1)	GLUTAMATE DECARBOXYLASE 1 (BRAIN, 67KD) AA018457
773	GF200:96(6A10):384(2A20)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, N POLYPEPTIDE 2 AA464590
774	GF201:96(93G6):384(12N12)	KIAA0711 GENE PRODUCT AA702544
775	GF201:96(63C5):384(23E9)	HOMO SAPIENS MRNA; CDNA DKFZP564F093 (FROM CLONE DKFZP564F093) W87710
776	GF202:96(114G1):384(16M2)	HOMO SAPIENS DNA SEQUENCE FROM COSMID ICK0721Q ON CHROMOSOME 6. CONTAINS A 60S RIBOSOMAL PROTEIN L35A LIKE PSEUDOGENE, A GENE CODING FOR A 60S RIBOSOMAL PROTEIN L12 LIKE PROTEIN IN AN INTRON OF THE HSET GENE CODING FOR A KINESIN AA457543
777	GF202:96(111C12):384(15F24)	625764 AA188366

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Table 1

778	GF201:96(64E7):384(23I14)	357298 W93688
779	GF201:96(100E12):384(14I24)	HNK-1 SULFOTRANSFERASE R16195
780	GF201:96(99A9):384(14A17)	INTERFERON STIMULATED GENE (20KD) AA150500
781	GF201:96(5G4):384(21I8)	ESTS, MODERATELY SIMILAR TO TRANSPORTIN [H.SAPIENS] R08897
782	GF200:96(19G6):384(5N12)	HUMAN MRNA FOR KIAA0264 GENE, PARTIAL CDS AA486524
783	GF201:96(55G2):384(21M3)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4894378) [H.SAPIENS] AA453591
784	GF201:96(59D2):384(22G3)	365536 AA009596
785	GF202:96(116G3):384(16N5)	ESTS, WEAKLY SIMILAR TO AXONEMAL DYNEIN HEAVY CHAIN [H.SAPIENS] AA486418
786	GF201:96(95B6):384(13C11)	ESTS, HIGHLY SIMILAR TO NAD(P) TRANSHYDROGENASE [H.SAPIENS] H22944
787	GF201:96(62B12):384(22D23)	487436 AA043360
788	GF201:96(56C2):384(21E4)	342522 W68559
789	GF200:96(24G6):384(6N11)	H.SPAIENS 3' MRNA FOR NEURONE-SPECIFIC ENOLASE (EC 4.2.1.11) AA450189
790	GF201:96(96D6):384(13G12)	CYSTATHIONINE-BETA-SYNTHASE AA430367
791	GF201:96(87E4):384(11I7)	NUCLEOLAR PROTEIN 1 (120KD) N50854
792	GF201:96(83H10):384(10O19)	ESTS, WEAKLY SIMILAR TO HUEMAP [H.SAPIENS] AA122022
793	PEROU:96(6A8):384(20A16)	HOMO SAPIENS MRNA; CDNA DKFZP586C201 (FROM CLONE DKFZP586C201) R12563
794	GF201:96(62D2):384(22H3)	503682 AA129974
795	GF200:96(1B6):384(1C11)	VALYL-TRNA SYNTHETASE 1 AA464470
796	GF202:96(112A2):384(15B3)	ESTS, WEAKLY SIMILAR TO ACID PHOSPHATASE [H.SAPIENS] AA160670
797	GF201:96(99C9):384(14E17)	75044 T51856
798	GF200:96(15D12):384(4H24)	THIOREDOXIN REDUCTASE 1 AA453335
799	GF201:96(56D5):384(21G10)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA404276
800	GF201:96(85A10):384(10B20)	IGF-II MRNA-BINDING PROTEIN 3 AA011347
801	GF200:96(23B11):384(6D22)	HIGH-MOBILITY GROUP (NONHISTONE CHROMOSOMAL) PROTEIN ISOFORMS I AND Y AA448261
802	GF201:96(95F1):384(13K1)	GLYCYL-TRNA SYNTHETASE AA629909
803	GF200:96(21H9):384(6O17)	HOMO SAPIENS CLONE 24636 MRNA SEQUENCE N79230
804	GF200:96(9D9):384(3G17)	CDC6 (CELL DIVISION CYCLE 6, S. CEREVISIAE) HOMOLOG HS9203
805	GF201:96(58F6):384(21L11)	ESTS, HIGHLY SIMILAR TO TAT BINDING PROTEIN 7, TBP-7 AA464568
806	GF202:96(112E10):384(15I19)	HOMO SAPIENS MRNA; CDNA DKFZP547C0410 (FROM CLONE DKFZP547C0410) N50079
807	GF200:96(9H6):384(3O11)	HOMO SAPIENS PESCADILLO MRNA, COMPLETE CDS R13806
808	GF200:96(16E10):384(4J19)	KALLIKREIN 3, (PROSTATE SPECIFIC ANTIGEN) AA490981
809	GF200:96(16G8):384(4N15)	ESTS, HIGHLY SIMILAR TO 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING [H.SAPIENS] AA598759
810	GF201:96(87F6):384(11K11)	NUCLEOPHOSMIN (NUCLEOLAR PHOSPHOPROTEIN B23, NUMATRIN) AA669758
811	GF201:96(90C11):384(11F21)	E2F TRANSCRIPTION FACTOR 3 N92519
812	GF200:96(7E12):384(2J24)	GAMMA-GLUTAMYL HYDROLASE (CONJUGASE, FOLYLPOLYGAMMAGLUTAMYL HYDROLASE) AA45580O
813	GF200:96(13G6):384(4M11)	CENTROMERE PROTEIN E (312KD) AA402431
814	GF200:96(7B2):384(2D4)	KIAA0042 GENE PRODUCT AA477501

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Table 1

815	GF200:96(13E4):384(4I7)	CYCLIN B1 R25788
816	GF201:96(96G1):384(13M2)	CELL DIVISION CYCLE 25C W95001
817	GF200:96(5G1):384(2M1)	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 12 AA497132
818	GF200:96(21C2):384(6E3)	HUMAN CLONE 23799 MRNA SEQUENCE AA489007
819	GF201:96(99B5):384(14C9)	HOMO SAPIENS CLONE 24703 BETA-TUBULIN MRNA, COMPLETE CDS AA427899
820	GF200:96(17C7):384(5E13)	METHYLENE TETRAHYDROFOLATE DEHYDROGENASE (NAD+ DEPENDENT), METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE AA480995
821	GF201:96(82D11):384(9H21)	430186 AA010188
822	GF201:96(87G10):384(11M19)	MUTT (E. COLI) HUMAN HOMOLOG (8-OXO-7,8-DIHYDROGUANOSINE TRIPHOSPHATASE) AA43998
823	GF201:96(87A10):384(11A19)	RIBONUCLEOTIDE REDUCTASE M1 POLYPEPTIDE AA633549
824	GF200:96(10H6):384(3O12)	HIGH-MOBILITY GROUP (NONHISTONE CHROMOSOMAL) PROTEIN 2 AA019511
825	GF200:96(11A6):384(3B12)	HOMO SAPIENS CLONE 24782 UNKNOWN MRNA AA430545
826	GF201:96(63E12):384(23I23)	126449 R06706
827	GF201:96(98A5):384(13B9)	APOPTOSIS INHIBITOR 4 (SURVIVIN) AA460685
828	GF200:96(13H12):384(4O23)	CTP SYNTHASE H09614
829	GF201:96(93F10):384(12L20)	BYSTIN-LIKE AA701929
830	GF201:96(64G8):384(23M16)	258761 N30185
831	PEROU:96(4B1):384(19D1)	PLASMINOGEN (CONTAINS ANGIOSTATIN) R91118
832	PEROU:96(7C2):384(20F4)	KIAA0101 GENE PRODUCT N29873
833	GF200:96(10D8):384(3G16)	CHK1 (CHECKPOINT, S.POMBE) HOMOLOG N73242
834	GF201:96(58D3):384(21H5)	TOPOISOMERASE (DNA) II ALPHA (170KD) AA026682
835	GF201:96(57D4):384(21H8)	KIAA0008 GENE PRODUCT W93717
836	PEROU:96(8H9):384(20P17)	ANTIGEN IDENTIFIED BY MONOCLONAL ANTIBODY KI-67 AA004872
837	GF200:96(1E5):384(1I9)	TISSUE INHIBITOR OF METALLOPROTEINASE 1 (ERYTHROID POTENTIATING ACTIVITY, COLLAGENASE INHIBITOR) H80215
838	GF200:96(15D4):384(4H8)	ESTS, HIGHLY SIMILAR TO TOPOISOMERASE II ALPHA {C-TERMINAL} [H.SAPIENS] AA504348
839	GF202:96(109F7):384(15K13)	TRAF INTERACTING PROTEIN AA186427
840	GF201:96(96C9):384(13E18)	HOMO SAPIENS MRNA; CDNA DKFZP434F222 (FROM CLONE DKFZP434F222) AA680129
841	GF200:96(3E7):384(1J14)	MINICHROMOSOME MAINTENANCE DEFICIENT (S. CEREVISIAE) 3 AA455786
842	GF201:96(90B10):384(11D19)	KIAA0166 GENE PRODUCT AA157787
843	GF201:96(87F8):384(11K15)	NUCLEAR AUTOANTIGENIC SPERM PROTEIN (HISTONE-BINDING) AA644128
844	GF200:96(22D3):384(6G6)	DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE 11 (S.CEREVISIAE CHL1-LIKE HELICASE) AA402879
845	GF200:96(10E1):384(3I2)	DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE 11 (S.CEREVISIAE CHL1-LIKE HELICASE) AA032090
846	GF201:96(89C4):384(11F8)	MINICHROMOSOME MAINTENANCE DEFICIENT (MIS5, S. POMBE) 6 AA663995
847	GF200:96(13C12):384(4E23)	DNA (CYTOSINE-5-)-METHYLTRANSFERASE 1 N43930
848	GF201:96(102B1):384(14D1)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] T63980
849	GF200:96(21A5):384(6A9)	ENHANCER OF ZESTE (DROSOPHILA) HOMOLOG 2 AA430744

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Table 1

850	GF201:96(99E1):384(14I1)	REPLICATION FACTOR C (ACTIVATOR 1) 4 (37KD) N93924
851	GF200:96(15B4):384(4D8)	V-MYB AVIAN MYELOBLASTOSIS VIRAL ONCOGENE HOMOLOG-LIKE 2 AA456878
852	GF201:96(86H10):384(10P19)	RIBONUCLEOTIDE REDUCTASE M2 POLYPEPTIDE AA187351
853	GF201:96(58D7):384(21H13)	CDC28 PROTEIN KINASE 2 AA010065
854	GF200:96(25H3):384(7O5)	CDC28 PROTEIN KINASE 2 AA397813
855	GF201:96(98D1):384(13H1)	PITUITARY TUMOR-TRANSFORMING 1 AA430032
856	GF200:96(4E4):384(1J7)	HUMAN UBIQUITIN CARRIER PROTEIN (E2-EPF) MRNA, COMPLETE CDS AA464729
857	GF201:96(88A12):384(11A24)	ESTS, HIGHLY SIMILAR TO MITOTIC KINESIN-LIKE PROTEIN-1 [H.SAPIENS] AA454098
858	GF200:96(26C11):384(7E22)	TROPHININ-ASSISTING PROTEIN (TASTIN) H94949
859	GF200:96(18H3):384(5O6)	CELL DIVISION CYCLE 20, S.CEREVISIAE HOMOLOG AA598776
860	GF202:96(109B4):384(15C7)	HOMO SAPIENS MRNA FOR KIAA0788 PROTEIN, PARTIAL CDS AA676460
861	GF201:96(94C2):384(12F3)	HOMO SAPIENS HPV16 E1 PROTEIN BINDING PROTEIN MRNA, COMPLETE CDS AA630784
862	GF201:96(92B8):384(12C16)	CENTROMERE PROTEIN F (350/400KD, MITOSIN) AA701455
863	GF201:96(59D12):384(22G23)	782283 AA432248
864	GF200:96(22E1):384(6I2)	POLYMYOSITIS/SCLERODERMA AUTOANTIGEN 1 (75KD) AA458994
865	GF200:96(25C6):384(7E11)	CYCLIN A2 AA608568
866	GF200:96(25E10):384(7I19)	HOMO SAPIENS MRNA FOR CDC2 DELTA T, COMPLETE CDS AA598974
867	GF201:96(92E2):384(12I4)	PROTEIN KINASE MITOGEN- ACTIVATED 13 AA157499
868	GF201:96(92F2):384(12K4)	POLO (DROSOPHILA)-LIKE KINASE AA629262
869	GF200:96(7A8):384(2B16)	HUMAN MRNA FOR KIAA0074 GENE, PARTIAL CDS N54344
870	GF201:96(92E6):384(12I12)	BUDDING UNINHIBITED BY BENZIMIDAZOLES 1 (YEAST HOMOLOG) AA446462
871	GF200:96(25H4):384(7O7)	MINICHROMOSOME MAINTENANCE DEFICIENT (S. CEREVISIAE) 4 AA485983
872	GF200:96(110C1):384(15E2)	FLAP STRUCTURE-SPECIFIC ENDONUCLEASE 1 AA620553
873	PEROU:96(7B8):384(20D16)	236142 H61303
874	GF200:96(22A8):384(6A16)	FORKHEAD (DROSOPHILA)-LIKE 16 AA129552
875	GF200:96(10A8):384(3A16)	ESTS, HIGHLY SIMILAR TO SERINE/THREONINE KINASE [H.SAPIENS] R19158
876	GF200:96(15G5):384(4N10)	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDES B AND B1 AA599116
877	PEROU:96(3F10):384(19L20)	PROLIFERATING CELL NUCLEAR ANTIGEN H13004
878	GF200:96(16F3):384(4L5)	PROLIFERATING CELL NUCLEAR ANTIGEN AA450265
879	GF201:96(59C9):384(22E17)	CALMODULIN 1 (PHOSPHORYLASE KINASE, DELTA) R76554
880	GF202:96(109C3):384(15E5)	NON-METASTATIC CELLS 1, PROTEIN (NM23A) EXPRESSED IN AA644092
881	GF201:96(86E5):384(10J9)	HUMAN MRNA FOR KIAA0098 GENE, PARTIAL CDS AA629692
882	GF202:96(116G8):384(16N15)	PROLIFERATION-ASSOCIATED 2G4, 38KD AA488332
883	GF200:96(1C3):384(1E5)	URACIL-DNA GLYCOSYLASE H15111
884	GF201:96(88A9):384(11A18)	MULTIFUNCTIONAL POLYPEPTIDE SIMILAR TO SAICAR SYNTHETASE AND AIR CARBOXYLASE N33274
885	GF202:96(113E7):384(16I13)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA088458
886	GF201:96(90F3):384(11L5)	MEMBRANE-ASSOCIATED TYROSINE- AND THREONINE-SPECIFIC CDC2-INHIBITORY KINASE AA478066
887	GF200:96(5G12):384(2M23)	292933 N69491

Table 1

888	GF201:96(96B11):384(13C22)	H.SAPIENS DHFR GENE, EXONS 1 & 2, AND JOINED CDS R00884
889	GF200:96(29B2):384(8C3)	244205 N52980
890	GF200:96(25B2):384(7C3)	PRIMASE, POLYPEPTIDE 1 (49KD) AA025937
891	GF201:96(90B12):384(11D23)	KIAA0159 GENE PRODUCT AA668256
892	GF200:96(17F10):384(5K19)	LAMIN B2 AA456868
893	GF201:96(86D3):384(10H5)	HOMO SAPIENS GENE FOR THYMIDYLATE SYNTHASE, EXONS 1, 2, 3, 4, 5, 6, 7, COMPLETE CDS AA663310
894	PEROU:96(7H9):384(20P18)	MCM5/CDC46 HOMOLOG AA075920
895	GF201:96(93B8):384(12D16)	CDC7 (CELL DIVISION CYCLE 7, S. CEREVISIAE, HOMOLOG)-LIKE 1 N62245
896	GF201:96(67C5):384(24E9)	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 EPSILON 1 N91962
897	GF200:96(23D12):384(6H24)	TRANSLIN AA61231
898	GF200:96(4D9):384(1H17)	HYALURONAN-MEDIATED MOTILITY RECEPTOR (RHAMM) R10284
899	GF201:96(96D9):384(13G18)	CYCLIN F AA676797
900	GF200:96(31E12):384(8J24)	ESTS, HIGHLY SIMILAR TO TOPOISOMERASE II ALPHA {C-TERMINAL} [H.SAPIENS] AA504348
901	GF201:96(96D10):384(13G20)	CYCLIN E1 T54121
902	GF201:96(58B3):384(21D5)	TRANSCRIPTION FACTOR COUP 2 (CHICKEN OVALBUMIN UPSTREAM PROMOTER 2, APOLIPOPROTEIN REGULATORY PROTEIN) R89308
903	GF202:96(115A5):384(16B10)	TYROSYL-TRNA SYNTHETASE AA102053
904	GF202:96(111C7):384(15F14)	HOMO SAPIENS EXPORTIN T MRNA, COMPLETE CDS AA211459
905	GF201:96(89C9):384(11F18)	ORIGIN RECOGNITION COMPLEX, SUBUNIT 1 (YEAST HOMOLOG)-LIKE R83277
906	GF200:96(19A11):384(5B22)	MAD2 (MITOTIC ARREST DEFICIENT, YEAST, HOMOLOG)-LIKE 1 AA481076
907	GF201:96(89G1):384(11N2)	HOMO SAPIENS DNA FOR APOER2 W80637
908	GF200:96(15G7):384(4N14)	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE B" AA521249
909	GF201:96(80C12):384(9E24)	770898 AA434411
910	GF202:96(113A7):384(16A13)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4877775) [H.SAPIENS] AA126951
911	GF200:96(26D4):384(7G8)	PHORBOLIN (SIMILAR TO APOLIPOPROTEIN B MRNA EDITING PROTEIN) T64880
912	GF202:96(116A6):384(16B11)	ESTS, WEAKLY SIMILAR TO PREGNANCY ZONE PROTEIN PRECURSOR [H.SAPIENS] AA600184
913	GF202:96(112G10):384(15N19)	ESTS, WEAKLY SIMILAR TO POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A [H.SAPIENS] AA130596
914	GF200:96(23D11):384(6H22)	CELL DIVISION CYCLE 25B H14343
915	GF200:96(17E12):384(5I23)	CELL DIVISION CYCLE 25B AA448755
916	GF200:96(11F5):384(3L10)	CHLORIDE CHANNEL, NUCLEOTIDE-SENSITIVE, 1A T52435
917	GF202:96(109A7):384(15A13)	THREONYL-TRNA SYNTHETASE AA630628
918	PEROU:96(2A10):384(19A20)	TRANSFERRIN RECEPTOR (P90, CD71) N27985
919	GF200:96(24D4):384(6H7)	GLUTAMIC-OXALOACETIC TRANSAMINASE 1, SOLUBLE (ASPARTATE AMINOTRANSFERASE 1) H22856
920	GF201:96(62E6):384(22I11)	308495 N95558
921	GF201:96(58D12):384(21H23)	CENTROMERE PROTEIN F (350/400KD, MITOSIN) T87341
922	GF201:96(80E5):384(9I10)	811069 AA485454
923	GF201:96(87F5):384(11K9)	NUCLEOSIDE PHOSPHORYLASE AA430382

Table 1

924	GF202:96(112F11):384(15L21)	731218 AA416724
925	GF201:96(89D12):384(11H24)	SOLUTE CARRIER FAMILY 16 (MONOCARBOXYLIC ACID TRANSPORTERS), MEMBER 3 AA129777
926	GF202:96(110D1):384(15G2)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] AA186804
927	GF200:96(16G10):384(4N19)	PHOSPHOFRUCTOKINASE, PLATELET AA608558
928	GF202:96(116G10):384(16N19)	511647 AA126947
929	GF200:96(4C4):384(1F7)	PROTEOLIPID PROTEIN 2 (COLONIC EPITHELIUM-ENRICHED) AA464627
930	GF200:96(9F10):384(3K19)	PROTEIN DISULFIDE ISOMERASE RELATED PROTEIN (CALCIUM-BINDING PROTEIN, INTESTINAL-RELATED) N59626
931	PEROU:96(7E12):384(20J24)	HEAT SHOCK 70KD PROTEIN 4 R85253
932	GF201:96(97F2):384(13L4)	ADDUCIN 3 (GAMMA) AA461325
933	GF201:96(88D2):384(11G4)	INTERLEUKIN 7 RECEPTOR AA485865
934	GF201:96(92B10):384(12C20)	CYCLIN-DEPENDENT KINASE INHIBITOR 2C (P18, INHIBITS CDK4) N72115
935	GF201:96(95A4):384(13A7)	ADIPOSE DIFFERENTIATION-RELATED PROTEIN; ADIPOPHILIN AA700054
936	GF201:96(83F6):384(10K11)	ESTS, WEAKLY SIMILAR TO CDNA EST EMBL:D70402 COMES FROM THIS GENE [C.ELEGANS] N62924
937	GF201:96(83G3):384(10M5)	ESTS, HIGHLY SIMILAR TO DEDUCED PROTEIN PRODUCT SHOWS SIGNIFICANT HOMOLOGY TO COACTOSIN FROM DICTYOSTELIUM DISCOIDEUM [H.SAPIENS] R78530
938	GF201:96(95G12):384(13M23)	INTERFERON, GAMMA-INDUCIBLE PROTEIN 30 AA630800
939	GF201:96(95F12):384(13K23)	GLUTAMATE DECARBOXYLASE 2 (PANCREATIC ISLETS AND BRAIN, 65KD) R44005
940	GF200:96(29G9):384(8M17)	SOLUTE CARRIER FAMILY 7 (CATIONIC AMINO ACID TRANSPORTER, Y+ SYSTEM), MEMBER 7 T98394
941	PEROU:96(6B7):384(20C14)	CHEMOKINE (C-X-C MOTIF), RECEPTOR 4 (FUSIN) AA479467
942	GF200:96(2A3):384(1A6)	SMALL INDUCIBLE CYTOKINE A4 (HOMOLOGOUS TO MOUSE MIP-1B) H62985
943	GF201:96(83G5):384(10M9)	ESTS, WEAKLY SIMILAR TO PUTATIVE P150 [H.SAPIENS] R74478
944	GF200:96(6F10):384(2K20)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.SAPIENS] T94293
945	GF200:96(8B7):384(2D13)	CHITINASE 1 T94272
946	GF200:96(8A6):384(2B11)	53341 R15934
947	GF200:96(10B8):384(3C16)	SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 18, PULMONARY AND ACTIVATION-REGULATED AA495985
948	GF200:96(10C8):384(3E16)	FOLYLPOLYGLUTAMATE SYNTHASE R44864
949	PEROU:96(6D4):384(20G8)	LYSOZYME (RENAL AMYLOIDOSIS) N63943
950	GF201:96(88B6):384(11C12)	LYSOZYME (RENAL AMYLOIDOSIS) N63943
951	GF201:96(86C12):384(10F23)	TRANSCRIPTION FACTOR AP-2 ALPHA (ACTIVATING ENHANCER-BINDING PROTEIN 2 ALPHA) N63770
952	GF201:96(88B10):384(11C20)	LIPASE A, LYSOSOMAL ACID, CHOLESTEROL ESTERASE (WOLMAN DISEASE) AA630104
953	GF200:96(25H8):384(7O15)	CD68 ANTIGEN AA421296
954	GF200:96(14H7):384(4O14)	ACID PHOSPHATASE 5, TARTRATE RESISTANT R08816
955	PEROU:96(6B2):384(20C4)	FC FRAGMENT OF IGE, HIGH AFFINITY I, RECEPTOR FOR; GAMMA POLYPEPTIDE R79170
956	GF202:96(114H10):384(16O20)	CATHEPSIN Z AA488341
957	GF200:96(14A4):384(4A8)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DM ALPHA H42679
958	GF201:96(94E9):384(12I17)	HUMAN MRNA FOR SB CLASSII HISTOCOMPATIBILITY ANTIGEN ALPHA-CHAIN AA634028
959	GF200:96(17E1):384(5I1)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DP BETA 1 AA486627

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Table 1

960	GF200:96(26C5):384(7E10)	HUMAN MHC CLASS II DQ-ALPHA ASSOCIATED WITH DRW6, DQW1 PROTEIN, COMPLETE CDS, CLONE B T63324
961	GF200:96(17E10):384(5I19)	HUMAN MHC CLASS II DQ-ALPHA ASSOCIATED WITH DRW6, DQW1 PROTEIN, COMPLETE CDS, CLONE B T63324
962	GF200:96(17F1):384(5K1)	LYSYL OXIDASE AA452916
963	GF200:96(8H10):384(2P19)	HUMAN MHC CLASS II DQ-BETA ASSOCIATED WITH DR2, DQW1 PROTEIN, COMPLETE CDS AA458472
964	GF200:96(32C10):384(8F19)	121275 T96731
965	GF201:96(63A7):384(23A13)	HOMO SAPIENS MRNA FOR KIAA0937 PROTEIN, PARTIAL CDS AA043790
966	GF201:96(88B3):384(11C6)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 1 AA664195
967	PEROU:96(6C5):384(20E10)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 5 H52245
968	GF201:96(88A2):384(11A4)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 5 AA485739
969	PEROU:96(6D9):384(20G18)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 5 AA037380
970	GF200:96(11A10):384(3B20)	HUMAN HLA-DR ALPHA-CHAIN MRNA R47979
971	PEROU:96(8A12):384(20B23)	KIAA0855 AI636699
972	GF200:96(15A12):384(4B24)	VASCULAR CELL ADHESION MOLECULE 1 H16637
973	GF200:96(1B4):384(1C7)	VASCULAR CELL ADHESION MOLECULE 1 H07071
974	GF200:96(11F3):384(3L6)	MACROPHAGE-ASSOCIATED ANTIGEN AA401693
975	GF200:96(3H9):384(1P18)	FC FRAGMENT OF IGG, LOW AFFINITY IIIA, RECEPTOR FOR (CD16) H20872
976	GF201:96(58D9):384(21H17)	ESTS, HIGHLY SIMILAR TO COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR [H.SAPIENS] N38801
977	GF200:96(32F6):384(8L11)	ESTS, HIGHLY SIMILAR TO COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR [H.SAPIENS] N90491
978	GF200:96(25D6):384(7G11)	COMPLEMENT COMPONENT 1, Q SUBCOMPONENT, BETA POLYPEPTIDE T71284
979	GF200:96(25D1):384(7G1)	COMPLEMENT COMPONENT 2 T71879
980	GF201:96(94H11):384(12P21)	FIBRINOGEN-LIKE PROTEIN 2 H56349
981	GF201:96(93A10):384(12B20)	HOMO SAPIENS MRNA FOR KIAA0290 GENE, PARTIAL CDS AA400186
982	GF201:96(97F3):384(13L6)	ADDUCIN 2 (BETA) AA019320
983	GF200:96(12D6):384(3H11)	GLUCAN (1,4-ALPHA-), BRANCHING ENZYME 1 (GLYCOGEN BRANCHING ENZYME, ANDERSEN DISEASE, GLYCOGEN STORAGE DISEASE TYPE IV) R09069
984	GF200:96(9F11):384(3K21)	GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 2 AA495724
985	GF200:96(12D2):384(3H3)	GLUCOSE-6-PHOSPHATE DEHYDROGENASE AA424937
986	GF200:96(23F6):384(6L12)	T-CELL ACTIVATION PROTEIN, EB1 FAMILY AA608576
987	GF201:96(84A8):384(10A16)	133518 R28608
988	GF200:96(2F12):384(1K24)	PROTEIN KINASE C, ALPHA AA030029
989	GF200:96(3E10):384(1J20)	MEMBRANE PROTEIN, PALMITOYLATED 1 (55KD) W01240
990	GF201:96(99F5):384(14K9)	52128 H22568
991	GF202:96(116C10):384(16F19)	34294 R44346
992	GF200:96(12F6):384(3L11)	FUCOSYLTRANSFERASE 4 (ALPHA (1,3) FUCOSYLTRANSFERASE, MYELOID-SPECIFIC) R28447
993	GF201:96(63G12):384(23M23)	366778 AA029722

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Table 1

994	GF201:96(83F9):384(10K17)	491644 AA150263
995	GF200:96(26G5):384(7M10)	NOVEL HUMAN GENE MAPPING TO CHOMOSOME 13 AA488718
996	GF200:96(21F12):384(6K23)	IQ MOTIF CONTAINING GTPASE ACTIVATING PROTEIN 2 W32272
997	GF201:96(97A2):384(13B4)	CD1D ANTIGEN, D POLYPEPTIDE AA451684
998	GF202:96(109A10):384(15A19)	SMALL INDUCIBLE CYTOKINE A5 (RANTES) AA486072
999	GF200:96(12B9):384(3D17)	NATURAL KILLER CELL GROUP 7 SEQUENCE T57859
1000	GF201:96(86D10):384(10H19)	TRYPTOPHANYL-TRNA SYNTHETASE AA664040
1001	GF201:96(88D9):384(11G18)	INTERCELLULAR ADHESION MOLECULE 1 (CD54), HUMAN RHINOVIRUS RECEPTOR R77293
1002	GF200:96(17A11):384(5A21)	768638 AA425352
1003	PEROU:96(6A5):384(20A10)	SMALL INDUCIBLE CYTOKINE A2 (MONOCYTE CHEMOTACTIC PROTEIN 1, HOMOLOGOUS TO MOUSE SIG-JE) T77817
1004	GF200:96(2A4):384(1A8)	SMALL INDUCIBLE CYTOKINE A2 (MONOCYTE CHEMOTACTIC PROTEIN 1, HOMOLOGOUS TO MOUSE SIG-JE) AA425102
1005	GF200:96(5E4):384(2I7)	SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 13 T64134
1006	GF201:96(86F11):384(10L21)	SMALL INDUCIBLE CYTOKINE SUBFAMILY A (CYS-CYS), MEMBER 11 (EOTAXIN) W69211
1007	GF201:96(92G4):384(12M8)	LEUKOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR 2 H54023
1008	GF201:96(98G1):384(13N1)	HOMO SAPIENS MRNA FOR KILLER ACTIVATING RECEPTOR ASSOCIATED PROTEIN, ISOFORM B H12338
1009	GF200:96(26F12):384(7K24)	FC FRAGMENT OF IGE, HIGH AFFINITY I, RECEPTOR FOR; GAMMA POLYPEPTIDE H79353
1010	GF202:96(109D3):384(15G5)	INTEGRIN, ALPHA X (ANTIGEN CD11C (P150), ALPHA POLYPEPTIDE) N64384
1011	GF201:96(88D11):384(11G22)	754406 AA436187
1012	GF201:96(95H9):384(13O17)	FC FRAGMENT OF IGG, LOW AFFINITY IIA, RECEPTOR FOR (CD32) AA634109
1013	GF200:96(25E12):384(7I23)	CATHEPSIN S AA236164
1014	GF200:96(1H9):384(1O17)	SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 5 H38650
1015	GF200:96(12D8):384(3H15)	GARDNER-RASHEED FELINE SARCOMA VIRAL (V-FGR) ONCOGENE HOMOLOG AA256231
1016	GF201:96(97B12):384(13D24)	BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN AA680249
1017	GF202:96(112B9):384(15D17)	783959 AA447383
1018	GF200:96(14F5):384(4K10)	AMINOLEVULINATE, DELTA-, SYNTHASE 1 AA453691
1019	GF201:96(87G9):384(11M17)	MYELOPEROXIDASE AA703058
1020	GF200:96(94A3):384(12B5)	KIAA0443 GENE PRODUCT AA702949
1021	GF201:96(87G8):384(11M15)	N-ACETYLTRANSFERASE, HOMOLOG OF S. CEREVISIAE ARD1 R55220
1022	GF200:96(28B12):384(7D23)	ESTS, WEAKLY SIMILAR TO DJ79C4.1.2 [H.SAPIENS] R69179
1023	GF201:96(94E10):384(12I19)	HEMOGLOBIN, ZETA N59636
1024	GF201:96(55A4):384(21A7)	PHOSPHOLIPASE C, BETA 2 AA464970
1025	GF200:96(27D10):384(7H20)	ESTS, WEAKLY SIMILAR TO E25B PROTEIN [M.MUSCULUS] AA034213
1026	GF201:96(95D8):384(13G15)	CORE-BINDING FACTOR, RUNT DOMAIN, ALPHA SUBUNIT 3 N67778
1027	GF201:96(102H7):384(14P13)	40296 R52082
1028	GF200:96(11B6):384(3D12)	RHO GTPASE ACTIVATING PROTEIN 4 H69620
1029	GF200:96(11H1):384(3P2)	RAS HOMOLOG GENE FAMILY, MEMBER H W38571

Table 1

1030	GF202:96(116B7):384(16D13)	HOMO SAPIENS IMMUNOGLOBULIN-LIKE TRANSCRIPT 7 MRNA, COMPLETE CDS N62837
1031	GF200:96(23C6):384(6F12)	HEMOPOIETIC CELL KINASE AA149096
1032	GF200:96(17A1):384(5A1)	CHEMOKINE (C-X-C MOTIF), RECEPTOR 4 (FUSIN) T62491
1033	GF200:96(4A11):384(1B21)	INTERCELLULAR ADHESION MOLECULE 3 AA478647
1034	GF201:96(100F4):384(14K8)	50619 H17517
1035	GF202:96(110D9):384(15G18)	742569 AA400074
1036	PEROU:96(6F11):384(20K22)	LYMPHOCYTE CYTOSOLIC PROTEIN 1 AA044266
1037	GF201:96(88B8):384(11C16)	ESTS, HIGHLY SIMILAR TO L-PLASTIN [H.SAPIENS] W73144
1038	GF200:96(15G1):384(4N2)	SPLEEN TYROSINE KINASE AA598572
1039	GF201:96(89A3):384(11B6)	RIBONUCLEASE, RNASE A FAMILY, K6 AA701545
1040	GF200:96(2E10):384(1I20)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, C POLYPEPTIDE H74265
1041	GF200:96(4A7):384(1B13)	INTERLEUKIN 2 RECEPTOR, GAMMA (SEVERE COMBINED IMMUNODEFICIENCY) N75745
1042	GF200:96(9D8):384(3G15)	CLK-ASSOCIATING RS-CYCLOPHILIN H14513
1043	GF202:96(116A8):384(16B15)	ESTS, WEAKLY SIMILAR TO RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSDR1 [H.SAPIENS] N79745
1044	PEROU:96(6B6):384(20C12)	INTEGRIN, BETA 2 (ANTIGEN CD18 (P95), LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 1; MACROPHAGE ANTIGEN 1 (MAC-1) BETA SUBUNIT) H17426
1045	GF200:96(16D6):384(4H11)	PROTEOGLYCAN 1, SECRETORY GRANULE AA278759
1046	GF200:96(24G11):384(6N21)	HUMAN EV12 PROTEIN GENE H93149
1047	GF202:96(110C3):384(15E6)	ECOTROPIC VIRAL INTEGRATION SITE 2B AA159620
1048	GF200:96(7A6):384(2B12)	LYSOSOMAL-ASSOCIATED MULTISPANNING MEMBRANE PROTEIN-5 AA410265
1049	GF201:96(79E8):384(9I15)	795544 AA459654
1050	GF200:96(9B2):384(3C3)	NOTCH (DROSOPHILA) HOMOLOG 4 AA419524
1051	GF201:96(90F8):384(11L15)	LEUKOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR 7 N63398
1052	GF201:96(86C4):384(10F7)	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 1B AA150416
1053	PEROU:96(6C8):384(20E16)	HEMATOPOIETIC CELL-SPECIFIC LYN SUBSTRATE 1 N32012
1054	GF200:96(11B2):384(3D4)	HEMATOPOIETIC CELL-SPECIFIC LYN SUBSTRATE 1 AA424575
1055	PEROU:96(6A12):384(20A24)	FC FRAGMENT OF IGG, LOW AFFINITY IIB, RECEPTOR FOR (CD32) R78403
1056	GF200:96(10A6):384(3A12)	HOMO SAPIENS MRNA FOR GALECTIN-9 ISOFORM, COMPLETE CDS AA434102
1057	GF200:96(3A1):384(1B2)	PHOSPHOINOSITIDE-3-KINASE, CATALYTIC, GAMMA POLYPEPTIDE AA464765
1058	GF201:96(17A9):384(5A17)	PLECKSTRIN AA490267
1059	GF201:96(91D11):384(12G21)	ALLOGRAFT INFLAMMATORY FACTOR 1 W69954
1060	GF201:96(18F7):384(5K14)	SRC-LIKE-ADAPTER AA485141
1061	GF201:96(100E11):384(14I22)	33293 R43956
1062	GF200:96(22A4):384(6A8)	POTASSIUM VOLTAGE-GATED CHANNEL, SHAKER-RELATED SUBFAMILY, BETA MEMBER 2 H14383
1063	GF200:96(25E2):384(7I3)	CYTOCHROME B-245, BETA POLYPEPTIDE (CHRONIC GRANULOMATOUS DISEASE) AA463492
1064	GF201:96(89G2):384(11N4)	H.SAPIENS MRNA FOR CORONIN AA047478
1065	PEROU:96(6C1):384(20E2)	CD53 ANTIGEN H70125
1066	GF200:96(25H10):384(7O19)	CD53 ANTIGEN AA132090

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Table 1

1067	GF200:96(26C7):384(7E14)	LYMPHOCYTE-SPECIFIC PROTEIN 1 T83159
1068	GF201:96(89E7):384(11J14)	HEMATOPOIETIC PROTEIN 1 AA668726
1069	GF200:96(6F12):384(2K24)	DEDICATOR OF CYTO-KINESIS 2 N70765
1070	GF201:96(96H11):384(13O22)	CD38 ANTIGEN (P45) R00276
1071	GF200:96(2F11):384(1K22)	PROTEIN KINASE C, BETA 1 AA479102
1072	GF201:96(10OC6):384(14E12)	51D29 H19330
1073	GF200:96(90A5):384(11B9)	51I78 H17121
1074	GF200:96(22B8):384(6C16)	RHO GDP DISSOCIATION INHIBITOR (GDI) BETA AA487634
1075	GF201:96(90B5):384(11D9)	KIAA0195 GENE PRODUCT W79511
1076	GF201:96(96H12):384(13O24)	CD37 ANTIGEN AA676453
1077	GF201:96(96F7):384(13K14)	CHEMOKINE (C-C MOTIF) RECEPTOR 1 AA036881
1078	GF200:96(6H11):384(2O22)	HUMAN MRNA FOR KIAA0128 GENE, PARTIAL CDS R76772
1079	GF200:96(17G3):384(5M5)	PROTEASE INHIBITOR 2 (ANTI-ELASTASE), MONOCYTE/NEUTROPHIL AA486275
1080	GF200:96(14C2):384(4E4)	CHEMOKINE (C-C MOTIF) RECEPTOR 2 H58254
1081	GF200:96(25D7):384(7G13)	704020 AA279147
1082	GF201:96(82C3):384(9F5)	504536 AA150043
1083	GF200:96(4F7):384(1L13)	INTERCELLULAR ADHESION MOLECULE 5, TELENCEPHALIN R87840
1084	GF200:96(7B7):384(2D14)	HUMAN MRNA FOR KIAA0006 GENE, COMPLETE CDS AA236617
1085	GF201:96(102B7):384(14D13)	PROSTATE CANCER OVEREXPRESSED GENE 1 T64312
1086	GF200:96(24D2):384(6H3)	GLUTAREDOXIN (THIOLTRANSFERASE) AA291163
1087	GF200:96(1G9):384(1M17)	T-CELL RECEPTOR, ALPHA (V,D,J,C) AA427667
1088	GF201:96(95E1):384(13I21)	GRANZYME K (SERINE PROTEASE, GRANZYME 3; TRYPTASE II) AA005382
1089	GF200:96(26C9):384(7E18)	CD79A ANTIGEN (IMMUNOGLOBULIN-ASSOCIATED ALPHA) T87012
1090	GF200:96(14A9):384(4A18)	CD8 ANTIGEN, ALPHA POLYPEPTIDE (P32) AA443649
1091	GF201:96(88D5):384(11G10)	INTERLEUKIN 10 RECEPTOR, ALPHA AA437226
1092	GF200:96(4B3):384(1D5)	INTEGRIN, ALPHA L, CD11A R48796
1093	GF200:96(1G8):384(1M15)	742143 AA406027
1094	GF201:96(98G4):384(13N7)	T-CELL RECEPTOR, BETA CLUSTER N91921
1095	GF201:96(86E4):384(10I7)	80186 T64192
1096	GF201:96(86E3):384(10J5)	T-CELL RECEPTOR, DELTA (V,D,J,C) AA670107
1097	GF200:96(98H4):384(13P7)	ESTS, WEAKLY SIMILAR TO S-ACYL FATTY ACID SUNTHETASE THIO ESTER HYDROLASE, MEDIUM CHAIN [R.NORVEGICUS] AA470066
1098	GF200:96(26B11):384(7C22)	LYMPHOCYTE-SPECIFIC PROTEIN TYROSINE KINASE AA420981
1099	GF201:96(88E6):384(10I11)	CD3D ANTIGEN, DELTA POLYPEPTIDE (TIT3 COMPLEX) AA055946
1100	GF200:96(14B2):384(4C4)	CD3G ANTIGEN, GAMMA POLYPEPTIDE (TIT3 COMPLEX) T66800
1101	GF200:96(22C5):384(6E10)	TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2) AA465444
1102	GF200:96(14D2):384(4G4)	TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 2 AA457114
1103	GF200:96(17C6):384(5E11)	NATURAL KILLER CELL TRANSCRIPT 4 AA458965
1104	GF200:96(14B3):384(4C6)	CD39 ANTIGEN H13577

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Table 1

ID	Clone	Description
1105	GF200:96(14E2):384(4I4)	APOLIPOPROTEIN C-II AA456474
1106	GF200:96(1D6):384(1G11)	TRANSKETOLASE (WERNICKE-KORSAKOFF SYNDROME) AA070357
1107	GF201:96(96B12):384(13C24)	SOLUTE CARRIER FAMILY 26 (SULFATE TRANSPORTER), MEMBER 2 N73101
1108	GF201:96(68A5):384(24A10)	ESTS, WEAKLY SIMILAR TO MBNL PROTEIN [H.SAPIENS] AA460149
1109	GF201:96(80B4):384(9C8)	ATROPHIN-1 INTERACTING PROTEIN 4 AA448286
1110	GF201:96(95A2):384(13A3)	GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 3 (34KD SUBUNIT) AA460838
1111	GF200:96(29E10):384(8I19)	ESTS, MODERATELY SIMILAR TO SIMILAR TO THYMIDINE DIPHOSPHOGLUCOSE 4,6-DEHYDRATASE [C.ELEGANS] H63455
1112	GF201:96(67D12):384(24G23)	282047 N48252
1113	GF202:96(114C5):384(16E10)	S-ADENOSYLMETHIONINE DECARBOXYLASE 1 AA425692
1114	GF201:96(98B6):384(13D11)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 3882205) [H.SAPIENS] AA425650
1115	GF202:96(112B7):384(15D13)	593239 AA165348
1116	GF202:96(115A6):384(16B12)	HOMO SAPIENS MRNA; CDNA DKFZP564M2423 (FROM CLONE DKFZP564M2423) AA487070
1117	PEROU:96(7G6):384(20N12)	TUMOR REJECTION ANTIGEN (GP96) 1 AA075290
1118	GF201:96(85F6):384(10L12)	257248 N26906
1119	GF202:96(110D11):384(15G22)	133454 R27457
1120	GF201:96(66D11):384(23H21)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4191594) [H.SAPIENS] AA464237
1121	GF200:96(10E6):384(3I12)	MAD (MOTHERS AGAINST DECAPENTAPLEGIC, DROSOPHILA) HOMOLOG 5 AA418999
1122	GF201:96(69C12):384(24F24)	782209 AA431986
1123	GF201:96(98B9):384(13D17)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 3954942) [H.SAPIENS] AA425297
1124	GF200:96(12D5):384(3H9)	GLUCOSAMINE (N-ACETYL)-6-SULFATASE (SANFILIPPO DISEASE IIID) AA035347
1125	GF202:96(116H7):384(16P13)	234977 H73640
1126	GF202:96(112F3):384(15L5)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4530437) [H.SAPIENS] AA457462
1127	GF201:96(57D7):384(21H14)	DCMP DEAMINASE W51951
1128	GF200:96(13F11):384(4K21)	CLATHRIN-ASSOCIATED/ASSEMBLY/ADAPTOR PROTEIN, LARGE, BETA 1 N72918
1129	GF201:96(102D4):384(14H7)	84229 T72825
1130	GF201:96(90F5):384(11L9)	IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 AA133187
1131	GF202:96(115C2):384(16F4)	CHONDROITIN SULFATE PROTEOGLYCAN 6 (BAMACAN) W40150
1132	GF201:96(97A12):384(13B24)	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (NADP+ DEPENDENT), METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE, FORMYLTETRAHYDROFOLATE SYNTHETASE AA633577
1133	GF201:96(58D11):384(21H21)	CITRATE SYNTHASE N67639
1134	GF201:96(99D6):384(14G11)	CITRATE SYNTHASE AA416759
1135	GF200:96(21F5):384(6K9)	HUMAN TB1 GENE MRNA, 3' END H11501
1136	GF202:96(116G4):384(16N7)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4240269) [H.SAPIENS] AA169411
1137	GF200:96(7F4):384(2L8)	FRAGILE X MENTAL RETARDATION, AUTOSOMAL HOMOLOG 1 N79708
1138	GF201:96(58B5):384(21D9)	SNARE PROTEIN AA457731
1139	GF201:96(57F2):384(21L4)	TRANSCRIPTION FACTOR 12 (HTF4, HELIX-LOOP-HELIX TRANSCRIPTION FACTORS 4) H98856
1140	GF201:96(56E6):384(21I12)	RAS-GTPASE ACTIVATING PROTEIN SH3 DOMAIN-BINDING PROTEIN 2 AA151214

Table 1

1141	GF202:96(114E1):384(16I2)	HOMO SAPIENS HUNTINGTIN-INTERACTING PROTEIN HYPA/FBP11 (HYPA) MRNA, PARTIAL CDS AA412712
1142	GF200:96(31D1):384(8H2)	CHAPERONIN CONTAINING TCP1, SUBUNIT 4 (DELTA) T98684
1143	GF201:96(98B5):384(13D9)	MYOSIN PHOSPHATASE, TARGET SUBUNIT 1 AA487028
1144	GF200:96(3B1):384(1D2)	HUMAN CLONE 23721 MRNA SEQUENCE R45056
1145	GF201:96(79F12):384(9K23)	TRANSCRIPTION FACTOR 6-LIKE 1 (MITOCHONDRIAL TRANSCRIPTION FACTOR 1-LIKE) AA150777
1146	GF201:96(98E4):384(13J7)	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4091980) [H.SAPIENS] H11938
1147	GF200:96(13G12):384(4M23)	CASEIN KINASE 2, ALPHA 1 POLYPEPTIDE T98414
1148	GF201:96(80H3):384(9O6)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] W04674
1149	GF200:96(8B1):384(2D1)	HOMO SAPIENS TRACHEA CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN (CSE1) MRNA, COMPLETE CDS N69204
1150	GF202:96(109F8):384(15K15)	HUMAN GLUCOSE TRANSPORTER PSEUDOGENE H03954
1151	GF201:96(55F6):384(21K11)	PROTEIN KINASE, AMP-ACTIVATED, BETA 2 NON-CATALYTIC SUBUNIT N78582
1152	GF201:96(57D11):384(21H22)	HOMO SAPIENS 14-3-3 PROTEIN MRNA, COMPLETE CDS AA609598
1153	GF200:96(10A1):384(3A2)	124781 R01118
1154	GF201:96(87F7):384(11K13)	NUCLEAR TRANSCRIPTION FACTOR Y, ALPHA AA412691
1155	GF200:96(14F8):384(4K16)	195903 R92227
1156	GF201:96(80D8):384(9G16)	DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE, Y CHROMOSOME AA447588
1157	GF201:96(85F3):384(10L6)	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A, Y CHROMOSOME N92611
1158	GF200:96(10C11):384(3E22)	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A, Y CHROMOSOME AA047039
1159	GF202:96(115D7):384(16H14)	842848 AA486281
1160	GF200:96(7H3):384(2P6)	HUMAN CLONE 23933 MRNA SEQUENCE H56918
1161	GF201:96(98H8):384(13P15)	ATP CITRATE LYASE H08548
1162	GF201:96(85F1):384(10L2)	345743 W72666
1163	PEROU:96(6E10):384(20I20)	MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR W87270
1164	GF200:96(5A11):384(2A21)	COMPLEMENT COMPONENT 3A RECEPTOR 1 AA464711
1165	GF201:96(88A10):384(11A20)	CD14 ANTIGEN AA701476
1166	GF200:96(5F5):384(2K9)	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 2 AA479093
1167	GF201:96(58D2):384(21H3)	MURINE LEUKEMIA VIRAL (BMI-1) ONCOGENE HOMOLOG T87515
1168	GF200:96(17D5):384(5G9)	MURINE LEUKEMIA VIRAL (BMI-1) ONCOGENE HOMOLOG AA478036
1169	GF201:96(102F3):384(14L5)	46448 H10673
1170	GF201:96(84G8):384(10M16)	ENDOTHELIAL DIFFERENTIATION-RELATED FACTOR 1 N69393
1171	GF201:96(81D1):384(9H2)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] H54263
1172	PEROU:96(4C5):384(19F9)	GDNF FAMILY RECEPTOR ALPHA 1 AA512935
1173	GF200:96(5G7):384(2M13)	PHOSPHOLIPASE C, EPSILON AA411387
1174	GF200:96(5G11):384(2M21)	NEL (CHICKEN)-LIKE 2 H45376
1175	GF201:96(94E12):384(12J23)	HUMAN HEART MRNA FOR HEAT SHOCK PROTEIN 90, PARTIAL CDS H88540
1176	GF202:96(109H11):384(15O21)	CALMEGIN AA778675
1177	GF201:96(101A7):384(14B14)	74223 T48412

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Table 1

1178	GF201:96(86F4):384(10L7)	ESTS, HIGHLY SIMILAR TO PUTATIVE [H.SAPIENS] AA022561
1179	GF201:96(101B7):384(14D14)	70203 T50083
1180	GF200:96(25F8):384(7K15)	CAPPING PROTEIN (ACTIN FILAMENT), GELSOLIN-LIKE AA486942
1181	GF200:96(24E8):384(6J15)	FORMYL PEPTIDE RECEPTOR 1 AA425249
1182	GF200:96(25G9):384(7M17)	COAGULATION FACTOR XIII, A1 POLYPEPTIDE AA448599
1183	GF200:96(26F10):384(7K20)	TUMOR NECROSIS FACTOR (LIGAND) SUPERFAMILY, MEMBER 10 H54629
1184	GF201:96(62E7):384(22J13)	PIGMENT EPITHELIUM-DERIVED FACTOR AA463946
1185	GF201:96(60B10):384(22C20)	811095 AA485674
1186	PEROU:96(6C4):384(20E8)	B-FACTOR, PROPERDIN H80257
1187	GF201:96(97C2):384(13F4)	B-FACTOR, PROPERDIN AA401441
1188	GF201:96(56A5):384(21A10)	RETINOIC ACID RECEPTOR RESPONDER (TAZAROTENE INDUCED) 3 W47350
1189	GF201:96(90E5):384(11J9)	BONE MARROW STROMAL CELL ANTIGEN 2 AA485371
1190	GF201:96(89C4):384(11E8)	FC FRAGMENT OF IGG, LOW AFFINITY IIB, RECEPTOR FOR (CD32) R68106
1191	GF201:96(88B4):384(11C8)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, A AA644657
1192	GF202:96(116F1):384(16L1)	72245 T50661
1193	GF201:96(88A5):384(11A10)	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, C AA464246
1194	GF201:96(88A6):384(11A12)	MACROPHAGE STIMULATING 1 (HEPATOCYTE GROWTH FACTOR-LIKE) T51539
1195	PEROU:96(7F2):384(20L4)	BETA-2-MICROGLOBULIN AI250654
1196	GF201:96(98F10):384(13L19)	INTERFERON-INDUCED PROTEIN 41, 30KD R54613
1197	GF201:96(66D6):384(23H11)	504372 AA142842
1198	GF202:96(113E6):384(16I11)	ESTS, WEAKLY SIMILAR TO NEURONAL THREAD PROTEIN AD7C-NTP [H.SAPIENS] AA099706
1199	GF200:96(32H9):384(8P17)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.SAPIENS] T64956
1200	GF201:96(98A2):384(13B3)	INTERFERON-INDUCED PROTEIN 17 AA058323
1201	GF201:96(88E11):384(11I22)	INTERFERON-INDUCED PROTEIN 17 AA419251
1202	GF201:96(88F10):384(11K20)	361899 AA001376
1203	GF201:96(88F3):384(11K6)	INTERFERON, ALPHA-INDUCIBLE PROTEIN 27 AA157813
1204	GF200:96(10B11):384(3C22)	HYPOTHETICAL PROTEIN, EXPRESSED IN OSTEOBLAST AA410567
1205	GF200:96(4A8):384(1B15)	HUMAN MRNA FOR 56-KDA PROTEIN INDUCED BY INTERFERON AA489743
1206	GF201:96(88E12):384(11I24)	289496 N63988
1207	GF200:96(1F9):384(1K17)	INTERFERON-STIMULATED TRANSCRIPTION FACTOR 3, GAMMA (48KD) AA291577
1208	GF200:96(17C9):384(5E17)	MYXOVIRUS (INFLUENZA) RESISTANCE 1, HOMOLOG OF MURINE (INTERFERON-INDUCIBLE PROTEIN P78) AA456886
1209	GF201:96(88F1):384(11K2)	INTERFERON-STIMULATED PROTEIN, 15 KDA AA406020
1210	PEROU:96(9F6):384(18L12)	INTERFERON-INDUCED 17 KD PROTEIN AA120862
1211	GF200:96(17H9):384(5O17)	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA448478
1212	GF200:96(26C8):384(7E16)	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA432030
1213	PEROU:96(9G1):384(18N2)	INTERFERON ALPHA-INDUCIBLE PROTEIN (CLONE IFI-6-16) AA075725
1214	PEROU:96(9G3):384(18N6)	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA AA079495
1215	PEROU:96(7G12):384(20N24)	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA AA076085

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Table 1

1216	PEROU:96(9G2):384(18N4)	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA AA076085
1217	GF200:96(15H8):384(4P16)	ESTS, HIGHLY SIMILAR TO SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA [H.SAPIENS] AA486367
1218	GF200:96(15C9):384(4F18)	TRANSPORTER 1, ABC (ATP BINDING CASSETTE) AA487637
1219	GF200:96(23B8):384(6D16)	MHC CLASS I REGION ORF T58146
1220	GF201:96(84C7):384(10E14)	207838 H60298
1221	GF200:96(17H10):384(5O19)	INTERFERON REGULATORY FACTOR 1 AA478043
1222	GF202:96(109B12):384(15C23)	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE, 8 (LARGE MULTIFUNCTIONAL PROTEASE 7) AA181300
1223	GF200:96(21D8):384(6G15)	BUTYROPHILIN, SUBFAMILY 3, MEMBER A3 AA478585
1224	GF201:96(92D11):384(12G22)	UBIQUITIN-CONJUGATING ENZYME E2L 6 AA292074
1225	GF200:96(32A10):384(8B19)	144916 R78509
1226	GF200:96(24B9):384(6D17)	MONOKINE INDUCED BY GAMMA INTERFERON AA131406
1227	GF200:96(11D9):384(3H18)	DIUBIQUITIN N49629
1228	GF201:96(63H7):384(23O13)	288807 N62522
1229	GF200:96(9B12):384(3C23)	G PROTEIN-COUPLED RECEPTOR R92239
1230	GF202:96(109G2):384(15M3)	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 3 BINDING PROTEIN (GALECTIN 6 BINDING PROTEIN) AA485353
1231	PEROU:96(7B2):384(20D4)	GLUTATHIONE S-TRANSFERASE M1 AA232417
1232	PEROU:96(7B1):384(20D2)	GLUTAMATE RECEPTOR, IONOTROPIC, N-METHYL D-ASPARTATE 1 AA351537
1233	GF201:96(96E5):384(13I10)	COLONY STIMULATING FACTOR 1 RECEPTOR, FORMERLY MCDONOUGH FELINE SARCOMA VIRAL (V-FMS) ONCOGENE HOMOLOG AA284954
1234	GF201:96(68B8):384(24C16)	795307 AA454159
1235	GF201:96(87A9):384(11A17)	RECOVERIN AA074224
1236	GF201:96(97C9):384(13F18)	ARYLSULFATASE A H45449
1237	GF200:96(17G5):384(5M9)	SERINE DEHYDRATASE T71363
1238	GF202:96(116F8):384(16L15)	265343 N20862
1239	GF201:96(101D5):384(14H10)	HOMO SAPIENS CLONE 643 UNKNOWN MRNA, COMPLETE SEQUENCE T53404
1240	GF201:96(83H11):384(10O21)	811020 AA485369
1241	GF200:96(25D10):384(7G19)	COLLAGEN, TYPE II, ALPHA 1 (PRIMARY OSTEOARTHRITIS, SPONDYLOEPIPHYSEAL DYSPLASIA, CONGENITAL) N66737
1242	GF201:96(83A8):384(10A15)	490718 AA115761
1243	GF200:96(4F1):384(1L1)	GATA-BINDING PROTEIN 6 H77652
1244	GF201:96(99B8):384(13D15)	ESTS, WEAKLY SIMILAR TO NUCLEAR PROTEIN SA-1 [H.SAPIENS] H17115
1245	GF201:96(12F11):384(3L21)	FOLATE RECEPTOR 1 (ADULT) R24635
1246	GF200:96(26E4):384(7I8)	HUMAN MRNA FOR KIAA0300 GENE, PARTIAL CDS AA405458
1247	GF200:96(9B10):384(3C19)	HUMAN GABA-A RECEPTOR EPSILON SUBUNIT (GABRE) RNA, ALTERNATIVE TRANSCRIPT H63934
1248	GF201:96(92B7):384(12C14)	SMALL INDUCIBLE CYTOKINE SUBFAMILY D (CYS-X3-CYS), MEMBER 1 (FRACTALKINE, NEUROTACTIN) R66139

Table 1

1249	GF201:96(92C8):384(12E16)	HUMAN DNA SEQUENCE FROM PAC 196E23 ON CHROMOSOME XQ26.1-27.2. CONTAINS THE TAT-SF1 (HIV-1 TRANSCRIPTIONAL ELONGATION FACTOR TAT COFACTOR TAT-SF1) GENE, THE BRS3 (BOMBESIN RECEPTOR SUBTYPE-3 (UTERINE BOMBESIN RECEPTOR, BRS-3) GEN AA700322
1250	GF201:96(92B2):384(12C4)	HUMAN DNA-BINDING PROTEIN ABP/ZF MRNA, COMPLETE CDS W88571
1251	GF201:96(95B1):384(13C1)	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, TYPE I, BETA R39069
1252	GF201:96(94H9):384(12P17)	51406 H18950
1253	GF201:96(55E8):384(21I15)	503051 AA149250
1254	GF201:96(58C8):384(21F15)	FATTY ACID BINDING PROTEIN 7, BRAIN N46862
1255	GF201:96(92H10):384(12O20)	FATTY ACID BINDING PROTEIN 7, BRAIN W72051
1256	GF201:96(99D9):384(14G17)	MACROPHAGE RECEPTOR WITH COLLAGENOUS STRUCTURE AA485867
1257	GF200:96(22G5):384(6M10)	HOMO SAPIENS MRNA FOR CALPAIN-LIKE PROTEASE CANPX AA457330
1258	GF201:96(79C4):384(9E7)	298662 N74313
1259	GF202:96(112C12):384(15F23)	FORKHEAD (DROSOPHILA)-LIKE 7 N22552
1260	GF201:96(82G11):384(9N21)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA459296
1261	GF200:96(19D3):384(5H6)	MEGAKARYOCYTE POTENTIATING FACTOR AA488406
1262	GF200:96(18G9):384(5M18)	PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA AA598817
1263	GF200:96(7F7):384(2L14)	EYES ABSENT (DROSOPHILA) HOMOLOG 2 AA402207
1264	GF201:96(55B7):384(21C13)	SYNAPTOGYRIN 1 AA007632
1265	GF200:96(2H9):384(1O18)	PHOSPHOLIPASE C, BETA 4 H22563
1266	GF200:96(4F3):384(1L5)	TRANSCRIPTION FACTOR AP-2 GAMMA (ACTIVATING ENHANCER-BINDING PROTEIN 2 GAMMA) AA399334
1267	GF201:96(88C6):384(11E12)	KERATIN 4 AA629189
1268	GF201:96(66E1):384(23I1)	BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) AA029597
1269	GF201:96(97B5):384(13D10)	BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1) W73473
1270	GF201:96(66H1):384(23P1)	KIAA0626 GENE PRODUCT N62737
1271	GF200:96(26E2):384(7I4)	HUMAN MRNA FOR KIAA0338 GENE, PARTIAL CDS R71689
1272	GF201:96(96F8):384(13K16)	CERULOPLASMIN (FERROXIDASE) H86554
1273	GF200:96(11A1):384(3B2)	HEPATIC LEUKEMIA FACTOR W00959
1274	GF201:96(98A9):384(13B17)	ESTS, WEAKLY SIMILAR TO VERY-LONG-CHAIN ACYL-COA SYNTHETASE [M.MUSCULUS] AA412064
1275	GF200:96(15F5):384(4L10)	SYNDECAN 2 (HEPARAN SULFATE PROTEOGLYCAN 1, CELL SURFACE-ASSOCIATED, FIBROGLYCAN) H64346
1276	GF201:96(79G7):384(9M13)	307050 N89673
1277	GF201:96(55F8):384(21K15)	CELLULAR RETINOIC ACID-BINDING PROTEIN 1 AA454702
1278	GF201:96(96F11):384(13K22)	CELLULAR RETINOIC ACID-BINDING PROTEIN 1 AA421218
1279	GF200:96(16G12):384(4N23)	PHOSPHODIESTERASE 4B, CAMP-SPECIFIC (DUNCE (DROSOPHILA)-HOMOLOG PHOSPHODIESTERASE E4) AA453293
1280	GF201:96(89G6):384(11N12)	S100 CALCIUM-BINDING PROTEIN A1 AA425934
1281	GF201:96(65C5):384(23F10)	SIGNAL TRANSDUCTION PROTEIN (SH3 CONTAINING) AA460282
1282	GF201:96(65B5):384(23D10)	134690 R28267

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Table 1

1283	PEROU:96(9E12):384(18J24)	ERYTHROCYTE MEMBRANE PROTEIN BAND 7.2 (STOMATIN) AI224884
1284	GF201:96(67C11):384(24E21)	782669 AA447583
1285	GF201:96(83C9):384(10E17)	416107 W85998
1286	GF201:96(95E4):384(13I7)	DEATH-ASSOCIATED PROTEIN KINASE 1 AA025275
1287	GF202:96(115A9):384(16B18)	773375 AA425723
1288	GF200:96(19C2):384(5F4)	ESTS, HIGHLY SIMILAR TO POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L3 [H.SAPIENS] AA481026
1289	GF201:96(84E10):384(10J20)	416676 W86504
1290	PEROU:96(6F10):384(20K20)	485760 AA039943
1291	PEROU:96(6D3):384(20G6)	290361 N64505
1292	GF201:96(93B4):384(12D8)	GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3 AA663910
1293	GF201:96(56F12):384(21K24)	ESTS, MODERATELY SIMILAR TO LASP-1 PROTEIN [H.SAPIENS] AA458882
1294	GF201:96(61A12):384(22B24)	795367 AA453271
1295	GF201:96(67D1):384(24G1)	268157 N30152
1296	GF200:96(25G4):384(7M7)	CYSTATIN B (STEFIN B) H22919
1297	GF201:96(101H4):384(14P8)	SUPEROXIDE DISMUTASE 2, MITOCHONDRIAL T61649
1298	GF201:96(86E10):384(10J19)	SUPEROXIDE DISMUTASE 2, MITOCHONDRIAL AA488084
1299	GF201:96(59E10):384(22I19)	309803 N94612
1300	GF200:96(14B8):384(4C16)	CHITINASE 3-LIKE 1 (CARTILAGE GLYCOPROTEIN-39) AA434115
1301	GF201:96(93B6):384(12D12)	EPHB6 AA609284
1302	GF201:96(96F6):384(13K12)	CHITINASE 3-LIKE 2 AA668821
1303	PEROU:96(7C4):384(20F8)	263815 N28486
1304	GF200:96(16D3):384(4H5)	H.SAPIENS MRNA FOR AN ACUTE MYELOID LEUKAEMIA PROTEIN (3917BP) AA425238
1305	GF200:96(14C6):384(4E12)	BILIARY GLYCOPROTEIN AA411757
1306	GF200:96(9A7):384(3A13)	APOPTOSIS INHIBITOR 2 H48706
1307	GF200:96(24F4):384(6L7)	FIBROBLAST GROWTH FACTOR RECEPTOR 2 (BACTERIA-EXPRESSED KINASE, KERATINOCYTE GROWTH FACTOR RECEPTOR, CRANIOFACIAL DYSOSTOSIS 1, CROUZON SYNDROME, PFEIFFER SYNDROME, JACKSON-WEISS SYNDROME) AA443093
1308	GF200:96(12G5):384(3N9)	FIBROBLAST GROWTH FACTOR RECEPTOR 2 (BACTERIA-EXPRESSED KINASE, KERATINOCYTE GROWTH FACTOR RECEPTOR, CRANIOFACIAL DYSOSTOSIS 1, CROUZON SYNDROME, PFEIFFER SYNDROME, JACKSON-WEISS SYNDROME) AA456160
1309	GF200:96(10B2):384(3C4)	IMMUNOGLOBULIN SUPERFAMILY CONTAINING LEUCINE-RICH REPEAT H62387
1310	GF202:96(116B10):384(16D19)	ESTS, WEAKLY SIMILAR TO KIAA0631 PROTEIN [H.SAPIENS] AA497001
1311	PEROU:96(4D3):384(19H5)	CYTOCHROME P450, SUBFAMILY I (DIOXIN-INDUCIBLE), POLYPEPTIDE 1 (GLAUCOMA 3, PRIMARY INFANTILE) AA029776
1312	GF200:96(25C2):384(7E3)	CYTOCHROME P450, SUBFAMILY I (DIOXIN-INDUCIBLE), POLYPEPTIDE 1 (GLAUCOMA 3, PRIMARY INFANTILE) AA448157
1313	GF201:96(83A9):384(10A17)	306420 N92699
1314	GF200:96(4E5):384(1J9)	POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 1 (TWIK-1) N62620

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1315	GF201:96(83H3):384(10O5)	KYNURENINE 3-MONOOXYGENASE (KYNURENINE 3-HYDROXYLASE) AA152183
1316	GF201:96(58F9):384(21L17)	UNTITLED R16098
1317	GF201:96(86H1):384(10P1)	S100 CALCIUM-BINDING PROTEIN A8 (CALGRANULIN A) AA086471
1318	GF201:96(86G1):384(10N1)	ESTS, HIGHLY SIMILAR TO STAT4 [M.MUSCULUS] R91570
1319	GF201:96(87F3):384(11K5)	OROSOMUCOID 1 AA700876
1320	GF201:96(95C5):384(13E9)	ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE AA676836
1321	GF201:96(91E7):384(12I13)	TOLL-LIKE RECEPTOR 2 T57791
1322	GF200:96(5B4):384(2C7)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, K R79082
1323	GF201:96(90B8):384(11D15)	KIAA0173 GENE PRODUCT AA682815
1324	GF201:96(87G1):384(11M1)	TRANSMEMBRANE GLYCOPROTEIN AA425450
1325	GF201:96(101B9):384(14D18)	77193 T50121
1326	GF200:96(30G3):384(8M6)	122982 R00332
1327	GF201:96(56C8):384(21E16)	268960 N24645
1328	GF200:96(12E7):384(3I13)	HUMAN GLUCOSE TRANSPORTER-LIKE PROTEIN-III (GLUT3), COMPLETE CDS AA406551
1329	GF200:96(24G12):384(6N23)	ETS VARIANT GENE 5 (ETS-RELATED MOLECULE) AA463830
1330	GF200:96(24G1):384(6N1)	HUMAN CLONE 23933 MRNA SEQUENCE H56918
1331	GF201:96(97E2):384(13I4)	ALDEHYDE DEHYDROGENASE 7 N93686
1332	GF201:96(96D1):384(13G2)	CYTOCHROME P450, SUBFAMILY XXVIIA (STEROID 27-HYDROXYLASE, CEREBROTENDINOUS XANTHOMATOSIS), POLYPEPTIDE 1 N66957
1333	GF201:96(66C11):384(23F21)	343400 W67199
1334	GF200:96(4C9):384(1F17)	GUANYLATE BINDING PROTEIN 2, INTERFERON-INDUCIBLE W77927
1335	PEROU:96(8B6):384(20D11)	TUMOR PROTEIN P53 (LI-FRAUMENI SYNDROME) H62385
1336	PEROU:96(10E10):384(18J19)	P53-ALU U94788
1337	GF201:96(80F3):384(9K6)	321488 W32509
1338	GF200:96(5D6):384(2G11)	LIVER X RECEPTOR, ALPHA H61935
1339	GF202:96(116E9):384(16I17)	ESTS, MODERATELY SIMILAR TO (DEFLINE NOT AVAILABLE 4105275) [H.SAPIENS] T60160
1340	GF201:96(102H8):384(14P15)	46180 H09105
1341	GF201:96(88B5):384(11C10)	MALIC ENZYME 1, SOLUBLE AA669689
1342	GF200:96(24D1):384(6H1)	GLUTATHIONE S-TRANSFERASE A2 T73468
1343	GF200:96(28B5):384(7D9)	EST, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] W47077
1344	GF202:96(112B10):384(15D19)	510736 AA099748
1345	GF200:96(14D10):384(4G20)	ARACHIDONATE 5-LIPOXYGENASE H51574
1346	GF200:96(32G3):384(8N5)	ESTS, HIGHLY SIMILAR TO AQUAPORIN 3 [H.SAPIENS] R91904
1347	GF201:96(99B8):384(14C15)	PARAOXONASE 3 T57069
1348	GF200:96(26G9):384(7M18)	PARAOXONASE 3 R95740
1349	GF202:96(109A3):384(15A5)	UDP GLYCOSYLTRANSFERASE 2 FAMILY, POLYPEPTIDE B4 N53031
1350	GF201:96(95G5):384(13M9)	GAP JUNCTION PROTEIN, BETA 1, 32KD (CONNEXIN 32, CHARCOT-MARIE-TOOTH NEUROPATHY, X-LINKED) N62394
1351	GF200:96(3D6):384(1H12)	DIAPHORASE (NADH/NADPH) (CYTOCHROME B-5 REDUCTASE) AA455538

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1352	GF200:96(13D4):384(4G7)	CYTOCHROME B-5 R92281
1353	GF201:96(81B5):384(9D10)	268258 N30006
1354	GF201:96(66H8):384(23P15)	504678 AA142942
1355	GF201:96(81D9):384(9H18)	HOMO SAPIENS MRNA; CDNA DKFZP564J142 (FROM CLONE DKFZP564J142) N75017
1356	PEROU:96(9F3):384(18L6)	299664 N75017
1357	GF201:96(91H4):384(12O7)	KYNURENINASE; L-KYNURENINE HYDROLASE H87471
1358	GF200:96(18B9):384(5C18)	TRYPTOPHAN 2,3-DIOXYGENASE T72422
1359	GF201:96(66H6):384(23P11)	810901 AA459293
1360	GF201:96(96E2):384(13I4)	ZA {REGION BETWEEN EXONS 35 AND 36 OF THE COMPLEMENT COMPONENT C4 GE} [HUMAN, FETAL ADRENAL GLAND, MRNA, 830 NT] AA664406
1361	GF201:96(91E8):384(12I15)	TRANSFORMING GROWTH FACTOR BETA-STIMULATED PROTEIN TSC-22 AA664389
1362	GF200:96(14H3):384(4O6)	ACTIVATED LEUCOCYTE CELL ADHESION MOLECULE R13558
1363	PEROU:96(7D3):384(20H6)	2338271 AI912047
1364	PEROU:96(7D4):384(20H8)	1944078 AI201945
1365	GF200:96(4B7):384(1D13)	ESTS, HIGHLY SIMILAR TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR [H.SAPIENS] H79047
1366	GF200:96(29A2):384(8A3)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] W20275
1367	GF201:96(80D11):384(9G22)	809503 AA454562
1368	GF201:96(87E10):384(11I19)	SILVER (MOUSE HOMOLOG) LIKE N67770
1369	GF200:96(7G1):384(2N2)	DYSTROBREVIN, ALPHA H09172
1370	GF201:96(92C12):384(12E24)	MYELOID/LYMPHOID OR MIXED-LINEAGE LEUKEMIA (TRITHORAX (DROSOPHILA) HOMOLOG); TRANSLOCATED TO, 4 N26539
1371	GF201:96(85B6):384(10D12)	359597 AA010818
1372	GF201:96(59A12):384(22A23)	364555 AA022601
1373	GF201:96(99H10):384(14O19)	47428 H11088
1374	GF201:96(83E6):384(10I11)	503602 AA131299
1375	GF202:96(112A1):384(15B1)	261194 H98215
1376	GF202:96(115G7):384(16N14)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] AA156821
1377	GF201:96(81G1):384(9N2)	282868 N50152
1378	GF201:96(97D8):384(13H16)	ANKYRIN 3, NODE OF RANVIER (ANKYRIN G) AA677185
1379	PEROU:96(8D3):384(20H5)	364209 AA021558
1380	GF200:96(8D1):384(2H1)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] H59915
1381	GF201:96(101G12):384(14N24)	81316 T60061
1382	GF201:96(89F3):384(11L6)	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), SHORT BASIC DOMAIN, SECRETED, (SEMAPHORIN) 3C AA042990
1383	GF200:96(4E1):384(1J1)	ENDOTHELIAL KRUPPEL-LIKE ZINC FINGER PROTEIN H45711
1384	GF201:96(90G4):384(11N7)	ESTS, MODERATELY SIMILAR TO (DEFLINE NOT AVAILABLE 4159884) [H.SAPIENS] AA001222
1385	GF200:96(26E12):384(7I24)	DESMOCOLLIN 2 AA074677
1386	GF201:96(69E2):384(24J4)	321902 W37448

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1387	GF201:96(79D8):384(9G15)	KERATIN 13 W60057
1388	GF200:96(4A3):384(1B5)	KERATIN 13 W23757
1389	GF201:96(65B11):384(23D22)	134011 R31262
1390	GF200:96(19A4):384(5B8)	49630 H29256
1391	GF200:96(15A9):384(4B18)	VITAMIN D (1,25- DIHYDROXYVITAMIN D3) RECEPTOR AA485226
1392	GF201:96(86E8):384(10J15)	SYNDECAN 1 AA074511
1393	GF201:96(80D12):384(9G24)	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), SHORT BASIC DOMAIN, SECRETED, (SEMAPHORIN) 3F AA454570
1394	GF200:96(16D9):384(4H17)	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, F AA598513
1395	GF200:96(12A10):384(3B19)	BUTYRATE RESPONSE FACTOR 1 (EGF-RESPONSE FACTOR 1) AA424743
1396	GF200:96(3F12):384(1L24)	ANTHRACYCLINE RESISTANCE-ASSOCIATED AA495766
1397	GF200:96(3E12):384(1I24)	MEMBRANE COMPONENT, CHROMOSOME 1, SURFACE MARKER 1 (40KD GLYCOPROTEIN, IDENTIFIED BY MONOCLONAL ANTIBODY GA733) AA454810
1398	GF200:96(19B4):384(5D8)	KERATIN 7 AA489569
1399	GF200:96(24B10):384(6D19)	813520 AA455591
1400	GF201:96(101C9):384(14F18)	HOMO SAPIENS MRNA; CDNA DKFZP586B2022 (FROM CLONE DKFZP586B2022) T52325
1401	GF202:96(115A1):384(16B2)	HOMO SAPIENS AGRIN PRECURSOR MRNA, PARTIAL CDS AA458878
1402	GF202:96(112E8):384(15J15)	ESTS, WEAKLY SIMILAR TO KIAA0319 [H.SAPIENS] AA101299
1403	GF200:96(14E5):384(4I10)	ANTIQUITIN 1 AA101299
1404	GF200:96(26H9):384(7O18)	HEXOKINASE 1 AA485272
1405	GF200:96(23B12):384(6D24)	HEXOKINASE 1 AA485271
1406	GF201:96(90F1):384(11L1)	LADININ 1 T97710
1407	GF200:96(26B1):384(7C2)	H.SAPIENS MRNA FOR RECEPTOR TYROSINE KINASE EPH (PARTIAL) N90246
1408	GF200:96(12A11):384(3B21)	144834 R77251
1409	GF200:96(19B1):384(5D2)	CREATINE KINASE, MITOCHONDRIAL 1 (UBIQUITOUS) AA019482
1410	PEROU:96(7B6):384(20D12)	364302 AA022462
1411	PEROU:96(7B4):384(20D8)	176461 H43515
1412	PEROU:96(10A7):384(18B13)	RECEPTOR PROTEIN-TYROSINE KINASE EDDR1 H41900
1413	GF201:96(64C8):384(23E16)	HOMO SAPIENS MRNA FOR INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE ISOENZYME, PARTIAL CDS N46828
1414	GF201:96(92G5):384(12M10)	PLEXIN 5 AA496565
1415	GF200:96(1H6):384(1O11)	810873 AA459197
1416	GF201:96(61A4):384(22B8)	504225 AA131934
1417	GF201:96(89H12):384(11P24)	SNF2-RELATED CBP ACTIVATOR PROTEIN AA419088
1418	GF200:96(11G1):384(3N2)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] H97778
1419	GF201:96(82H3):384(9P5)	ESTS, WEAKLY SIMILAR TO KIAA0281 [H.SAPIENS] N54395
1420	GF201:96(102D2):384(14H3)	85804 T72068
1421	GF200:96(17H1):384(5O1)	JUNCTION PLAKOGLOBIN R06417
1422	GF201:96(92B9):384(12C18)	CDP-DIACYLGLYCEROL SYNTHASE (PHOSPHATIDATE CYTIDYLYLTRANSFERASE) 1 R31562

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Table 1

1423	GF201:96(92F3):384(12K6)	PROLINE-RICH GLA (G-CARBOXYGLUTAMIC ACID) POLYPEPTIDE 2 AA430552
1424	GF201:96(56A6):384(21A12)	HUMAN DNA SEQUENCE FROM PAC 127B20 ON CHROMOSOME 22Q11.2-QTER, CONTAINS GENE FOR GTPASE-ACTIVATING PROTEIN SIMILAR TO RHOGAP PROTEIN. RIBOSOMAL PROTEIN L6 PSEUDOGENE, ESTS AND CA REPEAT AA037410
1425	GF200:96(21F9):384(6K17)	ESTS, WEAKLY SIMILAR TO LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR [H.SAPIENS] AA489246
1426	PEROU:96(9D8):384(18H16)	416386 W86859
1427	PEROU:96(10C10):384(18F19)	PLACENTAL BIKUNIN (KUNITZ-TYPE SERINE PROTEASE INHIBITOR) AA031287
1428	GF200:96(21G6):384(6M11)	SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2 AA459039
1429	PEROU:96(9E1):384(18J2)	HUMAN PLACENTAL BIKUNIN MRNA COMPLETE CDS AA031287
1430	GF201:96(67D3):384(24G5)	810728 AA457707
1431	GF200:96(30H5):384(8O10)	HOMO SAPIENS MRNA; CDNA DKFZP586F1318 (FROM CLONE DKFZP586F1318) T77847
1432	PEROU:96(9A6):384(18B12)	147447 R81173
1433	GF201:96(82D9):384(9H17)	365517 AA009593
1434	GF201:96(66C9):384(23F17)	HOMO SAPIENS MRNA; CDNA DKFZP586F1223 (FROM CLONE DKFZP586F1223) N59219
1435	PEROU:96(9B9):384(18D18)	281745 N51744
1436	GF201:96(97A9):384(13B18)	CALPAIN, LARGE POLYPEPTIDE L1 H15456
1437	GF201:96(97G1):384(13N2)	GLUCOSIDASE, ALPHA; ACID (POMPE DISEASE, GLYCOGEN STORAGE DISEASE TYPE II) AA44009
1438	GF200:96(31G9):384(8N18)	ESTS, HIGHLY SIMILAR TO HYPOTHETICAL PROTEIN B, 6.8K [H.SAPIENS] R63543
1439	GF201:96(57C10):384(21F20)	PUTATIVE PROSTATE CANCER TUMOR SUPPRESSOR H13424
1440	GF201:96(100A2):384(14A4)	HOMO SAPIENS MRNA; CDNA DKFZP564P0622 (FROM CLONE DKFZP564P0622) H15385
1441	GF200:96(18E6):384(5I12)	SIALYLTRANSFERASE AA497051
1442	GF200:96(4G10):384(1N19)	SIALYLTRANSFERASE AA497051
1443	GF200:96(6D8):384(2G16)	EGF-LIKE-DOMAIN, MULTIPLE 2 H39187
1444	GF201:96(79B12):384(9C23)	284355 N52136
1445	GF201:96(90F4):384(11L7)	IROQUOIS-CLASS HOMEODOMAIN PROTEIN R46202
1446	PEROU:96(5D7):384(20G13)	BHD-2
1447	PEROU:96(8A9):384(20B17)	ESTS, HIGHLY SIMILAR TO IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 [H.SAPIENS] R55185
1448	PEROU:96(9A7):384(18B14)	154654 R55184
1449	GF200:96(31C8):384(8F16)	137387 R38133
1450	GF202:96(114A4):384(16A8)	ESTS, MODERATELY SIMILAR TO MYSOIN HEAVY CHAIN 12 [H.SAPIENS] AA401349
1451	GF201:96(95A7):384(13A13)	148225 H13688
1452	GF200:96(26G6):384(7M12)	SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 1 H58873
1453	GF201:96(88F4):384(11K8)	SOLUTE CARRIER FAMILY 7 (CATIONIC AMINO ACID TRANSPORTER, Y+ SYSTEM), MEMBER 5 AA419177
1454	GF201:96(97D6):384(13H12)	HOMO SAPIENS CLONE 24551 MRNA SEQUENCE AA630794
1455	GF200:96(32A5):384(8B9)	DISCS, LARGE (DROSOPHILA) HOMOLOG 5 T77840
1456	GF200:96(16D7):384(4H13)	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE) AA173453
1457	GF200:96(5H8):384(2O15)	S100 CALCIUM-BINDING PROTEIN A11 (CALGIZZARIN) AA464731

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Table 1

1458	PEROU:96(9C2):384(18F4)	306136 N91023
1459	GF201:96(57B10):384(21D20)	MEMBRANE PROTEIN, PALMITOYLATED 3 (MAGUK P55 SUBFAMILY MEMBER 3) W44685
1460	GF200:96(19B3):384(5D6)	A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 15 (METARGIDIN) AA292676
1461	GF200:96(12E4):384(3J7)	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1 AA499936
1462	GF201:96(94A5):384(12B9)	KIAA0429 GENE PRODUCT AA676805
1463	PEROU:96(7C11):384(20F22)	KARYOPHERIN ALPHA 4 (IMPORTIN ALPHA 3) AI378946
1464	GF201:96(79C1):384(9E1)	277134 N40917
1465	GF201:96(60A12):384(22A24)	795832 AA461497
1466	GF201:96(86B6):384(10D11)	VASOACTIVE INTESTINAL PEPTIDE RECEPTOR 1 H73241
1467	GF201:96(89G7):384(11N14)	INTER-ALPHA (GLOBULIN) INHIBITOR H4 (PLASMA KALLIKREIN-SENSITIVE GLYCOPROTEIN) N73625
1468	PEROU:96(2D8):384(19G16)	SYNUCLEIN, GAMMA (BREAST CANCER-SPECIFIC PROTEIN 1) AA293803
1469	GF201:96(91D3):384(12G5)	ADIPOSE SPECIFIC 2 AA478298
1470	GF201:96(87H2):384(11O3)	MONOAMINE OXIDASE A AA011096
1471	GF202:96(109G3):384(15M5)	HOMO SAPIENS CLONE 23698 MRNA SEQUENCE AA680300
1472	GF200:96(12C7):384(3F13)	GLUTATHIONE S-TRANSFERASE THETA 2 AA490777
1473	GF201:96(89G11):384(11N22)	MYOSIN VI AA625890
1474	GF200:96(29E4):384(8I7)	470216 AA028987
1475	GF202:96(110B3):384(15C6)	S100 CALCIUM-BINDING PROTEIN A13 AA070489
1476	GF200:96(12A2):384(3B3)	LUTHERAN BLOOD GROUP (AUBERGER B ANTIGEN INCLUDED) H24954
1477	GF200:96(25C5):384(7E9)	CYCLIN D1 (PRAD1: PARATHYROID ADENOMATOSIS 1) AA487700
1478	GF200:96(25D3):384(7G5)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] AA598478
1479	GF200:96(25C3):384(7E5)	CYSTATIN C (AMYLOID ANGIOPATHY AND CEREBRAL HEMORRHAGE) AA599177
1480	GF201:96(82F1):384(9L1)	487831 AA045083
1481	GF201:96(94H3):384(12P5)	H.SAPIENS MRNA FOR MYOSIN-I BETA AA485871
1482	PEROU:96(8B11):384(20D21)	INTEGRIN, BETA 5 N29501
1483	GF201:96(65D7):384(23H14)	782547 AA431796
1484	GF200:96(28F5):384(7L9)	HOMO SAPIENS MRNA; CDNA DKFZP564E1616 (FROM CLONE DKFZP564E1616) H26176
1485	GF201:96(96A8):384(13A16)	ENDOTHELIN 1 H11003
1486	GF201:96(58G10):384(21N19)	SERUM-INDUCIBLE KINASE AA460152
1487	GF201:96(64F12):384(23K24)	795378 AA453495
1488	GF201:96(64F4):384(23K8)	138130 R53797
1489	GF201:96(97B1):384(13D2)	WASP FAMILY VERPROLIN-HOMOLOGOUS PROTEIN 3 AA629542
1490	GF200:96(23D5):384(6H10)	5-HYDROXYTRYPTAMINE (SEROTONIN) RECEPTOR 2A R55130
1491	GF200:96(14A8):384(4A16)	CD9 ANTIGEN (P24) AA412053
1492	GF200:96(8H11):384(2P21)	PROTEIN KINASE MITOGEN-ACTIVATED 10 (MAP KINASE) T75436
1493	GF201:96(88E6):384(11I12)	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 3 AA701976
1494	GF201:96(58H10):384(21P19)	809824 AA455519
1495	PEROU:96(6G5):384(20M10)	510165 AA053251

Table 1

1496	GF200:96(1H7):384(1O13)	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), ISOFORM 1 (ANTIPORTER, NA+/H+, AMILORIDE SENSITIVE) AA455369
1497	GF200:96(7H9):384(2P18)	HUMAN CLONE 23815 MRNA SEQUENCE AA424516
1498	GF200:96(22F9):384(6K18)	FILAMIN B, BETA (ACTIN-BINDING PROTEIN-278) AA486238
1499	GF200:96(27C3):384(7F6)	ESTS, WEAKLY SIMILAR TO OXYSTEROL-BINDING PROTEIN [H.SAPIENS] R31395
1500	GF200:96(25F1):384(7K1)	CATHEPSIN H AA487346
1501	GF202:96(110G8):384(15M16)	HOMO SAPIENS CHROMOSOME 16 BAC CLONE CIT987SK-A-575C2 T64469
1502	GF201:96(68D5):384(24G10)	415229 W91879
1503	GF201:96(95E10):384(13I19)	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA 15 (GQ CLASS) T99303
1504	GF201:96(83A5):384(10A9)	141726 R69584
1505	PEROU:96(63D8):384(19H16)	MATRIX GLA PROTEIN AA081250
1506	GF201:96(87H12):384(11O23)	MATRIX GLA PROTEIN AA155913
1507	GF201:96(93D9):384(12H18)	CREATINE TRANSPORTER [HUMAN, BRAINSTEM/SPINAL CORD, MRNA, 2283 NT] AA292226
1508	GF200:96(13F10):384(4K19)	CLUSTERIN (COMPLEMENT LYSIS INHIBITOR, SP-40,40, SULFATED GLYCOPROTEIN 2, TESTOSTERONE-REPRESSED PROSTATE MESSAGE 2, APOLIPOPROTEIN J) AA130017
1509	GF201:96(57H10):384(21P20)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4106368) [D.MELANOGASTER] AA454554
1510	GF201:96(102A11):384(14B21)	79576 T62849
1511	GF202:96(112G6):384(15N11)	ESTS, HIGHLY SIMILAR TO UNKNOWN [H.SAPIENS] AA046023
1512	GF201:96(92E11):384(12I22)	PROTEIN PHOSPHATASE 1D MAGNESIUM-DEPENDENT, DELTA ISOFORM.N33955
1513	GF201:96(56G1):384(21M2)	AMYLOID BETA PRECURSOR PROTEIN (CYTOPLASMIC TAIL)-BINDING PROTEIN 2 AA431206
1514	GF201:96(102B5):384(14D9)	RAD51 (S. CEREVISIAE) HOMOLOG C T64150
1515	GF200:96(28E10):384(7J19)	ESTS, WEAKLY SIMILAR TO HSP 27 [H.SAPIENS] H57494
1516	PEROU:96(10B11):384(18D21)	ESTS WEAKLY SIMILAR TO HEAT SHOCK 27 KD PROTEIN [H.SAPIENS] AA010110
1517	GF201:96(88A7):384(11A14)	MYOGLOBIN AA176581
1518	PEROU:96(6D12):384(20G24)	325165 W49759
1519	GF201:96(61B7):384(22D14)	283634 N52878
1520	GF202:96(114E5):384(16I10)	509462 AA056377
1521	GF201:96(99F11):384(14K21)	47264 H10713
1522	GF201:96(98A3):384(13B5)	UNCOUPLING PROTEIN 2 (MITOCHONDRIAL, PROTON CARRIER) H61243
1523	GF201:96(102D5):384(14H9)	84419 T73780
1524	GF201:96(64D5):384(23G10)	488431 AA047441
1525	GF201:96(93E11):384(12I22)	79935 T61475
1526	GF200:96(4C1):384(1F1)	INHIBITOR OF DNA BINDING 2, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN H82706
1527	PEROU:96(2G10):384(19M20)	TREFOIL FACTOR 1 (BREAST CANCER, ESTROGEN-INDUCIBLE SEQUENCE EXPRESSED IN) R83818
1528	GF200:96(17B11):384(5C21)	33045 R19478
1529	GF201:96(61B10):384(22D20)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] R05293
1530	GF202:96(115E9):384(16I18)	ATPASE, H+ TRANSPORTING, LYSOSOMAL (VACUOLAR PROTON PUMP), MEMBER J AA608567
1531	GF202:96(109D6):384(15G11)	CALCIUM CHANNEL, VOLTAGE-DEPENDENT, BETA 3 SUBUNIT R36947
1532	GF201:96(80A6):384(9A12)	809789 AA454756

Table 1

1533	GF201:96(97G3):384(13N6)	H.SAPIENS MRNA FOR TYROSINE KINASE RECEPTOR H15718
1534	GF202:96(111C4):384(15F8)	730439 AA469975
1535	GF201:96(95B2):384(13C3)	49351 H15445
1536	GF202:96(114A6):384(16A12)	ESTS, WEAKLY SIMILAR TO MEMBRANE GLYCOPROTEIN [M.MUSCULUS] AA159578
1537	GF201:96(99G1):384(14M1)	81449 T63490
1538	GF201:96(101C12):384(14F24)	71863 T52564
1539	GF201:96(101B12):384(14D24)	71863 T51290
1540	GF201:96(101B11):384(14D22)	71863 T51229
1541	GF201:96(61A3):384(22B6)	417081 W87826
1542	GF201:96(68E2):384(24I4)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4929751) [H.SAPIENS] AA004846
1543	GF201:96(64D4):384(23G8)	HOMO SAPIENS MRNA; CDNA DKFZP58612118 (FROM CLONE DKFZP58612118) R98407
1544	PEROU:96(8C4):384(20F7)	297604 N69835
1545	PEROU:96(9C1):384(18F2)	297604 N69835
1546	GF201:96(87E9):384(11I17)	DNA SEGMENT, SINGLE COPY PROBE LNS-CAI/LNS-CAII (DELETED IN POLYPOSIS H99681
1547	PEROU:96(3D1):384(19H2)	ESTROGEN RECEPTOR 1 AA164586
1548	GF201:96(62F10):384(22L19)	275798 R93185
1549	GF200:96(22E5):384(6I10)	TUMOR PROTEIN D52 AA459318
1550	GF200:96(9D4):384(3G7)	HUMAN D9 SPLICE VARIANT B MRNA, COMPLETE CDS AA453832
1551	PEROU:96(10E1):384(18J1)	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA733-2 PRECURSOR AA055808
1552	GF201:96(89H5):384(11P10)	KIAA0351 GENE PRODUCT AA402863
1553	GF201:96(91F7):384(12K13)	RAB2, MEMBER RAS ONCOGENE FAMILY-LIKE AA401972
1554	PEROU:96(8C5):384(20F9)	NEBULETTE N77806
1555	GF200:96(27B8):384(7D16)	ESTS, WEAKLY SIMILAR TO UNKNOWN [H.SAPIENS] R01499
1556	PEROU:96(8F1):384(20L1)	486828 AA042878
1557	PEROU:96(9E6):384(18J12)	486828 AA042878
1558	PEROU:96(10A2):384(18B3)	XMP T84249
1559	GF201:96(91E4):384(12I7)	EPITHELIAL MEMBRANE PROTEIN 2 T88721
1560	GF200:96(17G6):384(5M11)	KERATIN 8 AA598517
1561	GF202:96(160G7):384(17N13)	44292 H06273
1562	PEROU:96(3B1):384(19D2)	KERATIN 18 AA070385
1563	GF201:96(88C7):384(11E14)	KERATIN 18 AA664179
1564	GF201:96(93D3):384(12H6)	CLAUDIN 4 AA430665
1565	PEROU:96(9E9):384(18J18)	HCPE-R MRNA FOR CPE-RECEPTOR AA506754
1566	PEROU:96(9C7):384(18F14)	HCPE-R MRNA FOR CPE-RECEPTOR W74492
1567	GF200:96(10C10):384(3E20)	HOMO SAPIENS EPITHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1A (ESE-1) MRNA, COMPLETE CDS AA433851
1568	PEROU:96(10A5):384(18B9)	EPITHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1B (ESE-1) MRNA COMPLETE CDS H27938
1569	GF200:96(17G8):384(5M15)	SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1 AA464250
1570	GF200:96(15C11):384(4F22)	TRANSFORMING GROWTH FACTOR, BETA 3 AA040617

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1571	PEROU:96(9E5):384(18J10)	TRANSFORMING GROWTH FACTOR BETA 3 AA040616
1572	PEROU:96(10D5):384(18H9)	TRANSFORMING GROWTH FACTOR BETA 3 AA040616
1573	GF200:96(17F2):384(5K3)	LYSOSOMAL-ASSOCIATED MEMBRANE PROTEIN 1 H29077
1574	GF201:96(55A5):384(21A9)	ISLET CELL AUTOANTIGEN 1 (69KD) AA491302
1575	GF201:96(102A9):384(14B17)	ESTS, MODERATELY SIMILAR TO K02E10.2 [C.ELEGANS] T62552
1576	GF201:96(102B10):384(14D19	82869 T69270
1577	GF202:96(109D11):384(15G21	SELENIUM BINDING PROTEIN 1 T65736
1578	GF202:96(116D8):384(16H15)	HOMO SAPIENS MRNA FOR HYPOTHETICAL PROTEIN AA487488
1579	GF201:96(87B9):384(11C17)	PROLACTIN RECEPTOR R63647
1580	PEROU:96(8C7):384(20F13)	321658 W32933
1581	PEROU:96(9C3):384(18F6)	321658 W32933
1582	PEROU:96(8B3):384(20D5)	202658 H53479
1583	PEROU:96(9B3):384(18D6)	202658 H53479
1584	GF201:96(56H9):384(21O18)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] AA464739
1585	GF201:96(94D9):384(12H17)	197520 H52110
1586	PEROU:96(8E8):384(20I15)	KIAA0182 AA037466
1587	GF200:96(6G9):384(2M18)	HUMAN MRNA FOR KIAA0182 GENE, PARTIAL CDS H05563
1588	GF201:96(93D5):384(12H10)	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), ISOFORM 3 REGULATORY FACTOR 1 AA425299
1589	PEROU:96(8B2):384(20D3)	179211 H50224
1590	PEROU:96(9B2):384(18D4)	179211 H50224
1591	GF201:96(95H4):384(13O7)	FRUCTOSE-BISPHOSPHATASE 1 AA699427
1592	GF201:96(90H7):384(11P13)	HUMAN ENDOGENOUS RETROVIRUS ENVELOPE REGION MRNA (PL1) AA701655
1593	GF201:96(82C9):384(9F17)	X-BOX BINDING PROTEIN 1 W90128
1594	PEROU:96(7F6):384(20L12)	HEPATOCYTE NUCLEAR FACTOR 3, ALPHA T74639
1595	GF200:96(12E12):384(3J23)	GATA-BINDING PROTEIN 3 H72474
1596	PEROU:96(6A11):384(20A22)	GATA-BINDING PROTEIN 3 R31442
1597	PEROU:96(9A4):384(18B8)	GATA-BINDING PROTEIN 3 R31441
1598	GF200:96(12F12):384(3L23)	GATA-BINDING PROTEIN 3 AA058828
1599	PEROU:96(4D8):384(19H15)	ESTROGEN RECEPTOR 1 AA291702
1600	GF201:96(96A7):384(13A14)	ESTROGEN RECEPTOR 1 AA291749
1601	PEROU:96(8B8):384(20D15)	ANNEXIN XXXI N76688
1602	PEROU:96(9B5):384(18D10)	ANNEXIN XXXI N76688
1603	GF201:96(57B11):384(21D22)	HOMO SAPIENS MRNA; CDNA DKFZP434A091 (FROM CLONE DKFZP434A091) AA431988
1604	GF200:96(5E3):384(2I5)	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER C N80617
1605	GF200:96(6A3):384(2A6)	HOMO SAPIENS MRNA FOR NEUROBLASTOMA, COMPLETE CDS AA481950
1606	PEROU:96(10D1):384(18H1)	CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA036987
1607	GF200:96(25E7):384(7I13)	CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA598508
1608	PEROU:96(8E4):384(20J7)	CELLULAR RETINOIC ACID-BINDING PROTEIN 2 AA036986

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1609	GF201:96(88E10):384(11J20)	HUMAN SECRETORY PROTEIN (P1.B) MRNA, COMPLETE CDS N74131
1610	GF200:96(6A5):384(2A10)	MSH (DROSOPHILA) HOMEO BOX HOMOLOG 2 AA195636
1611	GF201:96(98C7):384(13F13)	HUMAN CHROMOSOME 16 BAC CLONE CIT987SK-254P9 H23265
1612	GF201:96(61F4):384(22L8)	204483 H58234
1613	GF201:96(88E3):384(11I6)	HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) MRNA T52830
1614	PEROU:96(9E8):384(18I16)	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) AA054451
1615	GF200:96(7D2):384(2H4)	HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 (IGFBP5) MRNA H08560
1616	GF201:96(90D2):384(11H3)	HUMAN MRNA FOR KIAA0061 GENE, PARTIAL CDS N33237
1617	GF201:96(90C2):384(11F3)	HUMAN MRNA FOR KIAA0143 GENE, PARTIAL CDS AA112057
1618	GF201:96(90E2):384(11J3)	CYSTEINE-RICH PROTEIN 2 AA485427
1619	PEROU:96(3A2):384(19B4)	PDGF BETA T49539
1620	GF200:96(16G1):384(4N1)	67654 T49539
1621	PEROU:96(6C7):384(20E14)	RAS HOMOLOG GENE FAMILY, MEMBER B H89046
1622	GF200:96(1F7):384(1K13)	RAS HOMOLOG GENE FAMILY, MEMBER B AA495846
1623	PEROU:96(8A4):384(20B7)	140018 R63971
1624	PEROU:96(9A5):384(18B10)	140018 R63971
1625	GF201:96(101A1):384(14B2)	81475 T63511
1626	GF201:96(96D4):384(13G8)	CYTOCHROME P450, SUBFAMILY IIJ (ARACHIDONIC ACID EPOXYGENASE) POLYPEPTIDE 2 H09076
1627	GF200:96(26H5):384(7O10)	P53-INDUCED PROTEIN H12189
1628	PEROU:96(10E9):384(18J17)	HOMO SAPIENS BREAST CANCER PUTATIVE TRANSCRIPTION FACTOR (ZABC1) MRNA, COMPLETE CDS AA460802
1629	PEROU:96(10E8):384(18J15)	HOMO SAPIENS BREAST CANCER PUTATIVE TRANSCRIPTION FACTOR (ZABC1) MRNA, COMPLETE CDS AA782528
1630	GF201:96(93C7):384(12F14)	SULFOTRANSFERASE FAMILY 2B, MEMBER 1 R73584
1631	PEROU:96(1F8):384(19K15)	HEREDITARY HEMOCHROMOTOSIS R07647
1632	GF200:96(17D7):384(5G13)	MUCIN 1, TRANSMEMBRANE AA488073
1633	PEROU:96(1G8):384(19M15)	156053 R72491
1634	GF201:96(94A4):384(12B7)	447786 AA702350
1635	GF201:96(62B2):384(22D3)	415317 W92160
1636	GF201:96(99A7):384(14A13)	IGG FC BINDING PROTEIN R52030
1637	GF200:96(24B11):384(6D21)	EPIDIDYMIS-SPECIFIC, WHEY-ACIDIC PROTEIN TYPE, FOUR-DISULFIDE CORE AA451904
1638	GF200:96(10A9):384(3A18)	SRC KINASE-ASSOCIATED PHOSPHOPROTEIN OF 55 KDA R01281
1639	GF200:96(28H2):384(7P3)	CARBONIC ANHYDRASE XI N52089
1640	GF201:96(87D4):384(11G7)	PHOSPHOFRUCTOKINASE, MUSCLE AA099169
1641	GF200:96(27C5):384(7F10)	HUMAN HEART MRNA FOR HEAT SHOCK PROTEIN 90, PARTIAL CDS AA064973
1642	GF200:96(26F1):384(7K2)	130843 R22306
1643	PEROU:96(8D12):384(20H23)	470105 AA029949
1644	GF201:96(8S5D6):384(10H12)	H2B HISTONE FAMILY, MEMBER Q AA010223
1645	GF200:96(7D9):384(2H18)	H2B HISTONE FAMILY, MEMBER Q AA456695

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1646	GF201:96(68E7):384(24114)	H2A HISTONE FAMILY, MEMBER L N50797
1647	GF200:96(11A12):384(3B24)	H1 HISTONE FAMILY, MEMBER 2 T66816
1648	GF201:96(68A3):384(24A6)	322461 W15305
1649	GF201:96(66B11):384(23D21)	289734 N62965
1650	GF201:96(91H2):384(12O3)	DUAL SPECIFICITY PHOSPHATASE 4 AA444049
1651	GF201:96(80G4):384(9M8)	CALCIUM CHANNEL, VOLTAGE-DEPENDENT, ALPHA 2/DELTA SUBUNIT 2 N53512
1652	GF200:96(14G9):384(4M18)	ACYL-COENZYME A DEHYDROGENASE, SHORT/BRANCHED CHAIN H96140
1653	PEROU:96(4B3):384(19D5)	CYTOCHROME P450, SUBFAMILY IIB (PHENOBARBITAL-INDUCIBLE), POLYPEPTIDE 6 H41908
1654	GF200:96(11C7):384(3F14)	PROTEASE INHIBITOR 12 (NEUROSERPIN) AA115876
1655	GF200:96(31C3):384(8F6)	HUMAN DNA SEQUENCE FROM CLONE 167A19 ON CHROMOSOME 1P32.1-33. CONTAINS THREE GENES FOR NOVEL PROTEINS, THE DIO1 GENE FOR TYPE 1 IODOTHYRONINE DEIODINASE (EC 3.8.1.4, TXD11, ITDI1) AND AN HNRNP A3 (HETEROGENOUS NUCLEAR RIBONUCLEOPR N74025
1656	GF200:96(14D5):384(4G10)	AUTOCRINE MOTILITY FACTOR RECEPTOR AA479243
1657	GF200:96(13D9):384(4G17)	CYTOCHROME P450, SUBFAMILY IIA (PHENOBARBITAL-INDUCIBLE), POLYPEPTIDE 7 T73031
1658	GF200:96(1F2):384(1K3)	ANGIOTENSIN RECEPTOR 1 H66116
1659	GF200:96(28H3):384(7P5)	ESTS, WEAKLY SIMILAR TO TUMOROUS IMAGINAL DISCS PROTEIN TID56 HOMOLOG [H.SAPIENS] T95268
1660	GF200:96(13B7):384(4C13)	QUINOID DIHYDROPTERIDINE REDUCTASE R38198
1661	GF201:96(90E9):384(11J17)	LYMPHOID NUCLEAR PROTEIN RELATED TO AF4 H99588
1662	GF201:96(94F3):384(12L5)	NUCLEOPORIN 88KD AA479888
1663	PEROU:96(6D8):384(20G16)	307220 N95180
1664	GF200:96(28D11):384(7H21)	HOMO SAPIENS MRNA; CDNA DKFZP564P0662 (FROM CLONE DKFZP564P0662) R27680
1665	GF200:96(26H10):384(7O20)	HEPSIN (TRANSMEMBRANE PROTEASE, SERINE 1) H62162
1666	GF200:96(29D11):384(8G21)	ESTS, HIGHLY SIMILAR TO TRANSCRIPTION ELONGATION FACTOR TFIIS.H [H.SAPIENS] R09980
1667	GF201:96(80E10):384(9J20)	795744 AA460298
1668	PEROU:96(6B10):384(20C20)	N-ACETYLTRANSFERASE 1 (ARYLAMINE N-ACETYLTRANSFERASE) R91803
1669	GF201:96(97H5):384(13P10)	N-ACETYLTRANSFERASE 1 (ARYLAMINE N-ACETYLTRANSFERASE) T67128
1670	GF201:96(64C11):384(23E22)	503581 AA131239
1671	GF200:96(8C12):384(2F23)	HUMAN BREAST CANCER, ESTROGEN REGULATED LIV-1 PROTEIN (LIV-1) MRNA, PARTIAL CDS H29407
1672	GF201:96(89B3):384(11D6)	N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAMIDASE) AA664155
1673	GF200:96(12H10):384(3P19)	EPOXIDE HYDROLASE 2, CYTOPLASMIC R73525
1674	GF201:96(97C6):384(13F12)	B-CELL CLL/LYMPHOMA 2 W63749
1675	GF201:96(100G11):384(14M22	ESTS, HIGHLY SIMILAR TO (DEFLINE NOT AVAILABLE 4929557) [H.SAPIENS] T74688
1676	GF200:96(22G7):384(6M14)	BASIC HELIX-LOOP-HELIX DOMAIN CONTAINING, CLASS B, 2 T62084
1677	GF201:96(62D11):384(22H21)	FORKHEAD (DROSOPHILA) HOMOLOG 1 (RHABDOMYOSARCOMA) AA448277
1678	GF201:96(91E3):384(12I5)	ACTIVATED P21CDC42HS KINASE AA427891
1679	GF200:96(6D3):384(2G6)	HUMAN MRNA FOR KIAA0303 GENE, PARTIAL CDS AA418846
1680	GF201:96(59A7):384(22A13)	487929 AA045481

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Table 1

1681	GF200:96(7D8):384(2H16)	ZINC FINGER PROTEIN HOMOLOGOUS TO ZFP103 IN MOUSE AA429297
1682	GF200:96(8D4):384(2H7)	CELL DIVISION CYCLE 4-LIKE AA041499
1683	PEROU:96(9B4):384(18D8)	ESTS, WEAKLY SIMILAR TO P1.11659_5 N47593
1684	GF202:96(111B9):384(15D18)	ESTS, WEAKLY SIMILAR TO (DEFLINE NOT AVAILABLE 4502327) [H.SAPIENS] T72850
1685	GF200:96(29D2):384(8G3)	ESTS, MODERATELY SIMILAR TO !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.SAPIENS] R70598
1686	PEROU:96(6C2):384(20F4)	220376 H86813
1687	GF201:96(100H8):384(14O16)	HOMO SAPIENS MRNA; CDNA DKFZP434H071 (FROM CLONE DKFZP434H071) T41078
1688	GF201:96(93D10):384(12H20)	ESTS, WEAKLY SIMILAR TO !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.SAPIENS] AA669222
1689	GF202:96(109A8):384(15A15)	T3 RECEPTOR-ASSOCIATING COFACTOR-1 [HUMAN, FETAL LIVER, MRNA, 2930 NT] AA400234
1690	GF201:96(63H11):384(23O21)	416556 W86987
1691	GF200:96(7H5):384(2P10)	HUMAN CLONE 23907 MRNA SEQUENCE R06567
1692	PEROU:96(6F3):384(20K6)	ESTS, WEAKLY SIMILAR TO KIAA0108 [H.SAPIENS] AA033947
1693	GF202:96(112E11):384(15I21)	ESTS, WEAKLY SIMILAR TO KIAA0108 [H.SAPIENS] AA600214
1694	GF200:96(16C10):384(4F19)	RAB2, MEMBER RAS ONCOGENE FAMILY T82414
1695	GF200:96(22C1):384(6E2)	TISSUE SPECIFIC TRANSPLANTATION ANTIGEN P35B AA421687
1696	GF201:96(55C3):384(21E5)	ESTS, WEAKLY SIMILAR TO RBCK2 [R.NORVEGICUS] AA434161
1697	GF200:96(29D10):384(8G19)	ESTS, WEAKLY SIMILAR TO ORF2 CONTAINS A REVERSE TRANSCRIPTASE DOMAIN [H.SAPIENS] R38239
1698	GF201:96(55F11):384(21K22)	ESTS, MODERATELY SIMILAR TO NMDA RECEPTOR GLUTAMATE-BINDING CHAIN [H.SAPIENS] AA455271
1699	PEROU:96(5C4):384(20E7)	HSP27
1700	GF201:96(82F6):384(9L11)	ESTS, HIGHLY SIMILAR TO TRANSDUCIN-LIKE ENHANCER PROTEIN 3 [H.SAPIENS] AA136692
1701	GF200:96(16H3):384(4P5)	PARVALBUMIN AA010609
1702	GF201:96(100C2):384(14E4)	50582 H17038
1703	GF201:96(99H6):384(14O11)	51700 H22854
1704	GF201:96(65C8):384(23F16)	CYTIDINE MONOPHOSPHATE-N-ACETYLNEURAMINIC ACID HYDROXYLASE (CMP-N-ACETYLNEURAMINATE MONOOXYGENASE) N29639
1705	GF201:96(91E1):384(12I1)	ADENOSINE A2A RECEPTOR N57553
1706	GF200:96(10C4):384(3E8)	HOMO SAPIENS INDUCIBLE PROTEIN MRNA, COMPLETE CDS H12043
1707	GF201:96(99F2):384(14K3)	46896 H09818
1708	GF200:96(9F2):384(3K3)	REGULATOR OF G-PROTEIN SIGNALLING 16 AA453774
1709	GF201:96(66D12):384(23H23)	418240 W90241
1710	GF200:96(6H10):384(2O20)	KIAA0130 GENE PRODUCT N76581
1711	PEROU:96(9C1):384(18F22)	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR AA025141
1712	GF200:96(24B4):384(6D7)	STEROIDOGENIC ACUTE REGULATORY PROTEIN RELATED AA504710
1713	PEROU:96(10E11):384(18J21)	ERBB2-POLYA X03363
1714	PEROU:96(6E5):384(20I10)	V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG) AA025141

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Table 1

1715	GF200:96(15B6):384(4D12)	V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2 (NEURO/GLIOBLASTOMA DERIVED ONCOGENE HOMOLOG) AA443351
1716	PEROU:96(2F1):384(19K2)	ERBB2 AA481939
1717	GF201:96(88H2):384(11O4)	GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 H53703
1718	PEROU:96(8A1):384(20B1)	68400 T57034
1719	PEROU:96(6A1):384(20A2)	68400 T57034
1720	PEROU:96(7F8):384(20L16)	SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY E, MEMBER 1 W63613
1721	GF201:96(65B12):384(23D24)	ESTS, WEAKLY SIMILAR TO ENVELOPE PROTEIN [H.SAPIENS] W37778
1722	GF201:96(69B5):384(24D10)	271076 N29918
1723	GF200:96(3H12):384(1P24)	GLYCINE AMIDINOTRANSFERASE (L-ARGININE:GLYCINE AMIDINOTRANSFERASE) R61229
1724	PEROU:96(7H11):384(20P22)	MOUSE MITOCHONDRION, COMPLETE GENOME NC_001569
1725	GF201:96(97D9):384(13H18)	AMYLO-1,6-GLUCOSIDASE, 4-ALPHA-GLUCANOTRANSFERASE (GLYCOGEN DEBRANCHING ENZYME, GLYCOGEN STORAGE DISEASE TYPE III) AA668425
1726	GF200:96(17B2):384(5C3)	ORNITHINE AMINOTRANSFERASE (GYRATE ATROPHY) AA446819
1727	GF200:96(13C5):384(4E9)	DAMAGE-SPECIFIC DNA BINDING PROTEIN 2 (48KD) AA406449
1728	GF201:96(87C8):384(11E15)	PLASTIN 1 (I ISOFORM) AA017379
1729	GF201:96(99C12):384(14E23)	ELECTRON-TRANSFER-FLAVOPROTEIN, BETA POLYPEPTIDE T62040
1730	GF201:96(82C4):384(9F7)	347276 W80996
1731	GF201:96(55A8):384(21A15)	ACYL-COENZYME A OXIDASE 2, BRANCHED CHAIN T71782
1732	PEROU:96(6C11):384(20E22)	6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BIPHOSPHATASE 3 N93901
1733	PEROU:96(1A6):384(19A11)	ERK3 PROTEIN KINASE AA603152
1734	GF201:96(100G5):384(14M10)	52339 H23278
1735	GF202:96(116H11):384(16P21)	CATENIN (CADHERIN-ASSOCIATED PROTEIN), ALPHA-LIKE 1 AA621315
1736	GF201:96(91A5):384(12A9)	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A SYNTHASE 2 (MITOCHONDRIAL) AA496149
1737	GF201:96(91A4):384(12A7)	470279 AA028905
1738	GF201:96(96G10):384(13M20)	CARNITINE ACETYLTRANSFERASE AA621218
1739	GF202:96(114C7):384(16E14)	78736 T61888
1740	GF201:96(101C2):384(14F4)	72498 T51936
1741	GF201:96(89D6):384(11H12)	NEUROGRANIN (PROTEIN KINASE C SUBSTRATE, RC3) H49511
1742	PEROU:96(9E3):384(18J6)	TRANSFORMING GROWTH FACTOR BETA AA033601
1743	GF201:96(79A6):384(9A11)	KIAA0057 GENE PRODUCT H59726
1744	GF201:96(84F4):384(10K8)	TRANSDUCIN (BETA)-LIKE 1 AA149637
1745	GF202:96(113B1):384(16C1)	837908 AA434090
1746	GF200:96(26H12):384(7O24)	H.SAPIENS MRNA FOR RAT HREV107-LIKE PROTEIN AA476543
1747	GF201:96(95F4):384(13K7)	GLUTATHIONE S-TRANSFERASE THETA 1 H99813
1748	GF201:96(86B7):384(10D13)	URACIL-DNA GLYCOSYLASE 2 AA425900
1749	GF200:96(11G7):384(3N14)	TRANSCRIPTION FACTOR AP-2 BETA (ACTIVATING ENHANCER-BINDING PROTEIN 2 BETA) AA018906
1750	GF200:96(31A5):384(8B10)	HOMO SAPIENS CLONE 23915 MRNA SEQUENCE H51765

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Table 1

1751	GF200:96(31A4):384(8B8)	785816 AA449048
1752	GF200:96(17A10):384(5A19)	PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE 1 (HOMOLOGOUS TO MOUSE LY-41 ANTIGEN) T70503
1753	GF200:96(5B3):384(2C5)	DUAL SPECIFICITY PHOSPHATASE 5 W65461

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
1	1	-0.00125	0.3059	0.3264	0.6647	0.6006	0.3391	0.9412	-0.4488
2	1	-0.6319	-0.2647	-0.1142	0.1341	6.39E-09	0.6085	0.1006	-0.1594
3	1	0.9575	0.5247	-0.7048	-0.1366	-0.3206	0.4679	-0.76	0.07
4	1	0.3475	1.895	-0.7348	-0.1866	-0.5406	0.03789		-3.85E-09
5	1	-0.6525	0.04469		0.7834	-0.2806		0.654	-3.85E-09
6	1	0.1815		-0.5808	0.5774	-0.2566	-0.3281	-0.102	
7	1	0.1455	-1.057	-0.9568	-0.6486	-0.5627	-0.1141	1.525	-0.322
8	1	-0.2875	-0.1203	0.1502	0.2984	0.1144	0.07289	0.2402	0.285
9	1	-0.1223	-0.5952	0.5654	0.5336	1.12	1.088		-0.6098
10	1	0.0075	0.07469	0.6352	0.3834	-0.3906	0.1279	1.635	-0.08
11	1	-0.5075	0.5497	0.4002	0.1584	-0.1656	-0.3071	1.173	0.035
12	1	-1.019	-0.1622	0.06832	0.5566	0.3025	-0.389	0.9358	0.3831
13	1	0.2733	0.4405	-0.129	0.4892	0.9052	0.4737	-0.18	-0.1842
14	1	0.2475	-0.03531	0.4552	0.1534	0.5394	0.3279		0.41
15	1	0.5373	0.7845	0.855	-0.4167	0.2592	0.01773	0.6194	0.3698
16	1	0.7169	0.5741	0.1346	-0.2072	0.2588	0.2073	0.2725	0.1294
17	1	1	-1.127	0.3277	-0.4841	0.1719	-0.2304	-2.285	-0.3875
18	1	-0.331	0.08621	-0.9133	-1.245	-0.0791	-0.7306		2.232
19	1	-0.5646	1.033	-0.01314	-0.07861	0.9973	0.4258	-0.2975	0.3679
20	1	0	-0.3028	0.1177	0.06594	0.8019	0.2804	-0.856	0.3325
21	1	-0.04852	0.04867	0.2692	0.3974	0.5834	-0.04812	0.1325	0.564
22	1	0	-1.453	-1.182	-0.8141	-0.1481	-0.7796	0.6787	-0.6775
23	1	0.9163	1.503	0.9639	0.3722	1.138	0.5766	0.015	1.349
24	1	2.033	2.23	0.9702	0.5084	2.564	2.413	1.528	1.055
25	1	2.455	0.7122	0.9227	0.7409	2.217			1.198
26	1	1.598	2.055	1.485	0.9834	2.269	1.968	0.8553	-0.5
27	1	0.04275	0.3299	0.0004492	-0.05131	0.2446	-0.05686	-0.03727	-0.1947
28	1	0.6302	1.387	0.7479	0.1162	0.6721	-0.3894	-0.55	0.5627
29	1	0.4375	0.9947	0.8652	0.2634	0.2794	-0.3421	-0.53	-0.02
30	1	-0.7225	-0.3253	-0.0948	-0.9266	-0.7006	1.768	-0.7989	-1.15
31	1	-0.5414	0.05578	-0.03371	-1.535	-1.18	-0.851		-1.209
32	1	-0.5862	0.1609	0.1814	0.5497	-0.05437	0.7841		-0.2837
33	1	-0.317	0.6802	-0.05926	0.09898	0.5949	-0.4266	-0.5264	1.246
34	1	0.1211	-0.5817	0.9988	-0.2166	0.273		-0.48	-0.3964
35	1	0.4375	-0.03531	-0.2948	0.1452	0.4394	0.4679		-0.53
36	1	-0.0007031	0.07648	-0.643		-0.1988	-0.04031		0.0618

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
37	1	0.2278	-0.935	-0.3745	-0.2363	0.3197	0.008203	1.45	-0.5597
38	1	0.8163	-0.1066	0.2039	-0.1378	0.6681	0.8266	1.359	0.6387
39	1	0.7475	-0.2153	0.1552	-0.1566	0.7094	0.9279	1.71	0.83
40	1	0.1725	-0.03031	0.4102	0.8384	-0.4156			-0.355
41	1	0.04031	-0.4325	-0.142	0.4862	-0.5678	0.0007031	0.07281	-0.05719
42	1	0.1986	-0.004219	0.1263	0.004531	-0.2095	0.309	0.4611	0.01109
43	1	-0.13	-0.02281	-0.4423	-0.1341	-0.3181	-0.1896	-0.8775	-0.1775
44	1	-0.2125	0.4547	0.3252	0.6634	-0.3906	0.5379	0.34	0.22
45	1	0.0075	0.7647	0.7952	1.453	-0.03063	0.5479	0.48	0.16
46	1	-0.2752	0.632	0.8425	1.111	-0.2934	1.725	1.377	0.5673
47	1	0.8686	1.736	1.556	0.3945	1.23	0.979	-0.3589	0.9011
48	1	-0.008203	0.329	0.2895	0.1377			0.8643	0.1343
49	1	-0.03375	-0.5366	-0.08605	-0.4878	-0.3919	-0.1734		0.2787
50	1	0.2875	0.3847	-0.2948	0.7834	-0.2406	0.01789	-2.65E-09	-0.02
51	1	-0.1775	0.7197	0.7802	0.2084	-0.1556	-0.07711	-0.965	0.205
52	1	0.6175	0.2647	0.0852	0.2634	0.9794	-0.09211	-0.15	0.4
53	1	-0.7566	0.3706	-0.2189	-0.9406	-0.7447	-0.4662		-0.1341
54	1	0.2831	1.17	0.3708	0.2391	-0.445	-0.7065	0.6156	-1.164
55	1	0.00375	-1.949	0.3314	0.4197	-0.3744		-0.5038	0.6162
56	1	-1.267	-0.3496	-0.0791	-0.07086	-0.7049	-0.4464	-1.204	0.6857
57	1	-0.1937	0.1634	-0.4861	-0.5278	-0.2019	-0.5634	0.6687	0.1687
58	1	0.0825	-0.7003	-0.1798	0.8884	-0.1256	-0.1171	0.195	-0.045
59	1	-0.2712	-0.03406	0.2564	-0.1953	0.000625	0.4091	-1.119	-0.1588
60	1	-0.3425	-0.5553	0.0852	0.1434	-0.02062	-0.1921	0.99	0.04
61	1	0.7747	-0.2381	0.2024	0.1806	-0.3234	-0.7149	-0.6128	0.2072
62	1	-0.1125	-0.3053	0.0552	0.02344	-0.1306	-0.7221		-0.5
63	1	-0.5266	-0.02938		-0.6206	-0.5947	-0.8062	-0.6441	0.05594
64	1	-0.18	1.087	0.5577	0.4159	0.04188	-0.1896	-0.1675	-0.1375
65	1	-0.2425	0.7247	0.3252	0.2634	0.01938	-0.1821		-0.07
66	1	-0.0775	0.7797	0.5602	0.4184	-0.1056	0.1129	-0.135	0.725
67	1	-0.3725		-0.1648	-0.6366	-0.2906			0.36
68	1	0.1125	0.2197		0.6084	-0.5156	0.5629	-0.445	1.515
69	1	0	-0.8428	0.1377	0.3259	-0.4181	0.09039	-0.1175	0.6425
70	1	-0.1425	-0.6653	-0.0148	0.1134	-0.4906	-0.3021	-1.56	0.46
71	1	-0.2175	-0.7503	-0.3498	0.3184	0.07437	0.09289	-0.135	0.335
72	1	0.4923	0.3295			-0.4158	-0.2973	-1.065	-0.3252

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
	1	1	1	1	1	1	1	1	1
73	1	0.6653	-0.6475	0.673	0.08125		-0.5843	0.4578	-1.262
74	1	0.0699	1.057	-0.0124	0.9958	0.1918		-0.5876	0.3624
75	1	0.2319	0.2691	0.7596	-0.2522	0.7637	0.5323	0.6244	0.4744
76	1	0.4328	0.55	1.171	-0.06125	0.7847	-0.006797	0.5253	0.4653
77	1	0.5741	0.6512	-0.1382	0.25	0.2559	0.4745		0.6566
78	1	0.0075	0.7147	0.3752	1.193	-0.5706	-0.08211		
79	1	0.2097	1.407	0.7174	0.7056	-0.3484	-0.5499	-0.6178	0.1222
80	1	0.2502	1.497	0.6679	0.9462	-0.1179	-0.6694		0.1227
81	1	0.3475	-0.5653	0.8452	-0.08656	0.5994	0.1779	0.48	-3.85E-09
82	1	0.5075	0.5047	0.5952	0.6534	0.6094	1.008	1.03	1.1
83	1	0.7375	1.195	0.7652	0.7134	-0.3406	0.8379	0.91	1.09
84	1	0.2225	1.05	0.6302	0.5784	-0.09563	0.2929	-0.965	
85	1	0.85	0.4872	1.108	0.1259	0.9219	0.4504	1.632	0.8725
86	1	0.7275	0.3647	1.155	0.2834	0.9294	0.9079	0.96	1.23
87	1	0.5925	0.5397	0.3902	0.2184	1.474	1.353	1.075	0.425
88	1	-0.09859	0.02859	0.5291	-0.2427	-0.1067	-0.7582		0.3039
89	1	0.1625	0.6897	0.0902	0.3784	0.08438	0.4829	0.025	0.395
90	1	-0.1184	0.4987	1.359	0.5475	-0.1766	-0.538		0.8941
91	1	0.2955	-0.3473	0.6832	0.5715	0.1774		1.058	0.668
92	1	0.8068	2.014	1.014	1.643	0.4787	0.7072	1.219	0.4693
93	1	0.07531	0.5125	-0.127	0.4513	0.4872	0.3457		0.6378
94	1	0.7566	0.8838	0.5143	-0.1574	0.4685		0.7791	0.1291
95	1	0.2375	0.06469	0.2652	0.1234	-0.3406	-0.2721	-0.18	0.49
96	1	0.1675	-0.07531	0.1952	0.2834	0.1894	0.5679	-0.11	-0.08
97	1	0.3875	0.4547	0.5352	0.6134	0.4094	0.4679	-0.07	0.19
98	1	0.6069	0.8241	0.5146	-0.1272	0.4088		0.7794	0.6494
99	1	0.5269	1.194	0.1446	0.2028	-0.4213		0.5594	0.9894
100	1	0.5775	0.5647	0.0952	0.2234	0.1594		0.47	0.51
101	1	0.4797	1.187	0.4874	-0.08437	-0.2084	0.3001	0.2222	0.7622
102	1	0.7386	1.086	0.1963	0.1745	1.27	0.369	0.8611	0.9911
103	1	0.6519	0.5491	0.5296	0.2678	0.9237		1.184	0.8444
104	1	0.6975	1.125	0.3952	-0.3866	1.299	1.038	0.89	1.31
105	1	1.005	1.683	0.863	1.241	1.537	1.116	1.198	1.178
106	1	-0.02125	0.5959	0.1664	0.3247	0.5306	0.5291	0.3212	1.191
107	1	-0.1977	-0.2405	1.46E-12	-0.06176	0.5642	0.4727	-0.1352	0.5848
108	1	0.1747	0.2319	0.08238	0.000625	0.8266	0.3151	0.2872	0.2672

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
	1	1	1	1	1	1	1	1	1
109	1	-0.2975	-0.3303	-0.1798	0.2584	-0.2356	-0.3171	-1.205	0.645
110	1	-0.2598	0.8074	-0.6321	0.3861	0.2021		-0.8073	1.153
111	1	-0.1035	0.5537	-0.3858	1.152	0.1184	0.6169	-0.661	1.129
112	1	-0.1502	0.357	-0.5125	0.4057	0.4316	0.1402	0.1623	-0.3977
113	1	-0.57	0.1872	0.0777	-0.4641	-0.2481	-0.3996		0.1225
114	1	0.3075	0.3147	0.1152	0.3034	-0.5206	0.05789	-1.37	0.03
115	1	-0.05375	0.9234	0.5139	-0.3878	0.4581	0.1666	0.9987	-0.03125
116	1	-0.2575	0.09969	0.2502	-0.5216	0.08438	0.2629	0.765	-0.175
117	1	-0.004219	1.503	0.3835	-0.07828	-0.04234	0.1562	0.6383	-0.2017
118	1	0.4347	1.522	-0.1776	0.000625	0.06656	0.5251	1.127	1.047
119	1	0.555	0.5022	0.5927	0.1809	-0.1031	-0.01461	0.9675	0.5875
120	1	0.358	0.8552	1.156	0.5139	0.7498	0.3884	0.5505	0.8705
121	1	0.0575	-1.035	0.0652	-0.2666	0.04937	-0.6779	-0.1	0.16
122	1	0.2403	-0.7925	0.218	-0.3937	-0.5278	-0.0107	0.002812	0.1128
123	1	-0.01031	-0.2831	0.4374	-0.05437	-0.02844	0.2301	0.1222	0.1122
124	1	0.2325	0.03969	0.5102		-0.005625	0.8929	-0.035	0.335
125	1	-0.06961	0.9076	0.5181	0.2263	-0.6477	0.6408		-0.7171
126	1	-0.2862	-1.069	-0.8086	0.07969	0.04562	-0.04586	-0.4038	-0.6538
127	1	-0.4853	-0.2081	-0.2876	0.000625	-0.4834	0.2651	-0.7028	-0.2728
128	1	0.472	-0.8908	0.02973	0.538	-0.4661	-0.1576	-0.09547	0.4345
129	1	-0.8073	-0.2802	1.28	-0.2114	-0.3755	-0.197	1.355	0.8852
130	1	-0.08375	-0.8466	0.04395	0.2222	0.3681	0.2566	0.3288	
131	1	-0.7575	-0.2303	-0.0398	-0.1416	-0.5456	-0.09711	0.735	1.595
132	1	1.608	1.855	-0.8848	-0.5766	0.1494	0.04789	-0.26	1.74
133	1	1.248	0.2556	-0.1339	-0.1556	-1.67	-1.671		0.1909
134	1	2.06	1.767	0.2275	-0.0143	-0.2184	-0.1898	-1.248	0.4323
135	1	1.774	0.6709	-0.09855	-0.01031	-0.3044	-0.2059	-0.1137	-0.3137
136	1	0.4608	-0.342	-0.8915	-0.2333	0.5327			0.4133
137	1	0.1592	0.5664	-0.1131	0.7352	0.1911	-0.2104	-0.1483	0.2717
138	1	0.4155	-0.9173	0.03324	-0.1785	0.4574	0.5859	0.788	-0.512
139	1	0	0.05719	0.6677	-0.1641	0.7119	0.7804	1.162	0.5925
140	1	0.6225	0.4597	0.2802	-0.3616	0.8444	-0.3071	0.045	0.255
141	1	0.7198	0.877	0.9975	-0.3443	0.7016	0.7902	1.212	1.062
142	1	1.208	1.495	-1.335	-1.777	0.6694	-0.6521	0.7	0.54
143	1	1.275	0.3619	1.212	0.000625	1.737	1.725	2.037	2.027
144	1	1.273	0.7497	1.58	0.7984	1.564	-0.2371		2.025

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
145	1	-0.08469	0.2025	-0.137	-0.03875	-0.3828	-0.3543	–	-0.1222
146	1	0.3247	0.3619	0.3024	1.271	-0.3434	-0.4949	0.7572	0.1172
147	1	1.354	0.2815	0.712	1.05	1.836	1.385	2.127	1.407
148	1	1.058	1.885	1.245	0.1634	0.3594	1.418		0.98
149	1	0.5175	-0.4553	1.135	0.6234		0.9779		2.1
150	1	0.8672	1.544	0.3849	-0.1269	1.089	0.1776	0.6597	0.7497
151	1	0.2847	0.3019	0.6924	0.000625	0.7966	0.1651	0.3472	1.047
152	1	0.5125	1.26		0.07844	0.8244		0.165	0.815
153	1	0.5925	0.3797	0.9002	0.008437	0.7944		0.635	0.705
154	1	0.9269	0.6841	0.4546	0.1828	0.7887	0.7573		0.8594
155	1	0.5375	-0.2953	0.3652	0.4634	0.1594	0.6179	0.68	0.73
156	1	0.3975	0.4647	0.3052	0.4234	0.03938	0.4879	0.72	0.75
157	1	0.8775	1.415	1.385	1.233	1.069	1.858	1.36	1.14
158	1	1.396	1.803	0.9839	0.7122	1.278		1.439	1.279
159	1	0.1525	0.8797	0.8402	0.6884	0.1944	0.3329	0.985	1.285
160	1	0.3661	-0.00668	0.7338	0.7521	-0.442	0.6365	-0.1814	1.029
161	1	0.8672	0.6344	1.145	-0.3469	-0.4309	0.4176	1.42	1.21
162	1	0.1114	0.6886	0.8491	0.02734	0.8433	-0.1718		1.124
163	1	0.2375	0.6547	0.2852	-0.1766	0.5894	1.138	0.56	0.53
164	1	0.3433	0.5705	-0.399	0.6692	0.3152	1.134	0.005781	0.4958
165	1	0.4569	-0.7159	1.135	–	1.389	-0.6027	1.929	0.3094
166	1	0.9075	1.025	0.7052	1.013	0.8294	0.7679	0.42	0.3
167	1	0.0875	0.6647	1.065	0.2934	0.2894	0.2679	0.02	0.83
168	1	0.6375	0.6747		0.5034	1.549	1.818	1.01	0.85
169	1	0.3454		1.143	-1.419	-1.053	0.4058		1.058
170	1	0.5954	-0.1274	0.6931	0.08133	0.4873	0.06578	1.678	0.4979
171	1	0.5475	-0.6153	1.265	-0.1266	1.339	1.088		1.16
172	1	1.252	0.5297	2.98	0.7084	2.034	0.3629	0.335	1.485
173	1	2.076	0.06297	1.983	0.05172	1.888	2.366		2.478
174	1	0.4973	-1.185	0.415	0.5333	0.8692		0.5798	0.4198
175	1	0.08449	0.4917	0.9722	-0.4296	0.5264	0.2749		0.327
176	1	0.2699	0.2071		0.1759	0.5018	0.8803	-0.3576	0.1324
177	1	0.2689	-0.1039	0.9966	-0.02516	0.4008	0.009297	-0.008594	1.091
178	1	0.0775	0.4847	1.605	-0.5266	0.8494	-0.3721		1.88
179	1	0.361	0.9982	-0.00127	-0.01303	0.4829	0.6014	0.01354	0.3735
180	1	0.7575	0.7647	0.1452	-0.1066	-0.1006	0.4279	0.58	0.06

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
181	1	0.5859	0.993	0.1936	0.0818	0.2277		0.4284	-0.2016
182	1	0.6875	1.455	1.115	-0.02656	0.1394	0.5579	1.83	1.04
183	1	1.375	1.802	0.9229	-0.3688	0.2871		1.768	1.438
184	1	-0.157	1.12	0.6707	0.1389	0.1248	0.1734	0.3255	0.8755
185	1	0.7027	1.61	1.59	0.07859	0.3645	0.293		1.295
186	1	0.5175	1.535	0.5752	-0.006562	-0.01063	0.007891	0.93	0.89
187	1	0.185	1.142	0.9527	0.1609	0.2869		0.7975	1.217
188	1	0.4614	1.709		0.2073	-0.1067	0.4418	1.244	1.154
189	1	0.3955	0.8927	0.5132	0.1214	-0.2727	-0.08414	0.488	0.878
190	1	0.5175	0.6747	0.6452	-0.04656	-0.1206	0.1279	0.9	0.88
191	1	0.4421	1.219	0.5998	0.1681	1.174	0.7125	1.235	0.7246
192	1	0.6134	0.7206	-0.08887	0.9094	1.055	0.7238	0.4659	0.8559
193	1	0.232	0.8392	1.3	1.648	0.8439	1.522	0.5345	1.405
194	1	-0.1069	0.5003	0.8108	-0.03094	0.595	0.7335	-0.6444	1.016
195	1	-0.1846	0.2126	0.7231	0.1414	0.7573		0.07793	0.9979
196	1	0.2579	-0.06486	0.02564	0.2839	0.7598	0.9283	0.4104	0.4504
197	1	0.1623	0.7295	0.27	-0.001797	1.004	0.6427	0.05477	1.115
198	1	-0.0225	-0.6953	0.2852	0.3234	1.069	0.7679	0.53	1.32
199	1	0.08332	0.7105	0.001016	0.1993	0.3952	-0.02629	-0.09418	-0.00418
200	1	-0.0075	0.3897	0.2502	-0.3216	-0.1056	-0.07711	0.585	0.005
201	1	-0.002344	-0.2752	-0.4046	-0.2564	0.3495		0.4002	-0.2898
202	1	-0.09141	-0.01422	-0.3937	0.4845	0.2205	0.359	0.5211	0.1211
203	1	-0.3525	-0.1753	0.4052	0.5634	-0.01062	-0.4521	0.09	0.27
204	1	0.4147	0.6919	0.6924	0.000625	0.1566	0.1251		0.5472
205	1	0.1345	0.3616	0.9821	1.17	1.226		1.167	0.607
206	1	0.3819	0.4491	0.2496	0.2978	0.9637		0.9944	1.034
207	1	-0.4397	0.9275	0.278	0.3162	0.5122	0.0007031	0.9428	0.5028
208	1	0	-0.1428	0.3377	-0.4341	0.5519	0.02039	0.7925	-0.2175
209	1	0.7122	0.4694	0.8599	1.598	0.8541		1.205	1.445
210	1	0.6375	-0.3353	0.7352	0.5234	0.5894	1.278	0.99	1.22
211	1	0.3008	0.508	0.7085	-0.01328	0.7527	1.621	1.043	0.8133
212	1	0.1031	1.06	0.6308	0.7991	-0.155	0.05352	-0.1744	0.7156
213	1	-0.0875	-0.4603	0.4902	-0.2016	0.9644	0.7129	0.925	1.475
214	1	-0.6145	0.3727	0.7732	-0.4837	0.07734	-0.7941		-0.002031
215	1	1.94	1.418	-0.01191	-0.2316	0.9023	1.211	0.9229	0.9529
216	1	0.8425	0.04969	1.02		1.654		1.135	1.785

Table 1

| | NORWAY 100-BE | NORWAY 100-AF | NORWAY 10-AF | NORWAY 10-BE | NORWAY 102-BE | NORWAY 102-AF | NORWAY 7-AF | NORWAY 17-BE |
	GWEIGHT	ARRY19X	ARRY18X	ARRY21X	ARRY20X	ARRY23X	ARRY22X	ARRY24X	ARRY25X
	1	1	1	1	1	1	1	1	1
217	1	0.8536	1.211	-0.6887	-0.7505		-0.976		0.4361
218	1	-0.1937	0.5434	0.9539	-0.6278	1.388	0.8766	-0.1313	0.3287
219	1	-0.2725	0.2447	0.2052	0.5834	0.07938	1.028		-0.18
220	1	-0.2225	-0.7253	0.6452	-1.377	0.1494	0.09789		0.32
221	1	-0.00875	0.02844	1.549		0.3231	-0.2384		1.024
222	1	0.2875	0.7447	1.295	0.5734	-0.3206	0.7079	-0.22	0.41
223	1	0	-0.2728	0.6977	-0.1041	-0.4181	0.4504	-0.5775	-0.3275
224	1	0.5258	-0.217	0.1835	0.9617	-0.5423	0.4062	0.7383	0.1383
225	1	-0.1684	0.1887	0.7193	0.4675	0.4234	-0.398		
226	1	-0.1075	-0.2203		0.1384	-0.5356	-0.3571	-0.045	0.095
227	1	-0.2175	-0.4203	0.4502		-0.1456	-0.3271	0.905	0.005
228	1	0.3975	0.6847	0.5452	-0.5266	-0.6906	-0.7521	-0.06	-0.38
229	1	0.6275	-0.2953	0.4252	-0.3366	-0.2406	-0.4921	1.52	-3.85E-09
230	1	0.7578	-0.295	0.1055	-0.04625	0.2097	-0.1018	0.2703	-0.3197
231	1	0.4434	0.6305	0.2411	0.6993	0.2852	-0.00625	0.05586	-0.01414
232	1	0.4125	0.06969	0.0802	0.02844	-0.5556	0.5829	0.325	0.545
233	1	0.3106	0.7478	-0.3817	0.3566	-0.1675	0.551		0.07312
234	1	-0.5625	-0.6053	-0.1148	-0.8766		-0.03211	-0.82	-0.5
235	1	-0.7555	-1.208	-0.8379	-1.6	-0.3337	-0.04516	-1.403	-0.323
236	1	0.9569	-0.3459	-0.4154	-0.8372	-0.2413	0.1373		0.8694
237	1	0.4231	1.11	-0.4792	0.2591	0.025	-0.02648	0.7456	-0.2344
238	1	-0.2247	0.1525		-0.2187	1.317	-0.2743	-0.06219	0.1778
239	1	-0.3778	-0.2406	0.2699	1.088	0.1741	0.6726		-0.1153
240	1	-1.011	-1.054	-0.2736	-1.425	0.000625	0.1491	-0.2288	0.2212
241	1	-0.8163	-0.7091	-0.3186	-0.3904	-0.04445	0.08406	0.1662	-0.1738
242	1	-0.0525	0.2447	-0.0948	-0.03656	-0.05062	0.06789	-0.24	0.45
243	1	0.02875	-0.4441	-0.1336	-0.3453	-0.1594	-0.5209	-0.08875	0.3312
244	1	0.608	1.115	-0.06426	0.204	-0.5301	0.3184	-0.9895	-0.01945
245	1	1.185	1.262	0.0527	0.1409	-0.2531	0.3954	-0.6625	-0.3625
246	1	0.682	0.4492	0.9197	0.858	0.3239	-0.1376	0.2245	0.3345
247	1	0.1093	-0.2535	-0.003027	-0.7648	-0.01885	0.04967	-0.2982	-0.06822
248	1	0.2316	-1.511	-0.3607	-1.552	0.2635	0.702	0.8241	0.06414
249	1	0.1425	-0.6703	0.3102		-0.4856	0.3629	1.375	-0.005
250	1	0.8245	-0.8184	2.562	0.8704	2.326	2.685		0.917
251	1	-1.564	-0.967	-0.3465	-0.6383	-1.042	-0.8038	1.758	-0.05172
252	1	-1.267	-1.47	-0.0298	-0.5716	-0.8556	-0.08711	1.345	0.725

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
253	1	0.6075	1.125	0.3252		0.07937	-0.4221		0.08
254	1	0.03242	0.6796	0.2501	0.5584	0.3243	-0.4272	-0.1951	-0.2751
255	1	-0.6003	0.3869	0.6974	1.486	-0.3084	-0.8299		0.4322
256	1	-0.06891	-1.382	0.2188	-0.423	-0.07703	0.7815	0.1436	1.124
257	1	-0.005703	-1.859	-0.368		0.1262	0.4747	-0.9832	0.9368
258	1	0.1658	-0.327	0.5635	-0.4983		-1.034		0.9783
259	1	2.227	1.534	-1.525	-0.3172	3.019		0.9994	-0.2306
260	1	1.726				2.618	0.1866		-0.03125
261	1	0.81	0.8072	0.2577	0.2859	-0.2181	-0.9496	0.4925	-0.3775
262	1	-0.3786	1.129	0.6091	0.9373	2.953	1.522		-0.3161
263	1	0.3336	1.361	0.2113	0.7995	0.3155		0.2361	-0.2739
264	1	-0.0175	0.2797	0.4802	0.5684	-0.4856	-0.7271		-0.555
265	1	0.7358	1.083	0.5335	-0.2583	-1.372	-1.314	-0.3817	-0.7817
266	1	-0.5597	0.4975	0.278	0.3162	0.5422	0.0007031	-0.7972	0.2428
267	1	-0.3451	0.2521	0.002598	0.6308	-0.1732	0.1753	-0.4426	-0.4226
268	1	-0.2964	-0.2693	0.4013	0.4195	-0.7946	-0.006055		-1.314
269	1	0.8297	-0.4431	1.487	0.5156	1.752	1.54	0.1522	-0.03781
270	1	0.3111	-0.1917	-0.4212	0.02703	-0.137	0.04148	-0.2564	-0.08641
271	1	0.05375	-0.8091	0.3414	-0.4203	0.3256	0.5041	-0.4637	-0.08375
272	1	-0.2625	-1.025	0.1952	-0.2566	0.3494	0.1079	0.9	0.39
273	1	-0.1966	0.4305	0.7711	-0.1907	0.03523	0.2138		-0.01414
274	1	0.9166	1.394	-0.6257	-0.06742	0.3385	-0.06297	-0.9809	-0.2309
275	1	0.1875	0.2747	-0.1948	-0.6366	-0.02063	-0.1521	0.75	0.12
276	1	0.2596	-0.01316	-0.2927	-0.9444	0.7215	0.18	-0.2079	-0.09785
277	1	-1.022	-0.2053	0.5552	0.5734	0.09937	1.598	0.35	-0.55
278	1	-0.03312	0.8641		-0.7372	0.2688	1.427	0.5094	0.2594
279	1	-0.1547	-0.4475	0.483		0.3372	0.8057	-0.002188	-0.5122
280	1	0.0275	0.5747	-0.0548	0.7734	-0.1306	0.2979	1.61	0.1
281	1	-0.3425	0.1547	1.005	0.6134	-0.8906	0.4379		-0.02
282	1	0.2853	0.6025	0.653	-0.3687	0.2072	-0.0743		0.07781
283	1	0.01219	0.2994	-0.5201	-0.7619	-0.8459	-1.167	0.01469	-0.5253
284	1	-0.1225	0.8647	0.2752	1.463	-0.7506	0.1879		0.27
285	1	0.1947	0.3419	1.332	0.000625	-0.3934	-0.5549	-0.3328	0.2872
286	1	1.92	1.287	0.7677	0.3159	-0.03812	-0.2296		-0.7675
287	1	2.023	0.1102	1.471	0.2089	0.03488	-0.8066	-1.014	0.03551
288	1	-0.1231	0.9341	-0.4354	-0.5672	0.3087	0.1373	0.3894	-0.2706

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
	1	1	1	1	1	1	1	1	1
289	1	0.6013	0.3284	0.7489	-0.2728	1.113	-1.368	-1.096	-0.5362
290	1	0.933	-0.1798	0.02072	-0.161	-2.275		-1.434	-3.524
291	1	0.8234	1.171	-0.3589	0.0993	-1.025	-0.6762		0.4259
292	1	-0.2225	1.315	0.2352	-0.1466	-0.02063	-0.7321	-0.49	0.29
293	1	-0.1339	0.5633	-0.07621	0.002031	-0.442	-0.7535	-0.5914	0.6686
294	1	-0.1825	-0.04531	0.2852	-0.02656	-0.3506	-1.352	-0.6	-0.38
295	1	-0.2325	0.7847	0.0352	-0.5766	-0.4006		0.27	-0.75
296	1	-0.7077	0.5895	-1.46E-12	-0.4618	-0.5658	-0.6473	0.3848	-0.6652
297	1	0.1292	-0.4236	-0.4431		-0.02891	0.2396	0.4417	-0.3083
298	1	-0.3725	0.2647	-0.0948	0.2234	-0.6506	-0.8621	-0.22	-0.16
299	1	-0.1047	1.312	-0.597	0.3112	-0.8628	0.0357		-0.6222
300	1	0	0.8172	0.8277	0.3059	-0.3281	0.6904		-0.0575
301	1	0.6175	1.275	0.4152	0.04344	0.6794	-0.1121		0.71
302	1	0.2895	-0.5234	-0.2429	-0.2246	0.1213	-0.4402	0.252	-0.468
303	1	0.78	-0.002813	0.8877	-0.1941		-0.5696		-0.4975
304	1	1.313	1.811		0.9493	-0.3348	-0.3163	-0.3342	0.4658
305	1	1.278	1.805	0.1852	0.9834	-0.2306	-0.4121	-0.22	-0.01
306	1	-0.09812	-0.3909	0.1796	0.3378	-0.4363	0.1723	0.1544	0.2244
307	1	0.1875	-0.5253	0.0952	-0.3466	0.7694	1.108	0.07	0.71
308	1	-0.01516	-0.178	1.333	0.2008	-0.4133	0.2552	-1.443	-0.3527
309	1	-0.935	-0.04781	0.3127	-0.1691	-0.1631	0.02539	0.4575	0.0075
310	1	-0.1079	0.3993	-0.3102	-0.8919	-0.226	-1.077	-0.2154	-1.105
311	1	-0.1322	-0.385	-0.2745	-1.056	-0.04031	-1.822	-0.04969	-0.5997
312	1	-0.3525	-0.1253	-0.6048	-0.8766	-0.07063	-0.9321	-0.02	-0.12
313	1	-0.1881	0.2591	-0.3104	-1.212	0.1737	-0.7877	-0.6756	-1.056
314	1	-0.006406	-0.06922	-0.7687	-0.9005		-0.896	-0.02391	-0.7739
315	1	-0.09215	-0.07496	-1.014	-0.8962	-0.07027	-0.9818	-0.02965	-0.6896
316	1	0.1275	-0.1353	-0.6348	0.2759	-1.061	-0.9821		-0.11
317	1	-0.42	-0.01281	0.0377	-0.9166	-0.4281			0.0125
318	1	-0.6725				-0.1006	-0.4621		0.04
319	1	1.272	1.31	-0.2798	0.4984	0.3644	0.3629	0.225	0.515
320	1	1.045	-0.418	-0.2375	0.9308	1.467	1.315	1.147	1.037
321	1	0.4347	0.3419	0.7524	0.000625	0.2766	-0.4549	0.1472	-0.2428
322	1	0.2925	0.6897	0.1302	0.7284	0.07438	0.2829	-0.285	0.825
323	1	-0.07672	-0.05953	-0.03902	0.05922	0.01516	-0.1063	-0.4342	0.9058
324	1	0.2975	0.05469	-0.9648	1.043	0.01937		0.17	-0.92

Table 1

	GWEIGHT	NORWAY 100-BE	NORWAY 100-AF	NORWAY 10-AF	NORWAY 10-BE	NORWAY 102-BE	NORWAY 102-AF	NORWAY 7-AF	NORWAY 17-BE
		ARRY19X	ARRY18X	ARRY21X	ARRY20X	ARRY23X	ARRY22X	ARRY24X	ARRY25X
		1	1	1	1	1	1	1	1
325	1	0.4225	0.5197	-0.2698	0.8284	0.004375	-0.1971	0.075	-0.685
326	1	0.08609	-0.7467	-0.07621	0.01203	-0.412	-0.5135		-0.1814
327	1	0.5697	1.187	0.2174	-0.03437	-0.3384	0.2201	-0.3678	-0.2578
328	1	0.6897	0.6769	-0.3826	-0.5244	-0.5884		-1.228	-3.85E-09
329	1	0.7675	1.135	-0.5048	0.2234	-0.3806		-1.04	-0.03781
330	1	0.6997	0.4969	-0.2826	-0.2344	-0.4984	-0.2699	-1.198	0.01
331	1	-0.2925	0.1347	0.9652	0.4334	-0.1806	0.8779		0.4825
332	1	0.54	0.4672	-0.6223	0.1559	0.1419	-0.5996	-0.4575	-0.015
333	1	0.9325	0.8597	0.1602	0.3384	0.4044	0.3229	0.275	0.58
334	1	0.2475	-0.3853	0.7652	0.4334	0.7194	0.8579	1.59	-0.3739
335	1	0.1836	0.02078	1.611	0.1495	-0.08453	-0.356	-0.2339	0.8553
336	1	1.673	0.4699	0.02045	-0.9013	0.4546	1.183	0.6253	0.6975
337	1	0.105	0.7322	0.2827	0.7409	0.1869	0.1954	0.6075	-0.4043
338	1	0.4232	0.9204	-0.4891	-0.3209	-0.2449	-0.3664	0.0657	1.09
339	1	0.3775	0.4247	0.3652	0.7134	0.4094	0.8179	0.88	0.08
340	1	-0.0325	-0.04531	0.005195	-0.05656	0.6494	0.8079	0.28	0.165
341	1	-0.0275	-0.5203	0.0902	-0.07156	-0.2156	0.3929	-0.055	0.7414
342	1	-0.06109	0.3361	0.8466	0.1148	0.3908	-0.0107	0.1314	0.3855
343	1	0.663	0.02023	0.1307	-0.871	0.2849	0.08344	-0.05445	0.33
344	1	0.7475	0.6547	0.2452	-0.5766	0.2094	-0.1321	-0.22	
345	1	1.095	0.2119	-0.08762	0.000625	0.5766		-0.3228	0.98
346	1	0.7875	0.8547	0.1952	0.1734	0.03937	0.1279	-1.08	0.67
347	1	1.348	1.385	0.3352	-0.7266	0.5294	0.7779	0.11	0.4878
348	1	-0.2747	0.1925	-0.367	-0.3488	-0.2528	0.0857		0.5975
349	1	0.065	0.002188	0.3827	-0.05906	-0.1231	0.3354		0.31
350	1	-0.2525	0.7747	0.2952		-0.3406	0.08789	-0.61	0.6258
351	1	-0.09672	0.4205	0.171	0.8692	-0.2948	-0.1163	-0.1942	0.5135
352	1	0.581		-0.02131		0.3629		0.2435	-0.31
353	1	-0.1225	0.004687	0.7252	0.7034	-0.7406	-0.8021	0.87	2.005
354	1	0.5825	0.9197	-0.2198	0.09844	0.7944	0.6129	-0.145	0.4525
355	1	0.36	0.02719	-0.6823	-0.2641	0.3119	0.04039	-0.8775	0.138
356	1	-0.9245	-0.01734	-0.7868	0.5414	-0.7727	-0.2741	-1.802	0.1072
357	1	-0.6453	0.1419	-0.03762		-0.8934	-1.005		-0.5477
358	1	0.2898	-0.08305	-0.9025	-0.6543	-1.638	-1.52	-0.6677	-0.1736
359	1	0.08391	-1.349	-0.9284	-0.02016	-1.244		-0.5536	0.3539
360	1	-0.01859	1.029	0.8291	0.6273	-0.3367	0.9718		

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
361	1	-0.1975	-0.1603	0.6402	0.2184	-0.8656	0.1629	-0.315	0.365
362	1	0.2336	-0.4792	0.2713	0.1295	0.2755	-0.476	-0.1839	0.4661
363	1	0.4	-0.6028	0.1177	0.09594	0.09188	0.3704	-0.1175	0.4125
364	1	0	0.9872	0.3677	0.3359	-0.2581	0.1904		-0.2475
365	1	-0.4225	0.06469	0.2052	0.2534	-0.1306	0.09789	-0.56	0.65
366	1	0.06781	0.795	0.4255	-0.1263	0.2697	0.6582	-0.009688	0.02031
367	1	1.188	0.7447	-0.0448	-0.1166	-0.02063	0.7879	0.31	-2.20E-08
368	1		-0.6468	-0.6163	-0.678	-0.02211	-0.1236	0.3785	-0.1515
369	1	-0.3425	0.1847	0.5552	0.9934	-0.6306	-0.4521		-0.54
370	1	-0.000625	-1.303		1.475	0.00125		0.6019	-0.1781
371	1	0.0475	0.4747	-0.0448	0.2534	-0.01063	-0.1221	-0.28	-0.53
372	1	0.2434	-0.4594	-0.04887	-0.1806	-0.5547	-0.1762	-1.104	-0.1341
373	1	-0.3225	0.3347	-0.6248	0.2534	-0.3506	-0.1221	-0.1	-0.08
374	1	0.08891	0.4561	-0.2634	0.3148	-0.1492	-0.0007031	0.4314	0.001406
375	1	-0.4803	0.6169	0.3174	-0.3344	0.03156	-0.03992	0.4122	0.7322
376	1	-0.3281	-0.4409	0.5596	-0.3022	-0.2962	-0.007734		-0.1256
377	1	-0.4425	0.4347	0.6652	0.01344	-0.7606	-0.7521	-0.21	0.45
378	1	0.1175	0.2047	0.4952	1.273	-0.6306	-0.4521	0.4	0.1
379	1	-0.1253	0.6319	0.2024	0.09063	-0.1834	0.1451	-0.1928	-0.04281
380	1	0.05344	0.6606	0.7011	-0.1206	-0.6547	0.4838	-1.074	0.5459
381	1	0	-0.3428	0.0477	0.6259	0.09187	0.3504	-0.0475	0.4325
382	1	0.4663	-0.5966	0.2839	1.012	0.9481	0.9766	1.079	0.07875
383	1	-0.3432	0.9639	0.2345	-0.0373	-0.4314	0.8471		-0.7807
384	1	0.4832	1.13	-0.3891	-0.4809	0.1651	0.2736	-0.5843	0.1557
385	1	0.49	0.9372	-0.6723	-0.4541	0.6019	0.5604	-0.6575	0.5025
386	1	0.2675	0.3947	0.7452	0.5134	-0.2406	0.07789		
387	1	0.01625	-0.8366	-0.5061	-1.398	-0.7119	-0.1734	-0.3613	-0.09125
388	1	-0.0825	-0.8153	-0.9148	-0.8466	-0.09063	-0.3321		0.02
389	1	-0.4163	-0.3591	-1.159	1.37	0.005547		-0.7138	0.4262
390	1	0.5432	0.8704	0.1109	-0.2609	-0.7249	-0.3664	-0.7743	-0.2643
391	1	0.6206	0.3978	0.4183	-0.8134	-0.3075		-0.1969	0.8031
392	1	0.2547	-0.8281	0.04238	0.000625	0.5866	-0.5849	-0.7728	0.7172
393	1	0.4859	-0.627	-0.1064	-0.3382	-0.1323	0.00625	-0.8516	-0.2716
394	1	0.2347	0.6519	-0.4176	-0.009375	-0.1634	-0.1149	-0.4928	0.1472
395	1	0.1364	0.9136	-0.4259	-0.4877	-1.052	-0.5932	-0.9111	-0.8411
396	1	0.5939	0.1511	-0.6184	-0.02016	-0.1442		0.7464	-0.06359

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Table 1

	GWEIGHT	NORWAY 100-BE	NORWAY 100-AF	NORWAY 10-AF	NORWAY 10-BE	NORWAY 102-BE	NORWAY 102-AF	NORWAY 7-AF	NORWAY 17-BE
		ARRY19X	ARRY18X	ARRY21X	ARRY20X	ARRY23X	ARRY22X	ARRY24X	ARRY25X
	1	1	1	1	1	1	1	1	1
397	1	0.2642	-0.06859	-0.1181	-0.1098	0.6961	0.4546	0.1767	-0.1533
398	1	0.4575	0.9247	0.5952	-0.6366	-0.06062	-0.1821		0.48
399	1	0.8197	0.4769	-0.1926	-0.7744	-0.2784	-0.02992	0.1622	0.3622
400	1	0.0475			-0.6666	0.1494	0.3379	0.66	0.04
401	1	0.7875	-0.2453	0.2752	-0.6066	0.009375	-0.3821		0.4
402	1	0.4938	-0.1291	1.191		-0.8944	0.8341		0.7263
403	1	-0.1925	0.2247	-0.1348	0.2034	0.4394	0.5379	0.26	0.13
404	1	-0.365	-0.7878	-0.2473	0.3409	0.8869	0.7154	0.8175	-0.2725
405	1	0.56	-0.002812	0.1877	1.036	-0.2181	-0.2596	-0.4375	0.0925
406	1	0.1455	-0.1273	0.03322	0.9615	-0.0326	0.1859	0.588	0.358
407	1	0.0475	0.5047	-0.3148	-1.107	-0.04063	-0.5021	0.04	0.25
408	1	-0.006406	0.6908	-0.2587	-0.2705	-0.7045	-0.146	0.4961	-0.8639
409	1	0.4675	0.3847	-0.3848	0.5834	-0.2006	0.3379	0.16	0.08
410	1	-0.09125	0.1459	-0.2736	0.5947	0.000625	0.3091	-0.3288	-0.2288
411	1	-0.6125	-0.1453	-0.3948	0.9234	-0.9406	-1.492	-1.87	-0.35
412	1	-0.3797	-0.6725	-0.04199	-1.424	-0.05781	0.4607	0.06281	-0.09719
413	1	-0.1112	-0.134	-0.3335	-0.1153	0.05066	0.3092	0.1013	-0.1987
414	1	-0.122	0.4152	0.3357	-0.2961	-0.3801	-0.1316	-0.8195	-0.4595
415	1	0.5375	0.8247		-2.167	-1.741		-0.12	-0.68
416	1	-0.1191	0.4881	-0.4914	-0.1832	-0.4172	-0.4687	-1.507	0.0134
417	1	0.2436	0.8908	0.04133	-0.5804	-0.8545	-0.516	-0.7739	-0.03387
418	1	0.4575	0.8147	0.9452	-0.3766	-0.3906	-0.9921	-0.91	-3.85E-09
419	1	-0.00625	-0.2791	0.1514	-1.03	0.6256	-1.146	0.3662	-0.9138
420	1	-0.1625	0.1547	0.4152	0.7134	0.4094	0.5279	0.28	-0.11
421	1	-0.1025	-0.005313	-0.5948	-0.1366	-0.7306	-0.5521	-2.65E-09	-0.52
422	1	2.296	3.253	-0.01605	-1.058	0.03813			-0.9713
423	1	0.1375	-0.2553		0.2834	-0.6906	-0.1321		0.12
424	1	1.408	0.7847	0.1052	0.3434	-0.4506	-0.7821	-0.38	0.41
425	1	1.608	0.9747	0.0852	0.1034	-1.481	-1.762		0.16
426	1	1.305	1.242	0.3225	-0.1993	0.02664	-0.5148		
427	1	1.556	1.333	-0.5361	-1.278	-2.222	-0.9434		-0.1512
428	1	1.756	1.003	-0.7261	-1.638	-1.332	-1.123	-3.151	-2.001
429	1	1.173	0.4297	-0.7098	-2.272	-0.8956		-2.645	
430	1	1.19	1.087	-0.5323	-1.884	-1.848	-2.07		-1.658
431	1	0.9681	0.9153	-0.2942		-1.11			
432	1	1.092	0.9197	-1.17	-0.8816	-0.9656	-1.307	-1.125	-1.415

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
433	1	1.715	1.902	-0.1473	-1.389	-2.003	-1.265		-0.6225
434	1	0.9091	-0.2037	0.09684	0.5451	-0.279	1.39	-0.6084	-0.08836
435	1	-0.06687	-1.57	0.08082	-0.1609	-0.505	0.7135	-0.03438	-0.3344
436	1	0.3334	0.5506	-0.6289	-0.3406	-0.5947		-0.004063	-0.3841
437	1	0.6475	1.215	-0.3448	0.6634	-0.6106		-0.36	-0.54
438	1	0.9354	1.113	-0.427	-1.369	-0.8628	-0.05426	-0.05215	0.1079
439	1	0.9498	1.207	0.07746	-0.3243	-0.5584	-0.1598	-0.4777	-0.7177
440	1	-0.5525	-0.1053	-0.0548	0.9734	-0.5806	0.4079		
441	1	-0.5125		1.215			0.04789		-0.04
442	1	-0.3875	0.7592	-0.6498	0.1284	-0.3556	-0.2071	-0.685	-0.145
443	1	0.09203	-0.3753	1.03	-0.002031	-0.6461	-0.1176		0.05453
444	1	-0.0525	0.2197	-0.6548	-0.01656	0.4394	0.1179	0.15	0.05
445	1	0.1525		-0.8298	-0.3716	-0.4256	0.04289	-0.095	-0.165
446	1	1.932	-2.201	-4.37E-12	-2.172	-0.2358	-0.1773	0.2548	1.045
447	1	0.28	-1.123	-0.0623	0.06594	-0.03812	-0.3996		0.1525
448	1	0.6659	0.553		-0.0482	0.2277	0.4462	-1.762	-0.8316
449	1	0.1968	-0.05602	-0.7755	-0.2673	-0.1113	-0.1328	-0.5807	-0.1807
450	1	0.6206	-1.182	0.9383	0.8066	-1.557	-1.519		0.5631
451	1	0.205	-0.3578	-0.4373	0.1609	-0.2731	-0.4346	-0.3725	-0.1525
452	1	0.5232	-0.05961	0.0409	0.2891	0.1651		0.3557	-0.1443
453	1	-0.4925	0.3147	-0.1648	0.4334	-1.161	-0.2221	-1.34	3.98
454	1	0.2723	-0.6105	-2.13E-11	-0.04176	0.6442	0.4427	0.3248	0.8948
455	1	-0.8637	0.2134	0.7839	-0.1478	-0.7519	0.6966	0.4487	-0.3413
456	1	0.9055	0.5227		-0.05859	-0.8427	0.1459		-0.752
457	1	0.6606	0.2678	-0.4517	0.7266	0.9325		0.6631	0.6931
458	1	0.7125	-1.67	0.8202	-1.082	1.034	-0.06711	0.655	0.885
459	1	-0.4825	-1.715	-0.2348	0.9634	-0.7206	-0.3921	-0.34	0.09
460	1	-1.259	-0.3817	-1.241	-0.413	0.323	0.1815	0.5636	-0.6864
461	1	-0.4225	-0.6153	-0.0748	0.1934	-0.1106		-2.65E-09	-0.32
462	1	-0.7775	0.3897	0.3702	-0.7516	-0.8656	-0.4171		0.525
463	1	0.4297	-0.2631	-0.4226	0.2656	0.1816	0.2301	-0.2578	-0.08781
464	1	-0.3325	-0.4753	-0.1648	-0.3866	-0.4606	0.08789	-0.39	0.05
465	1	0.002891	0.6001	-0.5094	-0.3712	-0.5352	-0.7667	0.3954	-0.5146
466	1	-0.01859	-0.1014	1.029	-0.9227	-0.4967	-0.0482		0.2939
467	1	0.2875	0.9447	-0.2848	0.7634	-0.1006	0.1579	0.38	-3.85E-09
468	1	-0.304	0.2232	0.7937	0.802	-0.6121			0.3285

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
469	1	2.293	3.24	0.5102	1.288	-0.9556		1.445	0.925
470	1	1.479	2.196	0.4164	0.8947	0.000625	-0.2009	0.7212	0.4112
471	1	-0.3664	-0.9192	1.031	-0.1104	-0.2745	0.584	0.1661	0.7361
472	1	-0.0025	-0.1153	0.2452	-0.2166	-0.06063	0.06789	0.33	0.29
473	1	0.6375	0.3747	0.5252	-1.017	-0.5406	-1.052	-0.67	-0.52
474	1	-0.307	-0.03977		0.699	-0.8951	-0.05656		0.2855
475	1	0.1977	-0.7951	0.4364	-0.3963	-0.2004	-0.1019	0.7002	-0.08977
476	1	0.3988	0.7059		0.8447	0.000625	0.1391	-1.699	-0.2388
477	1	-0.2977	0.3795	-4.37E-12	0.2682	-0.3558	0.1027		0.7848
478	1	0.3727	1.07	-0.06965	0.3786	0.3645	0.343	-0.1648	-0.3948
479	1	0.2253	-1.018	0.183	0.4212	0.8572	1.236	-0.1822	1.728
480	1	-0.1389	0.2383	-0.07121	-0.453	0.08297	-0.2885	-1.196	-0.05641
481	1	-0.7432	-0.656	0.2745	-0.8473	-0.2713	-0.8228	-2.381	-0.8907
482	1	0.6875	0.1747	-0.3748	-0.07656	-0.3906	-0.2721	-0.05	0.13
483	1	-0.03844	-0.01125	-0.5207	-0.5225	-0.1666	-0.828	0.04406	0.1041
484	1	0.1475	1.335	-0.1648	-1.237	-0.2106	-0.2221	-0.92	0.37
485	1	0.3275	0.5547	-1.115	-0.9366	0.2594	-0.5521	-0.04	0.04
486	1	0.1055	-0.6073	-0.3368	-0.2986	0.1773	-0.4141	-0.332	-0.03203
487	1	-0.3366	-1.479	-0.7489	-1.651	-0.2048	-0.9162	-0.2441	0.1359
488	1	-0.08375	-0.2266	-0.4861	-0.2878	-0.4419	-0.4534	-0.6613	0.3287
489	1	0.03328	-0.1295	-0.839	-1.061	-0.3948	-0.6663	-0.6842	0.5958
490	1	-0.3325	-0.09531	-0.2348	0.3934	-0.06062	-0.1221	-0.09	0.11
491	1	0.1014	0.1886	-0.0008984	0.2973	0.1933	0.7218	1.214	0.1839
492	1	-0.1319	0.2753	-0.3042	-0.1659	8.25E-09	0.1185	0.9506	0.1306
493	1	0.2064	0.6736	-0.2559	-0.1676	-0.4217	-0.4632	0.1389	0.02895
494	1	-0.8653	-1.718	0.03238	0.000625	0.3266	-0.2049	-0.06281	0.8772
495	1	-0.6974	-0.3802	0.3703	0.1086	-0.4155	-0.957	1.185	-0.3149
496	1	0.1653	0.8825	0.223		-0.3828	-0.6843		-0.3322
497	1	0.3575	0.8647	-0.004805	-0.2866	-0.3406	-0.6121		-0.13
498	1	-0.1239	-0.3067	-0.9162	0.002031	0.338	-0.07352	0.2586	-0.6614
499	1	0.2175	-0.04531	-0.1248	-0.5166	0.1794	-0.02211	-2.11	0.61
500	1	-0.2062	-0.4891	-0.8786	-1.12	-1.054	-0.3059	-1.444	-0.07375
501	1	1.101	1.448	-1.122	-0.4634	-0.7475	-0.739	0.4031	1.233
502	1	-0.0125	-0.5853	0.3752	0.1034	-0.3006	-0.1521	-0.73	-0.27
503	1	-0.2475	0.5697	0.2902	0.3484	-0.3556	0.7729		0.055
504	1	0.0523	-0.8705	-6.69E-12	0.7982	-0.2258	0.5427	-0.2552	0.6548

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Table 1

	GWEIGHT	NORWAY 100-BE	NORWAY 100-AF	NORWAY 10-AF	NORWAY 10-BE	NORWAY 102-BE	NORWAY 102-AF	NORWAY 7-AF	NORWAY 17-BE
		ARRY19X	ARRY18X	ARRY21X	ARRY20X	ARRY23X	ARRY22X	ARRY24X	ARRY25X
		1	1	1	1	1	1	1	1
505	1	0.7575	0.9247	-0.0648	-0.05656	0.1094		0.2	-0.22
506	1	-0.1075	0.2397	0.0802	0.4484	-0.2956	-0.8071		-0.615
507	1	-0.3814	0.2558	0.2563	0.5245	-0.9595	-0.681		0.09109
508	1	-0.5225	-0.1153	1.255	0.003437		0.2879		-0.94
509	1	-0.2025	-0.6553	0.1352	0.2934	-0.7106	-0.2221	-2.65E-09	-0.11
510	1	-0.5025	-0.3253	1.165	0.3934	-1.411	0.2479		
511	1	-0.1725	0.8447	0.4852	0.6334	0.3494	-0.3621		-0.5
512	1	0.6225	-0.2603	-0.1998	-0.5316	0.8344	-0.01711	-0.255	0.295
513	1	0.5458	0.04297	-0.2065	-0.3383	0.6877	0.03617	-0.2017	0.1283
514	1	-0.2375	0.2997	-0.3498	0.9784	-0.6456	-0.5271	-0.015	-0.675
515	1	0.4631	-0.1397	-0.01918	-0.4809	-0.265	-0.3465	-0.2344	0.8556
516	1	-0.3947	0.0725	0.533	0.1413	0.7472	-0.4343	-2.232	-0.3322
517	1	0.5648	0.272	0.9825	0.1008	-0.5633	-0.07477	0.2473	0.08734
518	1	1.273	0.7403	0.3808	-0.9109	-0.925	-0.6065		1.216
519	1	0.7647	-0.008125	0.8524	0.000625	0.8066	1.335	0.007187	1.357
520	1	0.3075	1.525	0.8352	0.05344	0.09937	0.3279	0.31	1.02
521	1	0.01203	-0.8408	-0.9003	0.168	0.1539	0.7524	-0.6555	0.1645
522	1	0.1305	0.3677	0.03816	-0.1236	-0.9477		-0.807	-0.007031
523	1	-0.2314	-0.1242	1.826	-0.1554	1.851	0.959	-0.3789	2.051
524	1	-1.087	-0.9903	1.68	-0.3616	0.4544	0.6329	0.605	0.005
525	1	-0.1725	-0.3553	1.175	-0.3766	0.1394	0.5079	1.77	0.55
526	1	0.2331	-1.05	0.2708	-0.6809	0.085	0.5935	-0.03437	0.1056
527	1	0.4339	0.2311	-0.0484	-1.4	0.2658	-0.005703		0.8764
528	1	-0.3962	0.2909	0.04145	-0.9503	-0.3644	-0.06586		0.6662
529	1	1.728	2.475	0.2652	0.04344	-0.4606	-0.3121	-1.16	0.25
530	1	2.404	3.051	0.2818	-0.67	-0.1041	-0.5055		1.087
531	1	1.925	1.952	1.513	0.5513	0.05719	0.2857		-0.002188
532	1	0.5975	1.105	0.2052	-0.4066	-0.3906	-0.1221	0.25	0.13
533	1	-0.8366	-0.4095	0.1811	0.0193	-1.505	-0.6362	1.956	1.416
534	1	-0.5914	-0.8642	-0.9537	-0.5455	-0.8795	1.349	1.321	0.6011
535	1	0.001563	0.7087	0.009258	0.3975	-0.7666	-0.448		1.404
536	1	1.93	1.477	0.0476	-1.294	-0.5682	-1.28	1.172	0.9424
537	1	0.6306	0.7578	-0.9117	0.1966	-0.7675	-1.099	1.013	1.703
538	1	0.1688	0.846	-0.6235	-0.5852	1.861	0.2992	1.331	2.681
539	1	0.01164	-1.391	0.7493	-0.7324	-1.146	-0.618		0.2841
540	1	-1.334	-0.547	2.333	1.542	-1.662	-1.824	1.048	-1.272

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
541	1	-0.1925	-0.1353	0.0652	1.023	-0.8006		-0.09	1.47
542	1	-0.1331	-0.5759	-0.09543	0.4428	-0.4512	-0.7127	0.4694	0.6694
543	1	-0.3725	0.5747	-0.1348		-0.6606	-0.1921	0.84	0.93
544	1	-0.3653	-0.5781	-1.088	0.000625	-0.3334	0.5851	2.417	0.7772
545	1	-0.4825	-1.875	-1.795	-0.7066	-0.5706	0.1779	2.21	0.38
546	1	0.4975	0.6247	-0.3548	1.933	0.6394	-0.01211	2.54	0.9
547	1	-0.3953	-2.068	0.8224	0.3606	-0.6134	-0.3949	1.247	0.1872
548	1	0.2977	0.3649	0.07541	0.7137	0.2596	1.188	1.01	-0.6298
549	1	0.4153	1.582	0.803	2.001	0.2372	0.3557	0.4778	0.4278
550	1	0.3575	-0.3453	0.6952	0.9634	2.669	2.288	1.68	-0.8
551	1	-0.0975	-0.5603	0.3802	0.008438	1.174	1.993		0.425
552	1	0.06469	-0.6481	0.7224	0.000625	0.9566	0.4551		0.6672
553	1	2.118	2.165	0.3252	-0.1066	-0.7821	-0.7821		-0.43
554	1	1.689	2.056	-0.3337	0.8545	1.96	0.309	0.04109	-0.1289
555	1	0.7175	1.465	0.7752	1.343	0.7594	1.348		0.99
556	1	1.403	2.03	0.6202	1.028	0.5144	0.4529	-0.055	0.995
557	1	1.493	2.85	0.5802	0.6584	0.9844	0.7029	-1.195	0.155
558	1	0.4275	0.8747	-0.5248	0.4934		-0.7421	1.09	-1.04
559	1	-0.3504	-0.03316	0.4873	0.5356	-0.07848	0.1	0.6021	-0.4879
560	1	0.7581	-0.4447	0.7558	0.4941	-0.48	0.4185		0.7506
561	1	-0.7325	0.2647	0.6752	0.3334	-0.7106	-0.2721		-0.42
562	1	-0.3025	-1.435	0.8852		-0.8606			
563	1	-0.2722	0.455	1.136	0.02375	-0.4903	-0.2218		-0.07969
564	1	-1.48	-1.443	0.8575	0.6257	-0.3884	-0.2098	-1.418	-0.4177
565	1	-0.2631	0.2541	1.185	0.7628	-0.1713	-0.1427		0.05937
566	1	-1.271	-0.8242	0.5263		-0.4495	-0.591		
567	1	-1.094	0.8934	0.3639	0.1122	-1.222	-0.6234		-0.2513
568	1	-0.3153	-0.9181		0.000625	-0.1134	-0.6849	0.2372	0.4272
569	1	-0.3009	-0.2638	1.007	-0.195	-0.7991	-0.7405		0.7216
570	1	-0.6294	0.7278	0.5583	0.7566	0.0425	-1.459	0.4531	0.2831
571	1	-0.1622	0.585	0.7355	-0.1563	0.1097	0.8182	0.4903	-0.04969
572	1	-0.4864	0.2908	0.6913	0.1195	-0.7445	0.04398		-0.2439
573	1	0.0309	1.398	0.7686	0.03684	-0.3572	0.4013		-0.3866
574	1	-0.2046	1.023	1.603	0.5414	-0.5427	-0.05418		-1.032
575	1	-0.6662		1.311	-0.5603		0.04414		-0.4838
576	1	-0.4517		-0.02404	0.4842	-1.07	1.109	-0.5592	-0.09924

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
577	1	-0.3025	0.5347		0.4534	-0.2106	0.02789	0.04	-0.3
578	1	-0.5555					-0.2852		-0.493
579	1	-0.9464			1.89	-1.645	1.094		
580	1	-0.8325	0.2747	0.5652	0.1634	-0.6706	0.1179	-0.29	-0.92
581	1	-0.5253	-0.2681	0.2324	0.000625	-0.01344	-0.2549	-1.043	0.1272
582	1	-0.1169	-0.9297	0.6308	0.2791	-0.025	0.4435		0.09562
583	1	0.6475	0.7847	-0.8148	0.3434	-1.261	-0.08211	-2.09	1.19
584	1	-0.4825	0.4547	0.5352	0.4234	0.7794	-0.04211	-1.1	1.58
585	1	-0.6919	-0.8947	0.8058	0.1741	0.03	-0.3315	0.4306	-0.5894
586	1	-0.7294	-0.9122	0.3783	-0.2334		0.161	-0.6669	0.08312
587	1	0.0775	0.3347	0.2752	-0.3966	-0.3706	0.3179		0.5
588	1	-0.7644	-0.6372	0.1733	-1.418	-0.0025	-0.114	-0.2019	-0.3919
589	1	0.1807	0.07793	0.8184	-0.09332	-0.6074	-0.6889	-1.047	-0.3168
590	1	3.393	1.34	0.6208	-0.3709	-0.235	-0.6265		2.406
591	1	1.023	-0.02953	1.021		0.3152	-0.1063		0.7458
592	1	3.033	2.66			1.024			-0.1249
593	1	2.302	2.739	-8.44E-12	1.108	-2.716	-0.0773	-4.405	2.175
594	1	-0.002266	0.7549	-0.2246	-0.3163	-0.5404	0.02813	4.01	0.1702
595	1	-0.6631	-0.8459	0.8146	0.7528	-0.1613	-0.5427	2.639	1.419
596	1	-0.8312	0.5659		1.275	0.000625	1.509		0.1212
597	1	-0.2425	0.1847	0.6752	0.9434	-0.8306	0.1979	-0.01	0.06
598	1	0.4425	-0.1503	-0.2398	-0.2716	-0.1656	0.4829	0.735	-0.045
599	1	-0.6225	-0.9053	0.5352	0.6234	0.2694	2.068	0.89	1.12
600	1	-0.2525	-0.6953	-0.5748	0.3734	-0.6406	0.9179	-0.29	0.09
601	1	0.3498	-0.453	-0.3525	-0.5043	0.3416	0.1002	0.2723	0.3823
602	1	-0.03695		-0.3193	-1.181	-0.3351	0.6334	0.9655	
603	1	1.453	-0.5603	0.7302	-0.4916	-0.3456	0.7229		0.735
604	1	0.0975	-0.8453	0.3752	0.2034	0.5594	1.148	0.22	0.67
605	1	0.5775	-2.505	-1.795	-1.137	-0.2306	-0.05211	3.44	-1.29
606	1	0.4133	-2.389	-0.879	-1.971	0.5652	0.1637	5.276	-1.174
607	1	0.705			-0.3891	0.6469	0.3354	1.738	-1.072
608	1	0.8542	-0.8686	-1.498	-1.8	0.4461	0.3246	1.497	-1.553
609	1	0.452	-1.661	-2.19	-1.262	0.6539		2.575	-2.585
610	1	1.633	-1.5	-2.469	-2.431	0.675		2.536	-1.974
611	1	1.276	-2.027	-2.296	-2.638	0.5981	-0.2234	2.469	-1.871
612	1	-0.426	-0.8188	-1.078	-1.27	0.1559		0.09648	-1.414

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
	1	1	1	1	1	1	1	1	1
613	1	-0.8753	0.7419	-1.158	-1.309	-0.2634		0.2672	-2.233
614	1	-0.5896	1.178	-0.5019	-0.9537	-0.1477	-0.9092	0.3429	-1.117
615	1	0.6686	-0.7042	-0.8137	-0.9855	0.4905		0.4211	-0.1689
616	1	-0.07215	0.03504	-1.764	-1.106	0.2497	-0.6818	1.77	-2.45
617	1	0.03688	0.03406	-1.595	-1.117	0.2887	-1.113	1.919	-2.341
618	1	0.3975	0.05469	-0.9848	-1.047	-0.3706	0.3979	1.94	-1.72
619	1	0.1775	-0.3353	-0.9248	-0.1966	-0.1906	-0.08211	0.12	0.32
620	1	0.4488	0.4559	-0.4736	-0.5053	0.000625	0.9091	-0.1088	1.341
621	1	-0.1475	-0.0003125	1.08	-0.1716	-0.05562	0.1529	1.245	-0.085
622	1	-0.1666	0.3705	1.011	-0.1407	-0.7948	-0.2762		0.9059
623	1	2.21	1.887	0.4574	0.1756	0.7816	1.66	-0.07781	0.3522
624	1	0.2363	-0.7866	1.344	0.5522	-0.5819	0.1866	-0.6913	0.5187
625	1	0.3333	-0.01949	0.871	0.6393	-0.2648	0.2337		0.9658
626	1	0.4625	-1.2	-0.0198	-0.8716	-0.8156	0.3129		-0.135
627	1	-0.5625	-0.9053	-0.6348	0.3734	0.6894	1.378	0.76	-0.28
628	1	1.038	-0.01531	-0.1048	-1.217	-0.07062	0.01789	-0.04	0.56
629	1	0.645	0.04219	-0.2673		0.2169	0.9254	-0.4425	-0.0725
630	1	0.03984	-0.263	0.8575	2.086	-0.3083	0.06023	-0.09766	-0.5977
631	1	-0.2994	1.028	0.5083	-0.4434	0.0225	0.381	0.2931	-0.1469
632	1	-0.8162	-0.5291	0.7414	0.2397	-0.2944	0.5941		-0.5038
633	1	0.3376	-1.465	1.065	-0.03648	-1.571	1.888	0.5301	
634	1	-0.2125	-0.2453	0.8652	0.2634	-1.051	1.488		-0.29
635	1	-0.005117	0.2121	1.123	1.461	-1.173	-0.2447		-0.1126
636	1	-0.4814	0.08578	0.8163	1.545	-0.1495	1.169		-0.9289
637	1	-0.0525	-0.4553		0.3834	0.05938	0.3579	0.73	0.31
638	1	-0.2697	-0.5825	0.508	-0.2738	-0.4878	0.0007031		-0.3872
639	1	-0.8462	-0.1891	1.251	1.95	0.005625	2.114		-0.1638
640	1	-0.1994	-1.262	0.7583	-1.303	-0.1175	0.08102	0.7831	-0.3169
641	1	-0.3332	-0.446	0.7145	1.543	-0.9813	0.9772	2.009	-0.3607
642	1	-0.1825	0.3147	1.835	1.543	-0.5306	0.8179		0.55
643	1	0.1463	-0.3866	0.3539	-0.4178	-0.2219	0.05664		-0.09125
644	1	0.5369	-2.536	0.1146	0.002813	0.2688	0.9573	1.999	0.5194
645	1	0.3061	-0.4067	0.5138	0.312	0.798	0.6565	1.139	0.8886
646	1	-0.00375	0.1434	-0.01605	-0.1378	-0.02187	0.1066	0.05875	-0.01125
647	1	-0.8273	-0.6702	-0.7896	1.129	-1.475	-0.917	-1.845	0.05516
648	1	0.1575	-0.9853	0.1552	1.703	-0.7306	-0.7721		0.11

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
649	1	-0.1525	-0.7853	-0.1848	0.08344	0.4294	0.6379	0.8	-0.09
650	1	-0.5964	-1.309	0.9013		0.5755	0.464	1.086	0.3961
651	1	-0.48	-0.02281		-0.6141	-0.9681	-0.6596	-0.4175	-0.8275
652	1	-1.107	-0.8696	-0.07904		-1.935	-1.496	-1.254	-1.554
653	1	-0.6536		1.754		0.08828	0.4368	0.8289	0.04891
654	1	0.2972	0.7444	1.405	0.5631	-0.4909	-0.1024	-0.04031	0.1597
655	1	-0.3825	-0.8553	-0.1148	-0.2466	0.2194	-0.02211	-0.23	-0.38
656	1	-0.7094	-0.8922	0.7183	0.4266	-0.1675	0.401		-0.7069
657	1	0.0625		0.0102	0.7984	0.5344	-0.5571	-0.055	-0.675
658	1	0.03875		1.176	0.6747	0.4406	-0.2809		0.2912
659	1	0.3411	-0.001719	-0.2312	-0.05297	-0.127	-0.3085	0.07359	0.3036
660	1	0	-0.6428	0.6477	0.1659	-0.7481		-1.978	0.5425
661	1	0.7109	-0.9219	1.539	-0.2131	-0.3772	-0.04867		1.153
662	1	-0.01625	-0.1291	-0.3086	-0.2703	0.4456	-0.2859	-0.6438	0.01625
663	1	-0.5278	-0.04063	0.06988	1.478	-1.436			1.155
664	1	-0.165	-1.348	0.2927	0.3509	-1.053	0.1054		1.328
665	1	-0.4095	-1.072	-0.1218	1.126	0.05242	-0.4191	0.213	-0.177
666	1	-0.5125	0.1947		1.293	-0.08063	0.09789		0.27
667	1	-0.4325	-0.3053	1.255	1.603	-0.5206	-0.2021		
668	1	-0.385	0.5122	0.8827	0.8009	0.05688	0.5454	-1.142	-0.1525
669	1	-0.4696	-1.022	-0.01186	0.9664	-0.1677	-0.2292	0.2629	0.02295
670	1	0.4475	-1.385	-0.0348	1.253	-0.4406	-0.9121	0.21	0.33
671	1	-0.678	-0.0007812	-0.3303	1.658	-0.5661	-0.7176		
672	1	-0.1202	-0.823	1.617	2.136	-0.7684	-0.3698	-1.058	-0.05773
673	1	-0.6714	-0.2142	0.1363	0.4245	-0.6695	-0.351		0.03109
674	1	-0.2925	-0.08531	0.6952	1.843	-0.1006	-0.4821		-0.42
675	1	-0.7447	-1.908	-0.04699	-0.6087	-0.2628	-0.6743		
676	1	-0.6125	-0.8853	0.0852	-0.2566	-0.1306	0.08789	0.57	-0.17
677	1	-0.5487	-1.072	0.1289	0.2672	-0.006875	0.2116	0.04375	0.09375
678	1	-0.8725	-0.7253	0.2352	-0.8066	-0.000625	0.2679	-0.34	0.55
679	1	-0.0225	0.5047	0.3652	0.6134	-0.8406	-0.7321	0.84	0.84
680	1	-0.0275	1.18	0.5602	0.6184	-0.1656	-0.3171		0.225
681	1	0.5053	-1.328			-0.8228	-0.6243	0.09781	
682	1	-0.6764	0.4908	-0.9987	-0.8105	-0.9045	-0.286	-1.644	-0.6539
683	1	-0.8902	0.347	-0.1625	-0.2943	-0.1584	0.06016	0.2323	-0.4577
684	1	-0.3125	0.7747	1.325	0.7534	-0.5906	-0.5021	0.09	0.58

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Table 1

	GWEIGHT	NORWAY 100-BE	NORWAY 100-AF	NORWAY 10-AF	NORWAY 10-BE	NORWAY 102-BE	NORWAY 102-AF	NORWAY 7-AF	NORWAY 17-BE
		ARRY19X	ARRY18X	ARRY21X	ARRY20X	ARRY23X	ARRY22X	ARRY24X	ARRY25X
		1	1	1	1	1	1	1	1
685	1	0.03625	0.5234	-0.4461	1.212	-0.07188	0.1566	0.3187	-0.2313
686	1	-0.2837	0.7334	0.06395	0.3922	0.1581		0.5887	-1.371
687	1	-0.4425	0.5647	-0.4448	0.8134	-0.04062	0.3479	0.04	-1.01
688	1	-0.6825	-1.335	0.0952	0.04344	-0.6506	-0.5021	-0.71	-0.05
689	1	-0.6553	1.012	-0.2476	-0.8594	-0.3034	-0.1649	0.2772	-0.4728
690	1	-0.1066	1.611	0.4711	0.6493	-0.3548	-0.3262	-0.6941	0.3259
691	1	-0.4437	-0.5866	0.4939	0.2522	0.1281	0.1466		-0.2313
692	1	-0.8522	0.585	0.3055	-0.4763	-0.7803	-0.7418	-0.4297	-0.6397
693	1	-0.4502		1.537	-0.1443	-0.6184	-0.1798	-0.5577	-0.6177
694	1	0.9334	0.3906		-0.3606	-0.05469	-0.3162		-0.6241
695	1	0.3238	0.02094	-0.6686	-0.09031	-0.09438		-0.05375	-0.7838
696	1	-0.3437	-0.1666	0.9139	-0.2478	-0.4419	-0.7134	-0.7513	0.2987
697	1	1.05	0.6269	0.5474	0.2956	-0.7284	-0.3399	-0.4078	0.1022
698	1	0.4905	-0.2923	0.3282	-1.074	0.8524	0.4809	-0.677	-0.217
699	1	0.1775	1.045	-1.105	-0.5766	-0.06063	-0.7321	0.78	-1.16
700	1	0.08406	0.2012	0.5918	0.22	0.2059	-0.03555	0.3366	-0.4234
701	1	0.7911	0.8983	-0.4412	-0.703	0.913	0.4615	-0.3664	0.1136
702	1	3.049	0.1758	-0.01371	-1.655	-1.36	-1.051	0.01109	-2.099
703	1	2.939	-0.01406	0.8864	-2.605	-1.349	-0.4409	0.4713	-0.8087
704	1	-0.3475	-1.1	1.19	0.2184	-0.6856	-0.2671	0.515	0.455
705	1	0.1736	-1.129	1.071			-0.396	-0.5739	2.216
706	1	-0.3822	0.205		0.9637	0.02965	0.1982	-0.1197	0.2503
707	1	-0.8402		0.09746	0.0357	-0.3084	-0.3298	-0.6877	0.3523
708	1	0.3325	1.04	1.05	1.078	0.7044	1.843	1.615	0.295
709	1	-0.5866	0.08062	0.7611	-0.06062	0.2853	1.164	0.1559	0.1059
710	1	-0.4847	-0.1675	0.683	0.2912	0.2772	-0.0843		0.7278
711	1	-0.6968	0.1104	1.151	0.3591	0.2251	-0.006406	-0.6843	0.5857
712	1	-0.4063	0.1309	1.281	-0.05039	0.005547	-0.5059		0.5262
713	1	-0.287	1.23	0.2607	0.359	0.2349	0.1234	0.2755	-0.6445
714	1	-0.2244	0.5328	0.5433	0.5116	0.6375	0.586	0.1081	-0.4419
715	1	-0.3725	1.185		0.3234	-0.3506	0.2079		-1.38
716	1	-0.1254	0.5218	0.5023	0.05059	0.2765	0.455	-1.453	-0.1329
717	1	-1.359	-0.9816	0.1989	-0.002813	-0.8669	-0.9384	-1.366	-0.3663
718	1	-0.6337	-0.5966	-0.1561	0.9922	-1.222	-0.1934		0.5987
719	1	0.2425	0.6997	0.3302	0.3884	0.004375	0.1529	0.685	0.235
720	1	-0.4425	-0.3653	-0.2948	0.03344	-0.5506	-0.8221	1.29	-0.16

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
721	1	-0.6875	0.1897	0.2202	-0.3416	-0.6856	-0.8771	-0.385	-0.715
722	1	-0.3728	-0.04563	-0.3351	0.02313	0.2691	0.3576	0.3097	-0.1303
723	1	-0.2125	-0.2153	-0.2748	0.7134	-0.6806	-0.1821		0.78
724	1	-0.9331		0.3646	0.04281	-0.5112	0.03727		0.4394
725	1	-0.3925	0.9847	0.6252	0.4634	-0.3006	0.5879		
726	1	-0.1498	0.1473	-0.2821	0.2761	-0.128	-0.1295	0.1127	0.1727
727	1	-0.575	0.1922	0.2527	-0.1991	0.1169	0.02539	-0.6025	-0.1025
728	1	-0.5268	0.3504	0.9309	0.9891	-1.435	-0.2164		
729	1	-1.23	0.4675	0.178		-0.3678		-0.3872	-0.3972
730	1	-1.458	-0.7409	-1.16	-1.562	0.4237	-0.04773	-1.626	0.39
731	1	-0.3025	0.1147	0.0852	-0.4766	0.2294	-0.5121	0.42	0.2341
732	1	-0.2084	-0.5212	-0.1907	0.2976	-0.03648		-1.676	-0.06
733	1	-0.1825	0.1447	0.9352	-1.047	-0.06063	-0.3921		-0.7073
734	1	-0.5798		0.3979	-0.3439	-0.968	-1.069	-3.147	-0.08492
735	1	-0.1074	0.2598	-0.09973	0.1885	-0.3155	0.183	0.5351	0.7197
736	1	0.1872	-1.696		0.6831	0.04906	0.7676	1.54	-0.5109
737	1	0.8366	0.7138	0.1343	0.7226	-0.5915	-0.253	-0.3409	-0.03
738	1	0.5375	0.6147	0.6252	-0.1766	0.3594	-0.09211	-0.9	0.9056
739	1	-0.06687	0.09031	0.01082	-0.5309	-0.175	-0.4065	-0.6444	0.4556
740	1	0.2831	-0.1997	-0.5092		0.885	1.104	0.4056	-0.03188
741	1	0.1056	-0.2072	0.2033	0.06156	0.0475	-0.08398	-0.8319	0.01
742	1	0.0575	0.6147	0.3752	-0.07656	-0.3306	-0.8721	0.23	0.45
743	1	0.1375	-0.1953	-0.1948	-0.3166	0.009375	-0.4221	1.4	-0.3175
744	1	-0.04	-0.1828	0.1877	0.4859	1.362	1.51	0.0225	0.1563
745	1	0.6338	-0.3191	-0.1486	0.01969	0.1656	-0.4559	-0.6337	0.1158
746	1	-0.3967	0.08051	-0.529	-0.1393	0.2752	0.2037	1.406	-1.392
747	1	-0.455	0.02219	-0.2573	0.5909	-1.193	-0.7646		
748	1	-0.8314	-1.204	-0.4937	0.05453	-1.21	-1.151	1.061	0.6711
749	1	-0.7361	-1.239	-0.4584	-1.19	-0.2342	0.0243	0.5464	-1.354
750	1	-0.4751	-0.8579	0.0126	-0.5892	-0.01322	0.5753	0.6874	-1.063
751	1	0.2687	-1.794	-0.9236	-0.9654	0.3305	0.1291	0.3612	0.2912
752	1	0.055	0.5022	0.1927	-0.1591	0.1869	0.2354	0.0575	-0.1425
753	1	0.3654	0.6925	1.183	1.921	0.5572	0.4857	0.6579	-0.07215
754	1	0.1742	0.6714	-0.1681	-0.6298	0.2161	0.1946	0.006719	-0.7433
755	1	-0.1358	0.3314	-0.08809	0.4302	1.016	0.1746	0.05672	-0.5933
756	1	-0.1375	-0.0003125	-0.5598	0.1784	0.1744	-0.08711	0.115	0.255

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
	1	1	1	1	1	1	1	1	1
757	1	-0.009609	0.5576	-0.6319	-0.6037	-0.2977		-0.3471	-0.1771
758	1	0.6231	-0.7197	-0.5092	-0.3909	-0.035	0.2935	0.3256	0.1656
759	1	1.038	-1.045	-0.9948	2.103	-0.6606	-0.9721	-1.37	3.67
760	1		-0.537	0.03348	1.252	0.2377		1.118	0.02828
761	1	-0.305	-0.2678	0.8327	-0.7791	-0.7931	0.08539	-0.0225	-0.3625
762	1	-0.4025	0.2147	-0.1648	-0.5566	-1.171	-0.7221	0.02	0.02
763	1	-0.5562	-0.6591	-0.2186	0.3097	-0.4744	0.7641	1.206	-0.9437
764	1	0.4455	-0.2173	-0.03684	0.1214	-0.4227	-0.1741	0.268	-0.692
765	1	-0.1958	0.03141	-0.2181	0.3002	-0.4539	-0.4654	-0.1033	-0.2833
766	1	-0.3653	-0.1481	0.6224	-0.7394	0.1166	-0.5749	-1.343	0.2672
767	1	0.3475	-0.06531	2.265	1.053	0.1694	0.7379		1.29
768	1	0.3472	0.4744	2.465	1.993	0.2691	0.4876		1.56
769	1	-0.3925	-0.2753	-0.5748		1.019	-1.122		-0.16
770	1	-0.1181	-0.5909	1.02	-0.08219	0.2638	0.4123	0.1544	0.004375
771	1	2.373	1.12	-0.06918	-0.06094	-1.375	-0.6165	0.02563	-0.3044
772	1	2.493	2.79	0.4008	0.01906	0.005	-0.3465	0.5256	1.696
773	1	-0.3375	1.1	0.2502	1.248	-1.026	-0.09711		
774	1	-0.025	0.5222	0.3927	1.081	-0.09312	0.5254		0.2375
775	1	-0.405	-0.4178	-0.1273	-0.3991	-0.02312	-1.285	-0.8325	0.4275
776	1	1.035	0.9527	0.2832	0.02141	1.167	0.4659	0.298	
777	1	0.6775	1.725	0.0952	-0.04656	0.7194	0.8179	0.2	-0.55
778	1	-0.2475	-0.9903	-0.8098	0.2684	-0.1856	-0.1971	-0.035	0.225
779	1	-0.005234	1.032	0.3625	0.4707	0.5266	1.265	-0.5527	-0.5527
780	1	-0.00375	-0.3466	-0.6261	-0.8578	0.1181	-0.5334		-0.3213
781	1	0.06336	1.001	0.05105	1.329	0.2752	0.5238	1.266	-0.2341
782	1	-0.3188	0.1284	0.5889	0.5371	0.473	0.6216		-0.1263
783	1	-0.3809	0.3763	0.2068	-0.03492	0.381	0.02953	0.6216	-0.1384
784	1	-0.4757	-0.5885	-0.01803	0.9202	0.2462	-0.3053	1.047	0.4368
785	1	-0.5125	0.7847	-0.004805	0.3434	-0.7106	1.228		0.81
786	1	-0.0175	-0.1603	-0.2698	-0.2116	-1.346	-0.9271	0.225	-0.375
787	1	-0.1467	-0.3695	-0.239	-0.07078	-0.004844	-0.09633	-0.2142	-0.3442
788	1	-1.105	-0.1175	-0.05699	0.8912	-0.5328	-0.1543		0.04781
789	1	0.0975	0.7447		0.2634	0.5594	0.7679	0.1	-0.28
790	1	-0.5425	0.1047	0.3652	-0.03656	-0.6106	0.06789	-0.55	-0.08
791	1	-0.3202	-0.533	-0.4025	0.2957	-0.2284	-0.2998	-0.8177	0.2823
792	1	-0.3652	-0.488	-1.007	-0.2592	-0.6633	-0.4848	-0.2227	-0.4127

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
793	1	-1.556	-1.719	-1.739	-0.5505	0.9355		2.786	-0.2139
794	1	-0.8175	-0.2503	-1.39	-0.8816	0.2344	-0.3271	0.315	-0.125
795	1	-0.3825	-0.9953	-0.2348	0.2634	-0.3306	-0.2021	0.1	-0.15
796	1	0.2938	0.4709	0.2714		-0.01438	-0.3159	0.1362	0.4962
797	1	-0.1925	-0.1253	0.1152	-0.1466	0.2794	0.07789	-1.07	0.03
798	1	-0.6997	-1.403	-0.832	-0.6738	-0.2278	0.0007031	-0.3772	-0.4972
799	1	-0.7614	-1.164	-0.3137	0.5445	0.1605		-0.008906	0.02109
800	1	-0.3461	0.3811	0.0816	0.2198	-0.7442	-0.005703	-0.1536	0.1264
801	1	-0.2512	-1.274	-0.07355	-0.3953	0.000625	-0.1009	0.1212	-0.07875
802	1	0	-0.4328	-0.8323	-0.3141	-0.1281	-0.4396	1.242	-0.0675
803	1	-0.7825	-1.645	-0.1148	-0.05656	0.2894	-0.2421	-0.2	-0.72
804	1	-0.8955	-0.7584	0.4521	-0.009609	-0.02367	-0.7252	-1.313	-0.243
805	1	-0.01695	-0.2498	-0.9293	-0.281	0.3249	-0.06656	0.4255	-0.1745
806	1	-0.0625	0.03469	-1.045		0.1194	-0.2521	-2.65E-09	-0.11
807	1	-0.2247	0.1425	-0.357	0.4212	0.1572	-0.004297	-1.032	-0.1122
808	1	-0.1069	0.3903	-0.2292	0.2791	-0.115	-0.04648	-0.3344	-0.2944
809	1	0.2675	0.7147	-0.8048	0.1534	-0.2906	-0.1721	-0.2	-0.2
810	1	-0.1597	-0.0825	-0.03199	-1.324	0.8022	0.0007031	-0.6972	-0.3172
811	1	-0.2014	0.2058	0.006289	0.5445	-0.5395	-1.191	-0.9689	-0.1389
812	1	-0.2237	0.2834	-0.05605	-0.7078	0.04816	-0.6634	1.449	0.1287
813	1	-0.6075	-0.1303	0.1802	0.9984	-0.4256	-1.027		
814	1	-0.3664	-0.1692	-0.06871	0.2795	0.1855	0.364	1.676	0.5261
815	1	-0.0075	0.2597		0.8384	0.2644	0.4729		0.705
816	1	-0.3819	-0.03469	-0.05418	-0.2759	0.22	-0.5015		-0.7094
817	1	0.1125	0.4397	-0.0198	-0.6516	-0.4656	-0.7171		-0.195
818	1	-0.5694	-0.5322	-0.4517	-0.1334	0.1925	-0.409		-0.6169
819	1	0.1363	-0.1466	0.03395	0.8122	1.218	0.3466	-0.3113	-0.3113
820	1	-0.4451	-0.02791	0.0226	-1.069	0.3268	-0.1747	0.7574	-0.3326
821	1	-0.8314	-2.114	-0.7037	-0.7855	-0.3395	-0.961		-1.409
822	1	-0.2225	-0.2753	-0.2448	0.03344	0.1194	0.08789	-0.53	-0.05
823	1	0.02242	0.3196	0.04012	-0.01164	0.0843	-0.4772	0.08492	-0.1351
824	1	-0.05687	0.8303	0.4208	-0.4209	0.035	0.3135	-0.3144	-0.6744
825	1	0.1739	0.5411		-0.3401	-0.5042	0.1643	0.1364	-0.2436
826	1	-0.4195	0.1777	-0.4018	-0.8935	0.2624	-0.4091	0.743	0.02305
827	1	0.1469	0.5241	-0.2454	-0.9572	0.1987	-0.8927	-0.2506	-0.6106
828	1	-0.2563	0.4508	0.001348	0.02959	0.01553	0.07404	1.646	-0.1338

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Table 1

	GWEIGHT	NORWAY 100-BE	NORWAY 100-AF	NORWAY 10-AF	NORWAY 10-BE	NORWAY 102-BE	NORWAY 102-AF	NORWAY 7-AF	NORWAY 17-BE
		ARRY19X	ARRY18X	ARRY21X	ARRY20X	ARRY23X	ARRY22X	ARRY24X	ARRY25X
		1	1	1	1	1	1	1	1
829	1	-0.1142	-0.587	-0.04652	-0.2683	0.07766	0.4262	-0.05172	-0.1017
830	1	-0.6895	0.8877	0.7582	-0.04359	-0.2977	1.231		-0.327
831	1	-0.4041	-0.07695	0.9436	-1.078	-0.1823	-0.4437		-0.01164
832	1	-0.04805	0.9491	0.4396	0.05789	0.5138		-0.3555	0.4245
833	1	-0.47	0.8372	-0.7323	0.5059	-0.2181	0.04039	0.4625	-0.0275
834	1	-0.6009	-0.4637	-0.09316	-0.4949	0.231	-1.23	-0.9784	-0.9784
835	1	-0.4656	0.4516	0.3621	-0.03969	0.1263	1.775	-0.08312	-0.6631
836	1	-0.1286	0.1986	-0.2509	0.1573	0.08328	0.001797	-0.006094	-0.5261
837	1	-0.0168	0.2704	0.1109	-0.1709	0.2151	-0.2064	-1.084	0.3257
838	1	-0.6725	-1.145	-0.4048	-0.7966	-0.05062	-0.3521	-0.61	-0.36
839	1	-0.4725	-0.2053	-0.3048	0.2734	-0.02063	-0.7321	0.02	0.06
840	1	-0.8974	-1.04	-0.2397	0.3485	-0.3155	-0.627		-0.05492
841	1	-0.6675	-0.1003	-0.3898	0.2884	-0.1756	-0.4571	0.585	-0.295
842	1	-0.6025	-0.5653	-0.3348	-1.087	-0.4406	-0.9221	0.79	0.02
843	1	-0.5482	-0.571	-0.4105	-0.5023	-0.4563	0.002187	-0.005703	-0.6857
844	1	-0.5222	-1.145	-0.3645	0.1437	-0.3803	-0.5118	-0.1497	-0.3197
845	1	-0.3252	-0.598	-0.2575	0.3208	-0.4333	-0.3648	-0.08266	0.1073
846	1	-0.6447	-0.0475	-0.06699	0.5013	-0.2128	-0.2943	-0.1822	0.6978
847	1	-0.05125	0.4859	-0.4036	0.4047	0.000625	0.2591	-0.3088	0.5112
848	1	-0.3842	-0.497	-0.04652	-0.8883	-0.7123	-0.7938	-1.242	-0.1517
849	1	0.2375	0.3847	0.2952	-0.07656	0.3294	-0.8621		0.17
850	1	-0.2725	-0.2353	0.1652	-0.2766	0.1494	-0.4321	0.46	0.17
851	1	-0.525	-0.8078	-0.4073	-0.3191	-0.6331	-0.4546	0.3375	0.0275
852	1	-0.5425	-0.5053	0.0952	0.003438	-0.2106	-0.7321	-0.48	0.14
853	1	-0.1137	0.3734	-0.1261	-0.9678	0.4281	-0.9534	-1.231	-0.3613
854	1	-0.1259	-0.00875	-0.1982	-0.42	0.2259	-0.7955	-1.703	-0.1534
855	1	-0.1037	0.06344	0.1639	-1.388	0.3481	-0.6434	-0.5312	-0.7312
856	1	0.09375	0.4909	0.1114	0.1997	0.1556	-0.08586	-0.1238	-0.01375
857	1	-0.3025	0.8047	0.1752	-0.1966	-0.2106	0.4279		-0.63
858	1	-0.7525	-0.3953	-0.2748	0.1534	-0.7606	-0.5821	0.66	-0.79
859	1	-0.4244	-0.1872	-0.6467	0.06156	-0.1925	-0.01398	1.658	-0.9819
860	1	-0.2775	-0.5903	-0.1998	-0.1716	0.3344	-0.7271	-0.495	-0.415
861	1	-0.3575	-0.0003125	-0.0198	-0.1716	0.1244	-0.08711	0.285	0.025
862	1	-0.1269	0.4403	0.1008	-0.2009	-0.035	0.02352	0.8456	-0.5344
863	1	-0.2253	-0.7081	-0.02762	0.000625	0.5866	-0.7749	0.7372	-0.2928
864	1	-0.3175	-0.3403	-0.2998	-0.1516	-0.2856	-0.8271	-0.195	-0.515

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
865	1	-0.1814	-0.07422	0.05629	-0.005469	-0.2595	-0.621	-0.3889	-0.03109
866	1	-0.2347	0.0825	-0.167	0.1012	0.08719	-1.014	-0.1222	-0.7822
867	1	-0.1416	0.5656	0.2661	0.2544	0.3403	1.419	0.2109	-0.2191
868	1	-0.03937	0.5578	0.1583	-0.3734	0.3925	0.331	-0.2969	-0.2969
869	1	-0.4497	0.3875		0.2162	0.1322	0.0007031	0.03281	-0.1172
870	1	-0.4297	0.5075	-0.232	-0.05375	-0.2378	0.4607		-0.6872
871	1	-0.2809	0.2263	0.6168	-0.5549	0.231	-0.01047	-0.06836	-0.06836
872	1	-0.2162	-0.4891	-0.5886	-0.3303	-0.1944	-0.7559	-0.08375	-0.3037
873	1	-0.7525	-0.7953	-0.4148	-0.2666	-0.08062	0.4379	0.92	-0.31
874	1	-0.523	0.2241	-0.5754	0.6929	-0.3512	-0.03266	0.7595	-0.1805
875	1	-0.545	0.03219	0.1827	-0.4391	-0.3331	-0.2746	1.608	-0.9425
876	1	-0.4225	-0.2753	-0.2248	0.2534	0.7994	-0.01211	-0.36	-0.57
877	1	-0.1142	-0.127	-0.2465	-0.7783	1.338		0.3783	-0.3217
878	1	0.0075	-0.5153	-0.1548	-1.387	1.119	0.2779	0.23	0.03
879	1	-0.4587	-0.02156	0.2689	-0.4128	0.5431	-0.5084	0.04375	-0.5762
880	1	-0.1977	0.2895	-1.02E-11	-0.9418	0.8242	-0.4973	-0.8852	-0.1652
881	1	0	0.2972	-0.1723	-0.4141	0.7419	-0.2996	-0.1275	-0.5575
882	1	-0.2564	-0.1192	-0.09871	0.2695	0.4855	0.504	-0.1439	-0.5139
883	1	-0.5352	0.222	0.1025	0.8108	0.2767	-0.1048		-0.3427
884	1	0.04563	0.1828	-0.1567	0.3016	0.6175	-0.244	-0.1719	0.008125
885	1	-0.2302	-0.413	0.1575		0.1916	-0.3698	2.152	
886	1	-0.3814	-0.5442	0.06629	0.2845	0.2505	-0.241	-0.1989	0.3111
887	1	-0.61	0.04719	0.0877	0.4259	-0.4681	0.7304	-0.6475	-0.6975
888	1	-0.7737	-1.277	0.5239	0.1822	0.3981	0.01664	-0.3213	-0.2513
889	1	-0.4389	-0.3017	1.019	0.187	0.493	0.1115	-0.3764	-0.1764
890	1	-0.4684	0.3388	-0.07066	0.1676	0.1535	0.05203	-0.07586	-0.1159
891	1	-0.1442	-0.497	-0.1265	0.2117	-0.05234	-0.2638	0.5283	-0.01172
892	1	-0.1236	0.3436	0.0341	0.6323	0.03828	0.0368	-0.3311	0.2289
893	1	0.009844	-0.373	0.4075	-0.5942	-0.02828	-0.3098	-0.6377	0.2223
894	1	-0.38	-0.3428		-0.5441	0.3919	-0.5796	1.813	-0.2475
895	1	-0.4612	-0.2541	0.5264	-0.4153	-1.369	-0.07086	-1.179	-0.3387
896	1	-0.01727	0.4699	0.4504	-1.131	0.3146	-0.8969	0.01523	0.04523
897	1	-0.4336	-1.116	0.5241		0.03828	0.1668	0.1489	-0.1911
898	1	0.1286	-0.9142	1.196	-0.8455	0.6605	-0.221	-1.089	-0.5689
899	1	-0.3625	-1.035	-0.3448	0.3534	0.6894	0.2279	-0.39	-0.26
900	1	-1.302	-0.08531	-0.2348	-0.1466	-0.1106	0.2779	1.01	-1.24

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
901	1	-0.6839	0.5333	-0.04621	-0.338	-0.302	-0.07352		-0.8414
902	1	-0.05141	-0.2342	-0.3437	-0.4455	0.5205	0.259	-0.8789	-0.1689
903	1	-0.4837	-0.3866	-1.046	0.1722	0.02812	0.05664	-0.3013	-0.9213
904	1	-0.4031	-0.2659	-0.6954	0.5828	-0.1113		0.4494	-0.6506
905	1	-0.5525	-0.5153	0.7552	0.7834	-0.6106	-0.8021	0.8	-0.73
906	1	-0.3169	0.3003	0.1308	-0.6709	-0.225	-1.286	0.2156	-0.8744
907	1	-0.7306		-0.3929	-0.5447	-0.4687	-1.46	-0.2081	-1.208
908	1	-0.1742	-0.407	-0.006523	-0.1083	0.4177	-0.07383	-0.3317	-0.3317
909	1	-0.3244	0.2928	-0.2267	1.022	-0.1025	0.266		-0.1819
910	1	0.2738	0.9509	-0.2786	-0.3803	1.876	0.7041	-2.884	-0.1238
911	1	-0.1666	0.5905	-0.2689		-0.6548	0.1038		-0.07414
912	1	-0.385	-0.2678		-1.089	-0.9631	0.3354	-0.2425	0.2475
913	1	0.425	0.9622	0.4927	0.2009	-0.5331	-0.4546	-0.1225	-0.3625
914	1	-0.2125	-0.3653	-0.4548	-0.1666	-0.000625	0.1179	-0.09	-0.56
915	1	-0.1053	-0.1081	-0.7376	0.000625	-0.05344	-0.1749		0.1572
916	1	-0.1742	-1.337	-0.3965	-0.8883	0.3077	0.05617	-0.4917	-0.6417
917	1	0.1475	0.1147	0.5752	-0.5866	0.3994	-0.2021	-2.36E-08	0.03
918	1	-0.6147	-0.1475	-1.217	-0.9287	0.3672		-0.9722	-0.3522
919	1	-0.3942	-0.677	-0.6365	-0.1883	0.1877	0.1462	0.7383	-0.4317
920	1	-0.08008	0.1871	-0.4324	-0.4441	0.3618	-0.5497		0.1824
921	1	-0.1125	0.3647	0.6552	-0.4166	0.02938	-1.322	0.79	-0.15
922	1	0.1433	-0.02953			-0.4548	-1.796	1.386	-0.6842
923	1	0.2747	0.001875	-1.018	-0.2694	-0.1034	-0.4249	-0.7528	0.4572
924	1	0.2434	-0.5194	-0.5389	0.1994	-0.4647	-0.09617		-0.1341
925	1	0.2797	-0.5031	-0.2926	0.2756	0.3716	0.3301	-0.3678	0.2122
926	1	-0.2003	-0.8331	-0.1226	-0.06437	-0.8784	0.01008	-0.3078	0.1222
927	1	0.1123	0.6595	-4.95E-12	-0.6018	-0.9258	-0.2473	-1.235	0.0948
928	1	0.2475	0.7347	-0.5848	0.7334	0.1794	1.138	-2.65E-09	0.15
929	1	0.6375	0.9647	-0.1848	0.2134	0.1694	0.05789	-0.23	-0.08
930	1	-0.2725	-0.7553	-0.8748	-0.09656	-0.1506	-0.08211	-0.49	-0.07
931	1	0	0.5172	-0.7523	-0.2041	-0.3481		-1.138	-0.1375
932	1	-0.6931	-0.8359	-0.6054	-1.127	0.1587	-0.2027	0.8194	-0.6306
933	1	-0.3751	0.7921	0.002598	0.5008	0.5968	0.3853	-0.1126	-0.0326
934	1	-0.3425	0.5947	0.005195	0.1634	-0.3706	-0.04211	0.08	-0.71
935	1	0.3901	0.1973	-0.2322	1.036	-0.01805	-0.1095	0.1926	-0.04742
936	1	0.1363	-0.3366	-0.7861	-0.2278	0.1981	0.2866	-0.5913	0.1087

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Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
		1	1	1	1	1	1	1	1
937	1	0.2289	-0.1339	-0.3334	0.4648	0.3208	-0.0107	-0.8786	0.06141
938	1	0.6091	0.3862	-1.443	0.465	0.08094	-0.2605	-0.7284	0.2216
939	1	0.3725	-0.7203	0.0502	0.1484	0.2144		-0.355	0.375
940	1	0.9375	0.1747	-0.7248	0.2734	0.06938	-0.3621	-0.04	-0.19
941	1	1.158	-1.755	-0.2848	0.4934	-0.05062		0.54	0.72
942	1	0.7755	0.1827	0.003164	-0.2286	-0.2927	-0.8241		0.278
943	1	0.3936	-0.2292	-0.3287	0.5296	0.4455	0.444	-0.4539	-0.3839
944	1	0.8586	-0.3342	0.1063	0.06453	0.4205	-0.371	-0.7589	0.02109
945	1	1.21	-1.153	-0.2425	-0.1843	0.3216	0.2402	0.03227	-0.6577
946	1	1.568	-0.1653	0.3552	0.2134	0.4794	0.5279	0.42	-0.47
947	1	0.3075	-1.625	-0.6648	-0.7666	0.5494	-1.142		-0.46
948	1	-0.1475	-0.0003125	-0.3498	0.1084	0.2744	-0.2771	1.115	-0.895
949	1	0.6475	-0.2653	-0.4148		0.8394		-0.15	-0.52
950	1	0.5186	-0.6942	-0.7137	0.1045	0.7405	0.06898	-0.1589	-0.2489
951	1	0.9236	-0.1492	-0.7687	0.04953	-0.2345	-0.106	0.9261	0.5761
952	1	0.7775	0.06469	-0.4548	0.1634	0.8794	0.8079	1.43	0.15
953	1	0.8319	0.06906	-0.7004	0.2578	0.3237	0.6923	0.3244	-0.07563
954	1	1.173	1.21	-0.5298	0.1184	0.09438	-0.8671	0.485	0.095
955	1	1.253	-0.6803	-0.1998	-0.5816	1.124	-1.427		0.765
956	1	0.3975	0.07469	-0.3748	0.5134	0.5194	0.1679	-0.09	-0.31
957	1	0.3947	-0.2881	-1.208	0.000625	0.6266	0.4451	0.1372	-0.6828
958	1	0.8636	0.1808	-0.7787	-0.6605	0.03547	0.354	0.7761	0.006094
959	1	0.8538	0.4509	-0.4186	-0.02031	0.1456	0.8141	0.6462	-0.2538
960	1	0.5034	-0.4194		-0.000625	0.5553	0.8538	1.016	0.09594
961	1	0.5375	-0.3853	-1.185	-0.4366	0.8894	0.7979		0.29
962	1	0.6528	-0.6		-0.1912	0.7547	0.5432	0.4253	-0.3047
963	1	1.024	-0.9286	-0.3481	-0.4898	0.9961	0.6246	1.327	-0.3333
964	1	0.7005	0.2777	-0.6918	0.1864	1.162	0.4409		0.133
965	1	0.5788		-1.094	-1.025	0.000625	-0.06086		-1.109
966	1	0.8269	-0.3859	-0.7254	-0.3572	0.2587	0.3873	0.009375	-0.1406
967	1	1.118	0.1347		0.1634	0.2294	0.6379	0.43	-3.85E-09
968	1	1.111	0.348	-0.3114	0.5568	0.4227	0.7913	0.7734	-0.006641
969	1	1.103	-1.08	-0.9892	0.4791	-0.125	0.5435	0.6956	-0.08438
970	1	0.7634	0.1105	-0.3189	0.0993	-0.2448	0.4838	0.8959	-0.05414
971	1	0.4214	-1.321	-0.9409	-0.4727	-0.5367	-1.018	0.1839	-0.3461
972	1	0.2724	-0.3204	-1.02	-1.282	-0.6357	0.1128	0.9949	0.06488

Table 1

	GWEIGHT	NORWAY 100-BE ARRY19X	NORWAY 100-AF ARRY18X	NORWAY 10-AF ARRY21X	NORWAY 10-BE ARRY20X	NORWAY 102-BE ARRY23X	NORWAY 102-AF ARRY22X	NORWAY 7-AF ARRY24X	NORWAY 17-BE ARRY25X
	1	1	1	1	1	1	1	1	1
973	1	0.3665	-0.6463	-1.026	-1.048	-0.7216	-0.1631	1.239	0.09902
974	1	0.002656	-2.29	-0.7496	-0.3614	0.3845	-0.107	0.5652	1.505
975	1	1.618	-1.355	-0.2148	0.01344	0.3494	0.8279	0.74	1.59
976	1	0.5025	-0.6003	-1.1	-0.7016	0.5544	-0.2171	2.285	-0.235
977	1	0.4763	-1.237	-0.7461	-0.5378	0.9681	-0.02336	0.6987	-0.07125
978	1	0.2102	-2.023	-0.3321	-1.084	0.252	0.5105		0.9827
979	1	0.0625	-0.9203	-0.8298	-0.3116	0.5044	-0.6571	0.465	-0.515
980	1	1.384		-0.4279	-0.4097	0.1963	0.5648		
981	1	-0.6925	0.4947	-0.6748	0.2434	-0.5306	0.4079	-1.22	-3.85E-09
982	1	-0.6132	-0.2561		1.173	0.05863	0.1371		
983	1	-0.1525	-0.3053	-0.5548	-0.7266	-0.06062	0.1179	-0.28	-0.02
984	1	-0.4466	-0.07937	0.04113	0.2594	-0.9847	-0.5462	-0.01406	0.1259
985	1	-0.3809			-0.495	-1.509	-0.1805		-0.1884
986	1	0.4234	0.1505	-0.6089	-0.1907	-0.6448	-0.3262		0.04586
987	1	0.93	1.347			-0.6881	-0.1096		0.1225
988	1	-0.0375	0.6097	0.1302	0.7984	-0.3556	0.09289	-0.465	-0.115
989	1	-0.0225	0.4747	-0.3648	0.2634	0.1794	-0.6821	0.08	1.46
990	1	0.39	0.1972	0.3277	0.2059	-1.058	-0.5396	-0.7475	0.1625
991	1	0.07881	0.426	0.006504		-1.009	0.3492	-1.109	0.3813
992	1	-0.2778	-1.241	0.1499	-0.6119	-0.3659	0.2126	-0.02531	0.1747
993	1	-0.4412	-0.3541	1.716	0.1247	0.000625	0.2691		0.1812
994	1	-0.1225	0.07469	-0.5048	-0.4166	-0.5906	1.458		-3.85E-09
995	1	-0.1375	-0.0003125	-0.2498	-1.182	-0.3656	-0.3871	-0.745	-1.115
996	1	0	0.3972	0.5977	-1.554	-0.7981	-0.2696	-0.1775	1.042
997	1	-0.08453	0.1827		0.4314	-0.2427	0.3359	0.288	-0.122
998	1	-0.2025	-0.1753	-0.9148	-0.3166	-0.4506	-0.4821	-0.49	-0.51
999	1	-0.1669	-1.78	-0.1292	-0.2109	-0.315	-0.4165	-1.474	-0.3144
1000	1	-0.3025	-1.265	-1.445	-0.3966	-0.3706	-0.5721	0.22	-0.73
1001	1	0.2223	0.4395	-9.61E-12	0.1282	-0.9258	-0.1073	-0.3752	0.9748
1002	1	-0.2523	-0.3452	-1.445	-1.256	-1.15	-0.452		0.7502
1003	1	-0.008359	-0.2212	-1.021	-1.552	-1.026	-0.208	0.05414	0.7841
1004	1	-0.2475	-0.08031	-0.9198	-0.6316	-0.5056		-1.155	0.965
1005	1	-0.6928	-0.4956	-0.4051	-0.2669	-0.9609	-0.2124		
1006	1	-0.2625	-0.8953	-0.3948	-1.277	-1.061	0.06789	0.92	0.48
1007	1	0.1675	-0.7553	-0.3948	-0.8566	-0.3006	-0.05211	0.1	0.21
1008	1	0.81	0.1872	-0.6323	-1.044	0.3719	-0.4496	0.6225	-1.188

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